

OM protein - protein search, using sw model  
Run on: August 3, 2006, 09:12:58 ; Search time 84 Seconds  
(without alignments)  
647.723 Million cell updates/sec

Title: US-10-015-967-2  
Perfect score: 644  
Sequence: 1 MKVLISLLLLPLMLMSV.....SRACQFLKQCQLRSPALPL 119  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2589679 seqs, 457216429 residues  
Total number of hits satisfying chosen parameters: 2589679  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database :  
A\_Geneseq\_8:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003ae:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

No. Score Match Length DB ID Description  
SUMMARIES

RESULT 1  
ID AAY66668 standard; protein; 119 AA.  
DE Membrane-bound protein PRO842.  
PN WQ963088-A2.  
PD 09-DEC-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 3; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 2  
ID RAY82453 standard; protein; 119 AA.  
DE Human TGC-440 secretory protein SEQ ID NO:1.  
PN WQ200014226-A1.  
PD 16-MAR-2000.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match 100.0%; Score 644; DB 3; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 3  
ID AAY87317 standard; protein; 119 AA.  
DE Human signal peptide containing protein HSPP-94 SEQ ID NO:94.  
PN WQ200000610-A2.  
PD 06-JAN-2000.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 100.0%; Score 644; DB 3; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 4  
ID AAB34728 standard; protein; 119 AA.  
DE Human secreted protein encoded by DNA clone vq8 1.  
PN WQ200053375-A1.  
PD 21-SEP-2000.  
PA (ALPH-) ALPHAGEN INC.  
Query Match 100.0%; Score 644; DB 3; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 5  
ID AAU29093 standard; protein; 119 AA.  
DE Human PRO polypeptide sequence #70.  
PN WQ200168848-A2.  
PD 20-SEP-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 6  
ID AAG63977 standard; protein; 119 AA.  
DE Amino acid sequence of a human Lng104 polypeptide.

PN WQ200161055-A2.  
PD 23-AUG-2001.  
PA (DIAD-) DIADEXUS INC.  
Query Match 100.0%; Score 644; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 7  
ID AAB87538 standard; protein; 119 AA.  
DE Human PRO842.  
PN WQ200116318-A2.  
PD 08-MAR-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 8  
ID AAB65191 standard; protein; 119 AA.  
DE Human PRO842 (UNQ473) protein sequence SEQ ID NO:165.  
PN WQ200073454-A1.  
PD 07-DEC-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 9  
ID ABG95863 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein PRO842.  
PN US2002119130-A1.  
PD 29-AUG-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 5; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 10  
ID ABP54931 standard; protein; 119 AA.  
DE Human cytokine PRO842 (CK27).  
PN WQ200270706-A2.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 5; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 11  
ID ABUS8469 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 12  
ID ABUS8017 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 13  
ID ABUS4332 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 14  
ID ABR66206 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003027278-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 15  
ID ABR65596 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 16

ID ABU99536 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 17  
ID ABU9806 standard; protein; 119 AA.  
DE Human PRO polypeptide #38.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 18  
ID ABU59084 standard; protein; 119 AA.  
DE Novel human secreted or transmembrane protein PRO842.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 19  
ID ABU82596 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein PRO842.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 20  
ID ABU82775 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 21  
ID ABU9896 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003036147-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 22  
ID ABR68145 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 23  
ID ABU60515 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein, #61.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 24  
ID ABU96198 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 25  
ID ABU92629 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 26  
ID ABO08706 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 27  
ID ABO02758 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 28  
ID ABR74912 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 29  
ID ABR94674 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 30  
ID ABU13897 standard; protein; 119 AA.  
DE Human PRO842 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 31  
ID ABU85647 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 32  
ID ABU9807 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 33  
ID ABU98022 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 34  
ID ABU91728 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 35  
ID ABU89421 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 36  
ID ABU86262 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.

PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 37  
ID ABR67475 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 38  
ID ABR0503 standard; protein; 119 AA.  
DE Human PRO protein #70.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 39  
ID ABR72482 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US200303531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 40  
ID ABR09888 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 41  
ID ABR33947 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein PRO842.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 42  
ID ABR99421 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 43  
ID ABR98811 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 44  
ID ABR016334 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 45  
ID ABR2234 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;

RESULT 46  
ID ABR018875 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 47  
ID ABR78296 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 48  
ID ABR71964 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 49  
ID ABR05032 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 50  
ID ABR00171 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 51  
ID ABR011503 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 52  
ID ABR02148 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 53  
ID ABR8722 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 54  
ID ABR83417 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 55  
ID ABR06218 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 56

ID ABR59254 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 57  
ID ABO09316 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 58  
ID ABO19180 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 59  
ID ABO11198 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 60  
ID ABR66816 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 61  
ID ABO16029 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 62  
ID ABO13735 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 63  
ID ABU71518 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 64  
ID ABU65638 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein, SEQ ID 140.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 65  
ID ABO07486 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 66  
ID ABO03673 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 67  
ID ABR67121 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 68  
ID ABO15724 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 69  
ID ABU56005 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein, PRO842.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 70  
ID ABU72299 standard; protein; 119 AA.  
DE Human PRO polypeptide #13.  
PN US2002182838-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 71  
ID ABU65333 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 72  
ID ABU95278 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 73  
ID ABU71181 standard; protein; 119 AA.  
DE Human PRO842 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 74  
ID ABO07791 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 75  
ID ABR70032 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 76  
ID ABR69365 standard; protein; 119 AA.



DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 77  
ID ABO01506 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 78  
ID ABU81308 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 79  
ID ABR60105 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 80  
ID ABU90972 standard; protein; 119 AA.  
DE Human PRO polypeptide #13.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 81  
ID ABR67840 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 82  
ID ABR65228 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 83  
ID ABR68450 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 84  
ID ABR71862 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 85  
ID ABUS9231 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein, #61.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 86  
ID ABUS5342 standard; protein; 119 AA.

DE Human PRO polypeptide #70.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 87  
ID ABUS9032 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 88  
ID ABUS3112 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 89  
ID ABUS9468 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 90  
ID ABUS0516 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 91  
ID ABUS4027 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 92  
ID ABUS3678 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 93  
ID ABO25928 standard; protein; 119 AA.  
DE Human PRO842 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 94  
ID ABR64923 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 95  
ID ABO27293 standard; protein; 119 AA.  
DE Human secreted/transmembrane polypeptide PRO842.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 96  
ID ABR68755 standard; protein; 119 AA.

DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 97  
ID ABO06571 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 98  
ID ABR99116 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 99  
ID ABU57000 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 100  
ID ABU5952 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 101  
ID ABU82239 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 102  
ID ABU87250 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 103  
ID ABU83722 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 104  
ID ABO08096 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 105  
ID ABU92488 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein PRO842.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 106  
ID ABU81807 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003032104-A1.

PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 107  
ID ABU65971 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 108  
ID ABU81158 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 109  
ID ABR59800 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 110  
ID ABU93988 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 111  
ID ABU99841 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 112  
ID ABR66511 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 113  
ID ABR90929 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 114  
ID AB053273 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 115  
ID ABU58937 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein, #61.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 116  
ID ABU94356 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.

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PN US2003017540-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 117
ID ABU79238 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 118
ID ABU86567 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 119
ID ABU86872 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 120
ID ABU94661 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 121
ID ABO4588 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 122
ID ABR70337 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 123
ID ABU92315 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 124
ID ABU98502 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 125
ID ABR65901 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 126
ID ABR64618 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 127
ID ABU59380 standard; protein; 119 AA.
DE Novel human secreted or transmembrane protein PRO839.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 128
ID ABU79543 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 129
ID ABU92934 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 130
ID ABU95893 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 131
ID ABU91113 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 132
ID ABU90206 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 133
ID ABO9621 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 134
ID ABO10893 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 135
ID ABR70947 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
RESULT 136
ID ABU98275 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
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RESULT 137  
ID ABU87555 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein #70.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 138  
ID ABU91423 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 139  
ID ABU89280 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 140  
ID ABU94637 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 141  
ID ABR69727 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 142  
ID ABU80104 standard; protein; 119 AA.  
DE Human PRO protein #70.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 143  
ID ABU82487 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 144  
ID ABU92146 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 145  
ID ABU93373 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 146  
ID ABO09926 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 147  
ID ABO09011 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 148  
ID ABU96451 standard; protein; 119 AA.  
DE Human PRO polypeptide #13.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 149  
ID ABU10852 standard; protein; 119 AA.  
DE Human PRO polypeptide #38.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 150  
ID ABU10579 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein #70.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 151  
ID ABU81604 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 152  
ID ABU72121 standard; protein; 119 AA.  
DE Human PRO polypeptide #13.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 153  
ID ABU95588 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 154  
ID ABU96797 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 155  
ID ABR70642 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 156  
ID ABO04993 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003008352-A1.  
PD 09-JAN-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 157  
ID ABO08401 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 158  
ID ABO08543 standard; protein; 119 AA.  
DE Human secreted and transmembrane polypeptide PRO842.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 159  
ID ABO34057 standard; protein; 119 AA.  
DE Human PRO842 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 160  
ID ABO05608 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 161  
ID ABR71997 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 162  
ID ABR9589 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 163  
ID ABR80886 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 164  
ID ABR81191 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 165  
ID ABO0887 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 166  
ID ABR88489 standard; protein; 119 AA.

DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 167  
ID ABO77310 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 168  
ID ABO28794 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 169  
ID ABO31539 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 170  
ID ABO07956 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 171  
ID ABO40436 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 172  
ID ABO35861 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 173  
ID ABO44000 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 174  
ID ADA77892 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 175  
ID ABO24795 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.

PN US2003104539-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 176  
ID ABO03063 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 177  
ID ABR90319 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 178  
ID ABR90319 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 179  
ID ABR94979 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 180  
ID ABR95284 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 181  
ID ADB17083 standard; protein; 119 AA.  
DE Human transmembrane PRO polypeptide (SeqID 26).  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 182  
ID ABO21522 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 183  
ID ABR97786 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 184  
ID ABR87574 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 185  
ID ABW77615 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 186  
ID ABM27845 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003064440-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 187  
ID ABM06126 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 188  
ID ABM03632 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 189  
ID ABM35083 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 190  
ID ABM26320 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 191  
ID ABO48102 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 192  
ID ABR92844 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 193  
ID ABO24605 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 194  
ID ADA37676 standard; protein; 119 AA.

DE Human secreted/transmembrane protein PRO842.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 195  
ID ABM11616 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 196  
ID ABM02717 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 197  
ID ABM16013 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 198  
ID ABO27574 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 199  
ID ABM29065 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 200  
ID ABM07041 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 201  
ID ABM21135 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 202  
ID ABM09481 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 203  
ID ABO41351 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 204  
ID ABO36166 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 205  
ID ABO43695 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 206  
ID ABM76395 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 207  
ID ABM76091 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 208  
ID ABM25710 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 209  
ID ABM26015 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 210  
ID ADA21362 standard; protein; 119 AA.  
DE Human secreted/transmembrane polypeptide PRO842.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 211  
ID ABO03368 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 212  
ID ABO02453 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 213  
ID ABO44251 standard; protein; 119 AA.

DE Human secreted/transmembrane polypeptide PRO 842.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 214  
ID ABR90624 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 215  
ID ABR73692 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 216  
ID ABO16944 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 217  
ID ABR94369 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 218  
ID ABR75876 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 219  
ID ABR71252 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 220  
ID ABR93149 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 221  
ID ABR93454 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 222  
ID ADA10149 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein, PRO842.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 223  
ID ABR87879 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 224  
ID ABO27879 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 225  
ID ABO30014 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 226  
ID ABO33223 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 227  
ID ABO4911 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 228  
ID ABO8871 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 229  
ID ABO36471 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 230  
ID ABO35556 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 231  
ID ABO39521 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;



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RESULT 232
ID ABO10396 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 233
ID ABO11921 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 234
ID ABO52067 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 235
ID ABO52372 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 236
ID ADA1988 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 237
ID ABO23690 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 238
ID ADB17271 standard; protein; 119 AA.
DE Human transmembrane PRO polypeptide (SeqID 26).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 239
ID ADA17693 standard; protein; 119 AA.
DE Human PRO842 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 240
ID ABR97176 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 241
ID ABR86964 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 242
ID ABO11006 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 243
ID ABO28150 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 244
ID ABO32149 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 245
ID ABO15276 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 246
ID ABO6431 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 247
ID ABO4242 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 248
ID ABO22355 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 249
ID ABO7651 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 250
ID ABO40741 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068684-A1.
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PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 251  
ID ABM35388 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 252  
ID ABM33151 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 253  
ID ABO52677 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 254  
ID ABO50237 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 255  
ID ABU99231 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 256  
ID ABO04283 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 257  
ID ABO05913 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 258  
ID ABM18453 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 259  
ID ADA27801 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein PRO842.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 260  
ID ABR97481 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003068773-A1.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 261  
ID ABR80581 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 262  
ID ABM01192 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 263  
ID ABR88794 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 264  
ID ABM13446 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 265  
ID ABM20830 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 266  
ID ABO41961 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 267  
ID ABO42571 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 268  
ID ABM10091 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 269  
ID ABO38606 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003068773-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 270  
ID ABM32846 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 271  
ID ABM22660 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 272  
ID ABM74871 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 273  
ID ADA79684 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003073173-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 274  
ID ABR96261 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 275  
ID ABM02412 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 276  
ID ABR86354 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 277  
ID ABR86659 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 278  
ID ABM16623 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 279  
ID ABM29675 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 280  
ID ABO29099 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003086693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 281  
ID ABM23980 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 282  
ID ABM23270 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 283  
ID ABM22050 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 284  
ID ABO37691 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 285  
ID ABM28455 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 286  
ID ABM28760 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 287  
ID ABM66404 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 288  
ID ABM75786 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003104547-A1.

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PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PD 13-MAR-2003.
RESULT 289
ID ABM34066 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PD 29-MAY-2003.
RESULT 290
ID ABM34371 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PD 29-MAY-2003.
RESULT 291
ID ABO20302 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PD 13-FEB-2003.
RESULT 292
ID ABO21217 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PD 20-MAR-2003.
RESULT 293
ID ABO22132 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PD 20-MAR-2003.
RESULT 294
ID ADA20060 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PD 27-MAR-2003.
RESULT 295
ID ABO34179 standard; protein; 119 AA.
DE Human secreted/transmembrane polypeptide PRO 842.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PD 27-MAR-2003.
RESULT 296
ID ABR96566 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PD 27-MAR-2003.
RESULT 297
ID ADA94381 standard; protein; 119 AA.
DE Human secreted/transmembrane protein PRO842.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PD 27-MAR-2003.
RESULT 298
ID ABR85744 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PD 13-MAR-2003.
RESULT 299
ID ABR99726 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PD 13-MAR-2003.
RESULT 300
ID ABM0277 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PD 17-APR-2003.
RESULT 301
ID ABM00582 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PD 17-APR-2003.
RESULT 302
ID ABO29709 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PD 10-APR-2003.
RESULT 303
ID ABM23575 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PD 10-APR-2003.
RESULT 304
ID ABM29370 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PD 10-APR-2003.
RESULT 305
ID ABO38301 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PD 10-APR-2003.
RESULT 306
ID ABO45601 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;
PD 17-APR-2003.
RESULT 307
ID ABM20525 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
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PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 308  
ID ADA81411 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 309  
ID ABO16639 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 310  
ID ABO18265 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 311  
ID ABO22692 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 312  
ID ABO22997 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 313  
ID ABR92539 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003084446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 314  
ID ABR81496 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 315  
ID ABR77920 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 316  
ID ABR89709 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003073171-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;

RESULT 317  
ID ABM26625 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 318  
ID ABM13751 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003084459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 319  
ID ABO28489 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 320  
ID ABO30319 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 321  
ID ABM07346 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003088702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 322  
ID ABM03937 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 323  
ID ABO37081 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 324  
ID ABO41656 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003088729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 325  
ID ABO35251 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 326  
ID ABM25100 standard; protein; 119 AA.

DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 336  
ID ABO20912 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 337  
ID ABR96871 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 338  
ID ADA38606 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein PRO842.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 339  
ID ABM12226 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 340  
ID ABU62090 standard; protein; 119 AA.  
DE Human PRO842 polypeptide.  
PN US2003065154-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 341  
ID ABM16318 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 342  
ID ABM24185 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 343  
ID ABM14666 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068596-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 344  
ID ABM04547 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 345  
ID ABM06736 standard; protein; 119 AA.

DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 327  
ID ABO47492 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 328  
ID ABO47797 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 329  
ID ABO48407 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 330  
ID ABO51457 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 331  
ID ABO51762 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 332  
ID ABO50542 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 333  
ID ABR79666 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 334  
ID ABM16928 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 6; Length 119;  
RESULT 335  
ID ABO17960 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003044918-A1.  
PD 06-MAR-2003.



Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 365  
ID ABO25655 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 366  
ID ABR94064 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 367  
ID ADA32727 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein PRO842.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 368  
ID ABR79971 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 369  
ID ABM11311 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 370  
ID ABO32918 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 371  
ID ABO30624 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 372  
ID ABO30929 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 373  
ID ABM27235 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 374  
ID ABM19610 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.

ID ABM29980 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 375  
ID ABM05516 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 376  
ID ABM15581 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 377  
ID ABM08566 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 378  
ID ABO42266 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 379  
ID ABO37996 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 380  
ID ABO45906 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 381  
ID ABM66709 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 382  
ID ADB20252 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 6; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 383  
ID ABM19610 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.



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PN US2003104552-A1.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 384
ID ABO49322 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 385
ID ABO49627 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 386
ID ABO49804 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 387
ID ABR88184 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 388
ID ADA00357 standard; protein; 119 AA.
DE Human secreted/transmembrane polypeptide PRO 842.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 389
ID ABM26930 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 390
ID ABM03327 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003058763-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 391
ID ABO39826 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 6; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 392
ID ABO49932 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003049776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 393
ID ABO50847 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 394
ID ABO05303 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 395
ID ABR74607 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 396
ID ABR77086 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 397
ID ABM17843 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 398
ID ABR95894 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 399
ID ABO21827 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 400
ID ABO19997 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 401
ID ABO24300 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 402
ID ABR86049 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
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PA  US2003049759-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 403
ID  ABM10701 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003064455-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 404
ID  ABM76700 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003054465-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 405
ID  ABR89404 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003073170-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 406
ID  ABM12531 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003073176-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 407
ID  ABM05821 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003068717-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 408
ID  ABO34946 standard; protein; 119 AA.
DE  Human PRO polypeptide #70.
PN  US2003068728-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 409
ID  ABM03022 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003068764-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 410
ID  ABM19000 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003104550-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 411
ID  ABM19305 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003104551-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 412
ID  ABO46516 standard; protein; 119 AA.
DE  Human PRO polypeptide #70.
PN  US2003049761-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 413
ID  ABO49017 standard; protein; 119 AA.
DE  Human secreted/transmembrane protein (PRO) #70.
PN  US2003049757-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 414
ID  ABR69060 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003027273-A1.
PD  06-FEB-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 415
ID  ABR89099 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003036119-A1.
PD  20-FEB-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 416
ID  ABR72472 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003036120-A1.
PD  20-FEB-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 417
ID  ABR74302 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003036161-A1.
PD  20-FEB-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 418
ID  ABO18570 standard; protein; 119 AA.
DE  Human secreted/transmembrane protein (PRO) #70.
PN  US2003044921-A1.
PD  06-MAR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 419
ID  ABR80276 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003049739-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 420
ID  ABM01497 standard; protein; 119 AA.
DE  Human secreted polypeptide PRO842, SEQ ID NO:140.
PN  US2003059882-A1.
PD  27-MAR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;
RESULT 421
ID  ABM02107 standard; protein; 119 AA.
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DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 422  
ID ABR87269 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 423  
ID ABR12836 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 424  
ID ABR30590 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 425  
ID ABR24490 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 426  
ID ABO29404 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 427  
ID ABO31234 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 428  
ID ABR14361 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 429  
ID ABR09786 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 430  
ID ABO38911 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.

PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 431  
ID ABR34676 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 432  
ID ABO51152 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 433  
ID ABO03978 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 434  
ID ABO10448 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 435  
ID ABO53143 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein PRO842.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 436  
ID ABR77691 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 437  
ID ABR78901 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 438  
ID ABO23995 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 439  
ID ABR93759 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 440  
ID ABR01802 standard; protein; 119 AA.

DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;  
RESULT 441  
ID ABM78225 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;  
RESULT 442  
ID ABR90014 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;  
RESULT 443  
ID ADA22288 standard; protein; 119 AA.  
DE Human secreted/transmembrane polypeptide PRO842.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;  
RESULT 444  
ID ABM7540 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;  
RESULT 445  
ID ABM13141 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;  
RESULT 446  
ID ABO31844 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;  
RESULT 447  
ID ABM14056 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068683-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;  
RESULT 448  
ID ABM08261 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;  
RESULT 449  
ID ABO40131 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003068681-A1.  
PD 10-APR-2003.

Query Match  
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;  
RESULT 450  
ID ABM74566 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;  
RESULT 451  
ID ABM33761 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;  
RESULT 452  
ID ABM20220 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;  
RESULT 453  
ID ABO48712 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;  
RESULT 454  
ID ABO22513 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein PRO842.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;  
RESULT 455  
ID ABR72777 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;  
RESULT 456  
ID ABO15419 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;  
RESULT 457  
ID ABR85134 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;  
RESULT 458  
ID ABO15114 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 644; DB 7; Length 119;  
RESULT 459  
ID ABO17249 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.

PN US2003040077-A1.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 460  
ID ABM17538 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 461  
ID ADA06454 standard; protein; 119 AA.  
DE Human secreted/transmembrane PRO polypeptide #38.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 462  
ID ADA39147 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein PRO842.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 463  
ID ABR85439 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 464  
ID ABM77005 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 465  
ID ABO28184 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 466  
ID ABM22965 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 467  
ID ABM30285 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 468  
ID ABM21745 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 469  
ID ABM21440 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 470  
ID ABM14971 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 471  
ID ABO41046 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 472  
ID ABO36776 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 473  
ID ABO37386 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 474  
ID ABM75176 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 475  
ID ABM33456 standard; protein; 119 AA.  
DE Human secreted polypeptide PRO842, SEQ ID NO:140.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 476  
ID ABO46211 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 477  
ID ADA82575 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 478  
ID ABO36776 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;

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ID ADB85599 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 479
ID ADB96173 standard; protein; 119 AA.
DE Human PRO polypeptide #38.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 480
ID ADBM31810 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 481
ID ADBM31200 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 482
ID ADB85893 standard; protein; 119 AA.
DE Human secreted/transmembrane protein (PRO) #70.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 483
ID ADBM32115 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 484
ID ADBM32420 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 485
ID ADB868278 standard; protein; 119 AA.
DE Human PRO842 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 486
ID ADB868085 standard; protein; 119 AA.
DE Human PRO842 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 487
ID ADBM31505 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 488
ID ADBM30895 standard; protein; 119 AA.
DE Human secreted polypeptide PRO842, SEQ ID NO:140.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 489
ID ADB90902 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 490
ID ADC57645 standard; protein; 119 AA.
DE Human PRO polypeptide #38.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 491
ID ADC55009 standard; protein; 119 AA.
DE Human PRO polypeptide #38.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 492
ID ADC11876 standard; protein; 119 AA.
DE Human secreted/transmembrane protein PRO842.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 493
ID ADC06982 standard; protein; 119 AA.
DE Human PRO842 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 494
ID ADC56298 standard; protein; 119 AA.
DE Human PRO polypeptide #38.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 495
ID ADC17161 standard; protein; 119 AA.
DE Mammalian PRO polypeptide (SeqID 26).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 496
ID ADC07353 standard; protein; 119 AA.
DE Human secreted/transmembrane protein PRO842.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 497
ID ADC11343 standard; protein; 119 AA.
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DE Human secreted/transmembrane protein PRO842.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 498  
ID ADC14859 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003073208-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 499  
ID ADC52354 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003138882-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 500  
ID ADC14465 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 501  
ID ADD07997 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003068623-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 502  
ID ADC81822 standard; protein; 119 AA.  
DE Human PRO polypeptide #38.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 503  
ID ADD07464 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 504  
ID ADC82355 standard; protein; 119 AA.  
DE Human PRO polypeptide #38.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 505  
ID ADD05613 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 506  
ID ADD08535 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003073090-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 507  
ID ADD06784 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 508  
ID ADC83031 standard; protein; 119 AA.  
DE Human PRO polypeptide #38.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 509  
ID ABR61571 standard; protein; 119 AA.  
DE Human VCC-1 polypeptide.  
PN WO2003087157-A2.  
PD 23-OCT-2003.  
PA (PHAA ) PHARMACIA CORP.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 510  
ID ADD55138 standard; protein; 119 AA.  
DE Human PRO polypeptide #38.  
PN US2003077593-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 511  
ID ADD36030 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 512  
ID ADD56096 standard; protein; 119 AA.  
DE Human PRO polypeptide #38.  
PN US2003077594-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 513  
ID ADD54534 standard; protein; 119 AA.  
DE Human PRO polypeptide #38.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 514  
ID ADE26688 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 515  
ID ADE26155 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 516  
ID ADF67092 standard; protein; 119 AA.  
DE Human PRO842 amino acid sequence SEQ ID NO:165.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;

Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 517  
ID ADG01031 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003078387-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 518  
ID ADG08584 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 519  
ID ADG02608 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 520  
ID ADG01315 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 521  
ID ADF95490 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 522  
ID ADF95205 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 523  
ID ADG12305 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003207392-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 524  
ID ADH24058 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 525  
ID ADH34084 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 526  
ID ADH24228 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 527  
ID ADH29917 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 528  
ID ADH23888 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 529  
ID ADH08965 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 530  
ID ADH24568 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 531  
ID ADH37424 standard; protein; 119 AA.  
DE Human secreted and transmembrane protein PRO842.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 532  
ID ADH02013 standard; protein; 119 AA.  
DE Human PRO polypeptide #13.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 533  
ID ADH37594 standard; protein; 119 AA.  
DE Human secreted and transmembrane protein PRO842.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 534  
ID ADG85632 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 535  
ID ADH24228 standard; protein; 119 AA.



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DE Novel human secreted and transmembrane protein PRO842.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 644; DB 7; Length 119;
  Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 536
ID ADH38522 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 644; DB 7; Length 119;
  Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 537
ID ADG83643 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 644; DB 7; Length 119;
  Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 538
ID ADH29451 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 644; DB 7; Length 119;
  Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 539
ID ADH27567 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 644; DB 7; Length 119;
  Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 540
ID ADH37764 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 644; DB 7; Length 119;
  Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 541
ID ADH37941 standard; protein; 119 AA.
DE Human secreted and transmembrane protein PRO842.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 644; DB 7; Length 119;
  Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 542
ID ADH57361 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 644; DB 7; Length 119;
  Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 543
ID ADH53503 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 644; DB 7; Length 119;
  Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 544
ID ADH53673 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 644; DB 7; Length 119;
  Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 545
ID ADH52009 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 644; DB 7; Length 119;
  Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 546
ID ADH49864 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 644; DB 7; Length 119;
  Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 547
ID ADI25374 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 644; DB 7; Length 119;
  Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 548
ID ADH90167 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 644; DB 7; Length 119;
  Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 549
ID ADI25544 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 644; DB 7; Length 119;
  Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 550
ID ADH97718 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 644; DB 7; Length 119;
  Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 551
ID ADI35346 standard; protein; 119 AA.
DE Human PRO polypeptide #38.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 644; DB 7; Length 119;
  Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 552
ID ADI03566 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 644; DB 7; Length 119;
  Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 553
ID ADI11923 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003181686-A1.
PD 25-SEP-2003.
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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 554
ID ADH98997 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 555
ID ADH98938 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 556
ID ADH98398 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 557
ID ADI11073 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 558
ID ADI11583 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 559
ID ADH98228 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 560
ID ADH98568 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 561
ID ADH98058 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 562
ID ADI05046 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 563
ID ADI03396 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 564
ID ADI04791 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 565
ID ADH78245 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 566
ID ADI19589 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 567
ID ADH90337 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 568
ID ADI03056 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 569
ID ADH77905 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 570
ID ADH97888 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 571
ID ADI01273 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
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DE Novel human secreted and transmembrane protein PRO842.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 591  
ID ADK65396 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 592  
ID ADH98738 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 593  
ID ADH79979 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 594  
ID ADH32746 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 595  
ID ADM30280 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 596  
ID ADL93710 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 597  
ID ADC52164 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003130483-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 7; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 598  
ID ADE74277 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 599  
ID ADE74899 standard; protein; 119 AA.  
DE Human secreted/transmembrane protein (PRO) #70.  
PN US2003211574-A1.

PD 13-NOV-2003.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 600  
ID ADF35291 standard; protein; 119 AA.  
DE Human PRO842 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 601  
ID ADG11541 standard; protein; 119 AA.  
DE Human PRO842 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 602  
ID ADF96102 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 603  
ID ADG04373 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 604  
ID ADG00533 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 605  
ID ADH06596 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 606  
ID ADH06426 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 607  
ID ADG68847 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 608  
ID ADH27737 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;



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DE Novel human secreted and transmembrane protein PRO842.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 628
ID ADH33540 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 629
ID ADH33880 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 630
ID ADH01090 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 631
ID ADG69697 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 632
ID ADH20904 standard; protein; 119 AA.
DE Human secreted/transmembrane protein PRO842.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 633
ID ADH02183 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 634
ID ADG69187 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 635
ID ADG85972 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 636
ID ADH24908 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 637
ID ADH39525 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 638
ID ADH19944 standard; protein; 119 AA.
DE Human secreted/transmembrane protein PRO842.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 639
ID ADH02523 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 640
ID ADG69017 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 641
ID ADH07620 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 642
ID ADG86142 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 643
ID ADH24738 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 644
ID ADH25786 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 644; DB 8; Length 119;
RESULT 645
ID ADH38352 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003180922-A1.
PD 25-SEP-2003.
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PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 646  
ID ADH57191 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003181642-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 647  
ID ADH52179 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 648  
ID ADH49545 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 649  
ID ADH90507 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 650  
ID ADI11243 standard; protein; 119 AA.  
DE Human PRO polypeptide #13.  
PN US2003181683-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 651  
ID ADH98908 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003190698-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 652  
ID ADI02138 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003190699-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 653  
ID ADH90677 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003181701-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 654  
ID ADK70554 standard; protein; 119 AA.  
DE Respiratory disease differentially expressed protein #120.  
PN WO2003101283-A2.  
PD 11-DEC-2003.  
PA (INCY-) INCYTE CORP.

Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 655  
ID ADJ54778 standard; protein; 119 AA.  
DE Human PRO polypeptide #70.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 656  
ID ADJ98552 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003187197-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 657  
ID ADJ98722 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 658  
ID ADH78881 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 659  
ID ADJ99115 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 660  
ID ADJ9285 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 661  
ID ADJ98903 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 662  
ID ADH79051 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 663  
ID ADK00911 standard; protein; 119 AA.  
DE Human PRO polypeptide #13.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 8; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;

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Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 664
ID ADK14432 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 665
ID ADL01573 standard; protein; 119 AA.
DE Human VEGF co-regulated chemokine-1 (VCC-1) polypeptide.
PN WO2004016224-A2.
PD 26-FEB-2004.
PA (PHAA ) PHARMACIA CORP.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 666
ID ADJ64549 standard; protein; 119 AA.
DE Human PRO polypeptide #70.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 667
ID ADM31445 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 668
ID ADM36492 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 669
ID ADM40297 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 670
ID ADM80881 standard; protein; 119 AA.
DE Human PRO polypeptide #13.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 671
ID ADN37905 standard; protein; 119 AA.
DE Novel human secreted and transmembrane protein PRO842.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 672
ID ADP07801 standard; protein; 119 AA.
DE Human secreted protein, seq id 284.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 673
ID ADF07856 standard; protein; 119 AA.
DE Human secreted protein, seq id 339.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 674
ID ADF07780 standard; protein; 119 AA.
DE Human secreted protein, seq id 263.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 675
ID ADP07879 standard; protein; 119 AA.
DE Human secreted protein, seq id 362.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 676
ID ADF07807 standard; protein; 119 AA.
DE Human secreted protein, seq id 290.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 677
ID ADF07852 standard; protein; 119 AA.
DE Human secreted protein, seq id 335.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 644; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 678
ID ADV77721 standard; protein; 119 AA.
DE Neoplastic disease detection protein PRO842.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 644; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 679
ID ADZ45057 standard; protein; 119 AA.
DE Human PRO842 encoding SEQ ID NO:2.
PN US2005100544-A1.
PD 12-MAY-2005.
PA (EATO/) EATON D L.
PA (PISA/) PISABARRO M T.
PA (SCHM/) SCHMIDT K N.
PA (VAND/) VANDLEN R.
PA (CHIA/) CHIANG N.
PA (DIEH/) DIEHL L.
Query Match 100.0%; Score 644; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-66;
RESULT 680
ID AEA38434 standard; protein; 119 AA.
DE Human secreted/transmembrane protein, #106.
PN US2005112725-A1.
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PD 26-MAY-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 9; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 681  
ID AED50135 standard; protein; 119 AA.  
DE Novel human secreted and transmembrane protein PRO842.  
PN US2005163766-A1.  
PD 28-JUL-2005.  
Query Match 100.0%; Score 644; DB 9; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 682  
ID AEF12552 standard; protein; 119 AA.  
DE Human PRO842 protein SEQ ID NO:26.  
PN US2006008901-A1.  
PD 12-JAN-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 644; DB 10; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 683  
ID AEF74241 standard; protein; 119 AA.  
DE Human PRO842 protein SEQ ID NO:26.  
PN US2005260647-A1.  
PD 24-NOV-2005.  
PA (EATO/) EATON D L.  
PA (FILV/) FILVAROFF E.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W L.  
Query Match 100.0%; Score 644; DB 10; Length 119;  
Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
RESULT 684  
ID ADY30566 standard; protein; 158 AA.  
DE Human splice variant protein expressed in ovary cells DEX0487\_006.orf.1.  
PN WO2005017102-A2.  
PD 24-FEB-2005.  
PA (DIAD-) DIADEXUS INC.  
Query Match 100.0%; Score 644; DB 9; Length 158;  
Best Local Similarity 100.0%; Pred. No. 4.6e-66;  
RESULT 685  
ID ADY30568 standard; protein; 170 AA.  
DE Human splice variant protein expressed in ovary cells DEX0487\_006.orf.2.  
PN WO2005017102-A2.  
PD 24-FEB-2005.  
PA (DIAD-) DIADEXUS INC.  
Query Match 100.0%; Score 644; DB 9; Length 170;  
Best Local Similarity 100.0%; Pred. No. 5.1e-66;  
RESULT 686  
ID ADY30568 standard; protein; 128 AA.  
DE Cancer related protein sequence #31.  
PN WO2004092338-A2.  
PD 28-OCT-2004.  
PA (DIAD-) DIADEXUS INC.  
Query Match 87.7%; Score 565; DB 8; Length 128;  
Best Local Similarity 100.0%; Pred. No. 5e-57;  
RESULT 687  
ID AAY82454 standard; protein; 97 AA.  
DE Mature human TGC-440 secretory protein SEQ ID NO:7.  
PN WO200014226-A1.  
PD 16-MAR-2000.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match 85.1%; Score 548; DB 3; Length 97;  
Best Local Similarity 100.0%; Pred. No. 3.3e-55;  
RESULT 688  
ID ABR61572 standard; protein; 97 AA.  
DE Human VCC-1 mature polypeptide.  
PN WO2003087157-A2.  
PD 23-OCT-2003.  
PA (PHAA ) PHARMACIA CORP.  
Query Match 59.9%; Score 386; DB 7; Length 97;  
Best Local Similarity 100.0%; Pred. No. 1.8e-36;  
RESULT 689  
ID AAM33953 standard; protein; 93 AA.  
DE Polypeptide encoded by gene 7 clone HJPDJ64.  
PN WO9845712-A2.  
PD 15-OCT-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 81.8%; Score 527; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 8.5e-53;  
RESULT 690  
ID ADT50870 standard; protein; 118 AA.  
DE Cancer related protein sequence #33.  
PN WO2004092338-A2.  
PD 28-OCT-2004.  
PA (DIAD-) DIADEXUS INC.  
Query Match 81.8%; Score 527; DB 8; Length 118;  
Best Local Similarity 100.0%; Pred. No. 1.1e-52;  
RESULT 691  
ID ADT50869 standard; protein; 94 AA.  
DE Cancer related protein sequence #32.  
PN WO2004092338-A2.  
PD 28-OCT-2004.  
PA (DIAD-) DIADEXUS INC.  
Query Match 80.9%; Score 521; DB 8; Length 94;  
Best Local Similarity 100.0%; Pred. No. 4.3e-52;  
RESULT 692  
ID ADT50871 standard; protein; 100 AA.  
DE Cancer related protein sequence #34.  
PN WO2004092338-A2.  
PD 28-OCT-2004.  
PA (DIAD-) DIADEXUS INC.  
Query Match 80.9%; Score 521; DB 8; Length 100;  
Best Local Similarity 100.0%; Pred. No. 4.6e-52;  
RESULT 693  
ID AAY82457 standard; protein; 119 AA.  
DE Mouse TGC-440 secretory protein SEQ ID NO:3.  
PN WO200014226-A1.  
PD 16-MAR-2000.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match 70.8%; Score 456; DB 3; Length 119;  
Best Local Similarity 71.4%; Pred. No. 1.9e-44;  
RESULT 694  
ID ABR61573 standard; protein; 119 AA.  
DE Mouse VCC-1 polypeptide.  
PN WO2003087157-A2.  
PD 23-OCT-2003.  
PA (PHAA ) PHARMACIA CORP.  
Query Match 70.8%; Score 456; DB 7; Length 119;  
Best Local Similarity 71.4%; Pred. No. 1.9e-44;  
RESULT 695  
ID ADT50873 standard; protein; 84 AA.  
DE Cancer related protein sequence #36.  
PN WO2004092338-A2.  
PD 28-OCT-2004.  
PA (DIAD-) DIADEXUS INC.  
Query Match 64.4%; Score 415; DB 8; Length 84;  
Best Local Similarity 80.9%; Pred. No. 6.8e-40;  
RESULT 696  
ID AAY82458 standard; protein; 97 AA.  
DE Mature mouse TGC-440 secretory protein SEQ ID NO:9.  
PN WO200014226-A1.  
PD 16-MAR-2000.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match 59.9%; Score 386; DB 3; Length 97;  
Best Local Similarity 71.1%; Pred. No. 1.8e-36;  
RESULT 697  
ID ABR61574 standard; protein; 97 AA.  
DE Mouse VCC-1 mature polypeptide.  
PN WO2003087157-A2.  
PD 23-OCT-2003.  
PA (PHAA ) PHARMACIA CORP.  
Query Match 59.9%; Score 386; DB 7; Length 97;  
Best Local Similarity 100.0%; Pred. No. 1.8e-36;

Best Local Similarity 71.1%; Pred. No. 1.8e-36;  
RESULT 698  
ID AAY82455 standard; protein; 119 AA.  
DE Rat TGC-440 secretory protein SEQ ID NO:2.  
PN WO200014226-A1.  
PD 16-MAR-2000.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match 59.9%; Score 386; DB 3; Length 119;  
Best Local Similarity 63.0%; Pred. No. 2.3e-36;  
RESULT 699  
ID AAY11732 standard; protein; 69 AA.  
DE Human 5' EST secreted protein SEQ ID No: 332.  
PN WO9906550-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 55.6%; Score 358; DB 2; Length 69;  
Best Local Similarity 100.0%; Pred. No. 2.1e-33;  
RESULT 700  
ID AAY82456 standard; protein; 97 AA.  
DE Mature rat TGC-440 secretory protein SEQ ID NO:8.  
PN WO200014226-A1.  
PD 16-MAR-2000.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match 53.1%; Score 342; DB 3; Length 97;  
Best Local Similarity 64.9%; Pred. No. 2.3e-31;  
RESULT 701  
ID AAW83938 standard; protein; 64 AA.  
DE Human secreted protein from gene 8 clone HLHCM89.  
PN WO9845712-A2.  
PD 15-OCT-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 46.0%; Score 296; DB 2; Length 64;  
Best Local Similarity 96.6%; Pred. No. 2.9e-26;  
RESULT 702  
ID AAY11731 standard; protein; 48 AA.  
DE Human 5' EST secreted protein SEQ ID No: 331.  
PN WO9906550-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 34.9%; Score 225; DB 2; Length 48;  
Best Local Similarity 97.9%; Pred. No. 3.4e-18;  
RESULT 703  
ID ADY30565 standard; protein; 57 AA.  
DE Human gp135 variant protein expressed in ovary cells DEX0487\_006.aa.1.  
PN WO2005017102-A2.  
PD 24-FEB-2005.  
PA (DIAD-) DIADEXUS INC.  
Query Match 18.6%; Score 119.5; DB 9; Length 57;  
Best Local Similarity 61.2%; Pred. No. 6.6e-06;  
RESULT 704  
ID ADY30567 standard; protein; 98 AA.  
DE Human gp135 variant protein expressed in ovary cells DEX0487\_006.aa.2.  
PN WO2005017102-A2.  
PD 24-FEB-2005.  
PA (DIAD-) DIADEXUS INC.  
Query Match 18.6%; Score 119.5; DB 9; Length 98;  
Best Local Similarity 61.2%; Pred. No. 1.3e-05;  
RESULT 705  
ID ABO68555 standard; protein; 620 AA.  
DE Pseudomonas aeruginosa polypeptide #730.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 13.1%; Score 84.5; DB 7; Length 620;  
Best Local Similarity 30.7%; Pred. No. 1.3;  
RESULT 706  
ID AAU66308 standard; protein; 191 AA.  
DE Propionibacterium acnes immunogenic protein #27204.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 12.2%; Score 78.5; DB 4; Length 191;  
Best Local Similarity 22.4%; Pred. No. 1.6;  
RESULT 707  
ID ABM62827 standard; protein; 191 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #27503.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 12.2%; Score 78.5; DB 6; Length 191;  
Best Local Similarity 22.4%; Pred. No. 1.6;  
RESULT 708  
ID ABO68031 standard; protein; 629 AA.  
DE Pseudomonas aeruginosa polypeptide #206.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 11.5%; Score 74; DB 7; Length 629;  
Best Local Similarity 30.2%; Pred. No. 21;  
RESULT 709  
ID AAP91996 standard; protein; 70 AA.  
DE Part of chick vitamin D receptor.  
PN WO9909223-A.  
PD 05-OCT-1989.  
PA (ARCH-) ARCH DEV CORP.  
Query Match 11.4%; Score 73.5; DB 1; Length 70;  
Best Local Similarity 35.5%; Pred. No. 1.8;  
RESULT 710  
ID AAR43657 standard; protein; 70 AA.  
DE Chicken vitamin D receptor.  
PN US5260199-A.  
PD 09-NOV-1993.  
PA (WISC ) WISCONSIN ALUMNI RES FOUND.  
Query Match 11.4%; Score 73.5; DB 2; Length 70;  
Best Local Similarity 35.5%; Pred. No. 1.8;  
RESULT 711  
ID ABO79771 standard; protein; 724 AA.  
DE Pseudomonas aeruginosa polypeptide #11946.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 11.3%; Score 72.5; DB 7; Length 724;  
Best Local Similarity 28.4%; Pred. No. 38;  
RESULT 712  
ID ADB64837 standard; protein; 752 AA.  
DE Human protein encoded by clone OCBF20166900.  
PN EPI308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 11.3%; Score 72.5; DB 7; Length 752;  
Best Local Similarity 28.0%; Pred. No. 39;  
RESULT 713  
ID ADE54405 standard; protein; 3313 AA.  
DE Rat Protein BAA32459, SEQ ID NO 208.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 11.3%; Score 72.5; DB 7; Length 3313;  
Best Local Similarity 27.6%; Pred. No. 2.3e+02;  
RESULT 714  
ID ADE54409 standard; protein; 3313 AA.  
DE Rat Protein BAA32459, SEQ ID NO 212.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 11.3%; Score 72.5; DB 7; Length 3313;  
Best Local Similarity 27.6%; Pred. No. 2.3e+02;  
RESULT 715  
ID ADN49433 standard; protein; 3313 AA.  
DE Rat seven-pass transmembrane receptor protein.  
PN US2004086931-A1.  
PD 06-MAY-2004.  
PA (SPAD/) SPADERNA S K.

PA (QUIN/) QUINN K E.  
PA (SHIM/) SHIMKETS R A.  
PA (PADI/) PADIGARU M.  
PA (SPYT/) SPYTEK K A.  
Query Match 11.3%; Score 72.5; DB 8; Length 3313;  
Best Local Similarity 27.6%; Pred. No. 2.3e+02;  
RESULT 716  
ID ABO70512 standard; protein; 689 AA.  
DE Pseudomonas aeruginosa polypeptide #2687.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 11.2%; Score 72; DB 7; Length 689;  
Best Local Similarity 40.5%; Pred. No. 41;  
RESULT 717  
ID AAO21337 standard; protein; 108 AA.  
DE Arabidopsis thaliana KCP-like protein, SEQ ID NO 92.  
PN WO200222821-A2.  
PD 21-MAR-2002.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 11.1%; Score 71.5; DB 5; Length 108;  
Best Local Similarity 25.9%; Pred. No. 5.1;  
RESULT 718  
ID ADG74889 standard; protein; 108 AA.  
DE Plant developmental pathway modulation-related RKS/ELS ligand protein 10.  
PN EP1382682-A2.  
PD 21-JAN-2004.  
PA (EXPR-) EXPRESSIVE RES BV.  
Query Match 11.1%; Score 71.5; DB 8; Length 108;  
Best Local Similarity 25.9%; Pred. No. 5.1;  
RESULT 719  
ID AEA49162 standard; protein; 651 AA.  
DE L. thamosus polypeptide #26.  
PN WO2005056801-A1.  
PD 23-JUN-2005.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FONT-) FONTERRA COOP GROUP LTD.  
Query Match 11.1%; Score 71.5; DB 9; Length 651;  
Best Local Similarity 23.8%; Pred. No. 43;  
RESULT 720  
ID AED03570 standard; protein; 651 AA.  
DE L. thamosus HexB protein SEQ ID NO:106.  
PN US2005202437-A1.  
PD 15-SEP-2005.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (VIAL-) VIALACTIA BIOSCIENCES NZ LTD.  
Query Match 11.1%; Score 71.5; DB 9; Length 651;  
Best Local Similarity 23.8%; Pred. No. 43;  
RESULT 721  
ID ADX69288 standard; protein; 188 AA.  
DE Human VEGF-B.  
PN WO2005016963-A2.  
PD 24-FEB-2005.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN) LICENTIA LTD.  
Query Match 11.0%; Score 71; DB 9; Length 188;  
Best Local Similarity 29.7%; Pred. No. 11;  
RESULT 722  
ID ADX68179 standard; protein; 249 AA.  
DE Plant full length insert polypeptide seqid 39022.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 11.0%; Score 71; DB 8; Length 249;  
Best Local Similarity 29.9%; Pred. No. 16;  
RESULT 723  
ID ABG25331 standard; protein; 330 AA.  
DE Novel human diagnostic protein #25322.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.0%; Score 71; DB 4; Length 330;  
Best Local Similarity 29.8%; Pred. No. 22;  
RESULT 724  
ID ADX89286 standard; protein; 330 AA.  
DE Plant full length insert polypeptide seqid 51950.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 11.0%; Score 71; DB 8; Length 330;  
Best Local Similarity 29.9%; Pred. No. 22;  
RESULT 725  
ID ADY04494 standard; protein; 330 AA.  
DE Plant full length insert polypeptide seqid 60309.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 11.0%; Score 71; DB 8; Length 330;  
Best Local Similarity 29.9%; Pred. No. 22;  
RESULT 726  
ID ADY06784 standard; protein; 351 AA.  
DE Plant full length insert polypeptide seqid 62599.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 11.0%; Score 71; DB 8; Length 351;  
Best Local Similarity 29.9%; Pred. No. 24;  
RESULT 727  
ID ADX77174 standard; protein; 356 AA.  
DE Plant full length insert polypeptide seqid 46540.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 11.0%; Score 71; DB 8; Length 356;  
Best Local Similarity 29.9%; Pred. No. 24;  
RESULT 728  
ID ADX68580 standard; protein; 604 AA.  
DE Plant full length insert polypeptide seqid 39423.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 11.0%; Score 71; DB 8; Length 604;  
Best Local Similarity 33.3%; Pred. No. 45;  
RESULT 729  
ID ADX95182 standard; protein; 777 AA.  
DE Plant full length insert polypeptide seqid 57846.

PA US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIU//) LIU J.  
PA (ZHOU//) ZHOU Y.  
PA (KOVAC//) KOVALIC D K.  
PA (SCRE//) SCREEN S B.  
PA (TABAK//) TABASKA J E.  
PA (CAOY//) CAO Y.  
Query Match 11.0%; Score 71; DB 8; Length 777;  
Best Local Similarity 33.3%; Pred. No. 61;  
RESULT 730  
ID AAM50896 standard; protein; 1798 AA.  
DE Human laminin B2 chain.  
PN WO9815179-A1.  
PD 16-APR-1998.  
PA (UNIW ) UNIV WASHINGTON.  
Query Match 11.0%; Score 71; DB 2; Length 1798;  
Best Local Similarity 28.4%; Pred. No. 1.7e+02;  
RESULT 731  
ID ADE60385 standard; protein; 1798 AA.  
DE Human protein P55268, SEQ ID NO 6294.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEOH ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 11.0%; Score 71; DB 7; Length 1798;  
Best Local Similarity 28.4%; Pred. No. 1.7e+02;  
RESULT 732  
ID AAB84634 standard; protein; 3190 AA.  
DE Amino acid sequence of CBP protein of Drosophila.  
PN WO200147981-A1.  
PD 05-JUL-2001.  
PA (INSR ) INST ROUSSY GUSTAVE.  
PA (CNRS ) CENT NAT RECH SCI.  
Query Match 11.0%; Score 71; DB 4; Length 3190;  
Best Local Similarity 26.7%; Pred. No. 3.3e+02;  
RESULT 733  
ID ABB70437 standard; protein; 3275 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 38103.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 11.0%; Score 71; DB 4; Length 3275;  
Best Local Similarity 26.7%; Pred. No. 3.4e+02;  
RESULT 734  
ID ADK11301 standard; protein; 3275 AA.  
DE Drosophila CREB binding protein (p300/CBP) protein.  
PN WO2003040301-A2.  
PD 15-MAY-2003.  
PA (CYCL-) CYCLACEL LTD.  
Query Match 11.0%; Score 71; DB 7; Length 3275;  
Best Local Similarity 26.7%; Pred. No. 3.4e+02;  
RESULT 735  
ID AAU83095 standard; protein; 146 AA.  
DE Novel secreted protein Z3038GIP.  
PN WO200202621-A2.  
PD 10-JAN-2002.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 10.9%; Score 70.5; DB 5; Length 146;  
Best Local Similarity 32.5%; Pred. No. 9.5;  
RESULT 736  
ID AED54309 standard; protein; 160 AA.  
DE Peanut conglutinin-like allergen.  
PN WO2005100995-A2.  
PD 27-OCT-2005.  
PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.  
Query Match 10.9%; Score 70.5; DB 9; Length 160;  
Best Local Similarity 22.1%; Pred. No. 11;  
RESULT 737  
ID ABO78864 standard; protein; 420 AA.  
DE Pseudomonas aeruginosa polypeptide #11039.  
PN US6551795-B1.  
PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.9%; Score 70.5; DB 7; Length 420;  
Best Local Similarity 24.8%; Pred. No. 34;  
RESULT 738  
ID ABG61841 standard; protein; 117 AA.  
DE Prostate cancer-associated protein #42.  
PN WO20020268-A2.  
PD 18-APR-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 10.9%; Score 70; DB 5; Length 117;  
Best Local Similarity 29.5%; Pred. No. 8.4;  
RESULT 739  
ID ABM82165 standard; protein; 117 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO23238, SEQ:5589.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.9%; Score 70; DB 8; Length 117;  
Best Local Similarity 29.5%; Pred. No. 8.4;  
RESULT 740  
ID ADY20193 standard; protein; 117 AA.  
DE PRO polypeptide SEQ ID NO 5993.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 10.9%; Score 70; DB 9; Length 117;  
Best Local Similarity 29.5%; Pred. No. 8.4;  
RESULT 741  
ID AAY66165 standard; protein; 121 AA.  
DE Human bladder tumour EST encoded protein 23.  
PN DE19818619-A1.  
PD 28-OCT-1999.  
PA (META-) METAGEN GBS GENOMFORSCHUNG MBH.  
Query Match 10.9%; Score 70; DB 2; Length 121;  
Best Local Similarity 29.5%; Pred. No. 8.7;  
RESULT 742  
ID AAS56893 standard; protein; 121 AA.  
DE Human prostate cancer antigen protein sequence SEQ ID NO:1471.  
PN WO200055174-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.9%; Score 70; DB 3; Length 121;  
Best Local Similarity 29.5%; Pred. No. 8.7;  
RESULT 743  
ID ADR66888 standard; protein; 121 AA.  
DE Human prostatic carcinoma derived DNA SEQ ID 186 #4.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ//) HINZMANN B.  
PA (DAHL//) DAHL E.  
PA (ROSE//) ROSENTHAL A.  
PA (HERM//) HERMANN K.  
PA (PILA//) PILARSKY C.  
Query Match 10.9%; Score 70; DB 8; Length 121;  
Best Local Similarity 29.5%; Pred. No. 8.7;  
RESULT 744  
ID ADR65990 standard; protein; 121 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 186 #1.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ//) HINZMANN B.  
PA (DAHL//) DAHL E.  
PA (ROSE//) ROSENTHAL A.  
PA (HERM//) HERMANN K.  
PA (PILA//) PILARSKY C.  
Query Match 10.9%; Score 70; DB 8; Length 121;  
Best Local Similarity 29.5%; Pred. No. 8.7;  
RESULT 745  
ID AAY08283 standard; protein; 167 AA.  
DE Human growth factor protein fragment VEGF-B167.  
PN DE19748734-A1.  
PD 06-MAY-1999.

PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
Query Match 10.9%; Score 70; DB 2; Length 167;  
Best Local Similarity 28.4%; Pred. No. 13;  
RESULT 746  
ID AAB24082 standard; protein; 167 AA.  
DE Human PRO834 mature VEGF-b protein sequence SEQ ID NO:69.  
PN WO200053755-A2.  
PD 14-SEP-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 10.9%; Score 70; DB 3; Length 167;  
Best Local Similarity 28.4%; Pred. No. 13;  
RESULT 747  
ID AAM00726 standard; protein; 188 AA.  
DE Vascular endothelial growth factor-like protein SOM175-e6.  
PN WO9627007-A1.  
PD 06-SEP-1996.  
PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
Query Match 10.9%; Score 70; DB 2; Length 188;  
Best Local Similarity 28.4%; Pred. No. 15;  
RESULT 748  
ID AAW04829 standard; protein; 188 AA.  
DE Fibrosarcoma vascular endothelial growth factor-B167.  
PN WO9626736-A1.  
PD 06-SEP-1996.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.  
Query Match 10.9%; Score 70; DB 2; Length 188;  
Best Local Similarity 28.4%; Pred. No. 15;  
RESULT 749  
ID AAY33442 standard; protein; 188 AA.  
DE Parapox virus VEGF growth factor homologue protein fragment 9.  
PN DE19813774-A1.  
PD 30-SEP-1999.  
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
Query Match 10.9%; Score 70; DB 2; Length 188;  
Best Local Similarity 28.4%; Pred. No. 15;  
RESULT 750  
ID AAW80493 standard; protein; 188 AA.  
DE Human vascular endothelial growth factor (VEGF)-B167.  
PN US5840693-A.  
PD 24-NOV-1998.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.  
Query Match 10.9%; Score 70; DB 2; Length 188;  
Best Local Similarity 28.4%; Pred. No. 15;  
RESULT 751  
ID AAB10647 standard; protein; 188 AA.  
DE Human VEGF protein.  
PN WO200037641-A2.  
PD 29-JUN-2000.  
PA (JANC ) JANSSEN PHARM NV.  
Query Match 10.9%; Score 70; DB 3; Length 188;  
Best Local Similarity 28.4%; Pred. No. 15;  
RESULT 752  
ID AAB24083 standard; protein; 188 AA.  
DE Human PRO834 proVEGF-b protein sequence SEQ ID NO:69.  
PN WO200053755-A2.  
PD 14-SEP-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 10.9%; Score 70; DB 3; Length 188;  
Best Local Similarity 28.4%; Pred. No. 15;  
RESULT 753  
ID AAU08440 standard; protein; 188 AA.  
DE Polypeptide for human VEGF-B.  
PN WO200162942-A2.  
PD 30-AUG-2001.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA OY.  
Query Match 10.9%; Score 70; DB 4; Length 188;  
Best Local Similarity 28.4%; Pred. No. 15;  
RESULT 754  
ID AAG77791 standard; protein; 188 AA.  
DE Human vascular endothelial growth factor B-167 protein (VEGFB-167).

PN WO200164233-A1.  
PD 07-SEP-2001.  
PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
Query Match 10.9%; Score 70; DB 4; Length 188;  
Best Local Similarity 28.4%; Pred. No. 15;  
RESULT 755  
ID AAU83407 standard; protein; 188 AA.  
DE Human vascular endothelial growth factor VEGF-B167.  
PN US6331301-B1.  
PD 18-DEC-2001.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.  
Query Match 10.9%; Score 70; DB 5; Length 188;  
Best Local Similarity 28.4%; Pred. No. 15;  
RESULT 756  
ID ABB07952 standard; protein; 188 AA.  
DE Human VEGF-B167 protein.  
PN WO200207514-A2.  
PD 31-JAN-2002.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
Query Match 10.9%; Score 70; DB 5; Length 188;  
Best Local Similarity 28.4%; Pred. No. 15;  
RESULT 757  
ID ADH53391 standard; protein; 188 AA.  
DE Human VEGF-B167 protein.  
PN US2003170253-A1.  
PD 11-SEP-2003.  
PA (UYHE-) UNIV HELSINKI LICENSING LTD.  
Query Match 10.9%; Score 70; DB 7; Length 188;  
Best Local Similarity 28.4%; Pred. No. 15;  
RESULT 758  
ID ADR31420 standard; protein; 188 AA.  
DE Human vascular endothelial growth factor B (VEGF-B) protein #1.  
PN WO2004070018-A2.  
PD 19-AUG-2004.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (UYFL-) FLANDERS INTERUNIVERSITY INST BIOTECHNOL.  
Query Match 10.9%; Score 70; DB 8; Length 188;  
Best Local Similarity 28.4%; Pred. No. 15;  
RESULT 759  
ID ADY86488 standard; protein; 188 AA.  
DE Human VEGF - B167 protein, SEQ ID NO: 11.  
PN US2005064493-A1.  
PD 24-MAR-2005.  
PA (LICN ) LICENTIA LTD.  
Query Match 10.9%; Score 70; DB 9; Length 188;  
Best Local Similarity 28.4%; Pred. No. 15;  
RESULT 760  
ID AED26693 standard; protein; 188 AA.  
DE Human VEGF-B isoform 1.  
PN WO2005087808-A2.  
PD 22-SEP-2005.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
Query Match 10.9%; Score 70; DB 9; Length 188;  
Best Local Similarity 28.4%; Pred. No. 15;  
RESULT 761  
ID AEF19782 standard; protein; 188 AA.  
DE Human vascular endothelial growth factor B (VEGF-B) isoform 2 protein.  
PN WO2006001888-A2.  
PD 05-JAN-2006.  
PA (ACUT-) ACUTY PHARM INC.  
Query Match 10.9%; Score 70; DB 10; Length 188;  
Best Local Similarity 28.4%; Pred. No. 15;  
RESULT 762  
ID AAE09217 standard; protein; 189 AA.  
DE Hexa-His-tagged human VEGF-B167 protein.  
PN WO200160861-A1.  
PD 23-AUG-2001.  
PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
Query Match 10.9%; Score 70; DB 4; Length 189;

Best Local Similarity 28.4%; Pred. No. 15;  
RESULT 763  
ID AEF19783 standard; protein; 192 AA.  
DE Human VEGF-B isoform 2 protein with KDEL signal.  
PN WO2006001888-A2.  
PD 05-JAN-2006.  
PA (ACUI-) ACUTY PHARM INC.  
Query Match 10.9%; Score 70; DB 10; Length 192;  
Best Local Similarity 28.4%; Pred. No. 15;  
RESULT 764  
ID ABP41889 standard; protein; 216 AA.  
DE Human ovarian antigen HRAFP38, SEQ ID NO:3021.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 10.9%; Score 70; DB 5; Length 216;  
Best Local Similarity 28.4%; Pred. No. 17;  
RESULT 765  
ID AAB99889 standard; protein; 491 AA.  
DE Physcomitrella patens 78\_pproti\_092\_e12-260rev protein.  
PN WO200144276-A2.  
PD 21-JUN-2001.  
PA (BADI) BASF PLANT SCI GMBH.  
Query Match 10.9%; Score 70; DB 4; Length 491;  
Best Local Similarity 24.8%; Pred. No. 46;  
RESULT 766  
ID ABB71263 standard; protein; 543 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 40581.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 10.9%; Score 70; DB 4; Length 543;  
Best Local Similarity 26.7%; Pred. No. 52;  
RESULT 767  
ID ABO81764 standard; protein; 626 AA.  
DE Pseudomonas aeruginosa polypeptide #13939.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.9%; Score 70; DB 7; Length 626;  
Best Local Similarity 29.6%; Pred. No. 62;  
RESULT 768  
ID AAU29777 standard; protein; 795 AA.  
DE Novel human secreted protein #268.  
PN WO200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.9%; Score 70; DB 4; Length 795;  
Best Local Similarity 28.4%; Pred. No. 82;  
RESULT 769  
ID ADE08948 standard; protein; 935 AA.  
DE Novel protein-related contig polypeptide sequence #14.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.9%; Score 70; DB 7; Length 935;  
Best Local Similarity 28.4%; Pred. No. 1e+02;  
RESULT 770  
ID ADY09512 standard; protein; 204 AA.  
DE Plant full length insert polypeptide seqid 65327.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ) LIU J.  
PA (ZHOU) ZHOU Y.  
PA (KOVA) KOVALIC D K.  
PA (SCRE) SCREEN S E.  
PA (TABAS) TABASKA J E.  
PA (CAOY) CAO Y.  
Query Match 10.8%; Score 69.5; DB 8; Length 204;  
Best Local Similarity 27.0%; Pred. No. 19;  
RESULT 771  
ID AAU64571 standard; protein; 361 AA.  
DE Propionibacterium acnes immunogenic protein #25467.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 10.8%; Score 69.5; DB 4; Length 361;  
Best Local Similarity 28.0%; Pred. No. 37;  
RESULT 772  
ID ABM61090 standard; protein; 361 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #25766.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 10.8%; Score 69.5; DB 6; Length 361;  
Best Local Similarity 28.0%; Pred. No. 37;  
RESULT 773  
ID AAR45335 standard; protein; 461 AA.  
DE Thrombomodulin analogue Q336N, Q365E.  
PN WO9325675-A1.  
PD 23-DEC-1993.  
PA (SCHD) SCHERING AG.  
Query Match 10.8%; Score 69.5; DB 2; Length 461;  
Best Local Similarity 23.5%; Pred. No. 49;  
RESULT 774  
ID AAR45347 standard; protein; 462 AA.  
DE Thrombomodulin analogue 398-417X.  
PN WO9325675-A1.  
PD 23-DEC-1993.  
PA (SCHD) SCHERING AG.  
Query Match 10.8%; Score 69.5; DB 2; Length 462;  
Best Local Similarity 23.5%; Pred. No. 49;  
RESULT 775  
ID AAR45349 standard; protein; 462 AA.  
DE Thrombomodulin analogue 423-461X.  
PN WO9325675-A1.  
PD 23-DEC-1993.  
PA (SCHD) SCHERING AG.  
Query Match 10.8%; Score 69.5; DB 2; Length 462;  
Best Local Similarity 23.5%; Pred. No. 49;  
RESULT 776  
ID AAR45337 standard; protein; 462 AA.  
DE Thrombomodulin analogue R456X, H457X.  
PN WO9325675-A1.  
PD 23-DEC-1993.  
PA (SCHD) SCHERING AG.  
Query Match 10.8%; Score 69.5; DB 2; Length 462;  
Best Local Similarity 23.5%; Pred. No. 49;  
RESULT 777  
ID AAR45339 standard; protein; 462 AA.  
DE Thrombomodulin analogue Q365X, L369X, M388X, R456X, H457X.  
PN WO9325675-A1.  
PD 23-DEC-1993.  
PA (SCHD) SCHERING AG.  
Query Match 10.8%; Score 69.5; DB 2; Length 462;  
Best Local Similarity 23.5%; Pred. No. 49;  
RESULT 778  
ID AAR45343 standard; protein; 462 AA.  
DE Thrombomodulin analogue D349N.  
PN WO9325675-A1.  
PD 23-DEC-1993.  
PA (SCHD) SCHERING AG.  
Query Match 10.8%; Score 69.5; DB 2; Length 462;  
Best Local Similarity 23.5%; Pred. No. 49;  
RESULT 779  
ID AAR45355 standard; protein; 462 AA.  
DE Thrombomodulin analogue 408-461X.  
PN WO9325675-A1.  
PD 23-DEC-1993.  
PA (SCHD) SCHERING AG.  
Query Match 10.8%; Score 69.5; DB 2; Length 462;  
Best Local Similarity 23.5%; Pred. No. 49;  
RESULT 780  
ID AAR45341 standard; protein; 462 AA.  
DE Thrombomodulin analogue 349-461X.  
PN WO9325675-A1.

PD 23-DEC-1993.  
PA (SCHD ) SCHERING AG. 10.8%; Score 69.5; DB 2; Length 462;  
Query Match 23.5%; Pred. No. 49;  
Best Local Similarity 23.5%; Pred. No. 49;  
RESULT 781  
ID AAR45342 standard; protein; 462 AA.  
DE Thrombomodulin analogue 349-461X.  
PN WO9325675-A1.  
PD 23-DEC-1993.  
PA (SCHD ) SCHERING AG. 10.8%; Score 69.5; DB 2; Length 462;  
Query Match 23.5%; Pred. No. 49;  
Best Local Similarity 23.5%; Pred. No. 49;  
RESULT 782  
ID AAR45336 standard; protein; 462 AA.  
DE Thrombomodulin analogue Q365X, Q369X.  
PN WO9325675-A1.  
PD 23-DEC-1993.  
PA (SCHD ) SCHERING AG. 10.8%; Score 69.5; DB 2; Length 462;  
Query Match 23.5%; Pred. No. 49;  
Best Local Similarity 23.5%; Pred. No. 49;  
RESULT 783  
ID AAR45348 standard; protein; 462 AA.  
DE Thrombomodulin analogue 423-461X.  
PN WO9325675-A1.  
PD 23-DEC-1993.  
PA (SCHD ) SCHERING AG. 10.8%; Score 69.5; DB 2; Length 462;  
Query Match 23.5%; Pred. No. 49;  
Best Local Similarity 23.5%; Pred. No. 49;  
RESULT 784  
ID AAR45350 standard; protein; 462 AA.  
DE Thrombomodulin analogue 349-359X.  
PN WO9325675-A1.  
PD 23-DEC-1993.  
PA (SCHD ) SCHERING AG. 10.8%; Score 69.5; DB 2; Length 462;  
Query Match 23.5%; Pred. No. 49;  
Best Local Similarity 23.5%; Pred. No. 49;  
RESULT 785  
ID AAR45345 standard; protein; 462 AA.  
DE Thrombomodulin analogue 349-385X.  
PN WO9325675-A1.  
PD 23-DEC-1993.  
PA (SCHD ) SCHERING AG. 10.8%; Score 69.5; DB 2; Length 462;  
Query Match 23.5%; Pred. No. 49;  
Best Local Similarity 23.5%; Pred. No. 49;  
RESULT 786  
ID AAR45354 standard; protein; 462 AA.  
DE Thrombomodulin analogue 408-461X.  
PN WO9325675-A1.  
PD 23-DEC-1993.  
PA (SCHD ) SCHERING AG. 10.8%; Score 69.5; DB 2; Length 462;  
Query Match 23.5%; Pred. No. 49;  
Best Local Similarity 23.5%; Pred. No. 49;  
RESULT 787  
ID AAR45338 standard; protein; 462 AA.  
DE Thrombomodulin analogue R456G, H457Q.  
PN WO9325675-A1.  
PD 23-DEC-1993.  
PA (SCHD ) SCHERING AG. 10.8%; Score 69.5; DB 2; Length 462;  
Query Match 23.5%; Pred. No. 49;  
Best Local Similarity 23.5%; Pred. No. 49;  
RESULT 788  
ID AAR45353 standard; protein; 462 AA.  
DE Thrombomodulin analogue 363-402X.  
PN WO9325675-A1.  
PD 23-DEC-1993.  
PA (SCHD ) SCHERING AG. 10.8%; Score 69.5; DB 2; Length 462;  
Query Match 23.5%; Pred. No. 49;  
Best Local Similarity 23.5%; Pred. No. 49;  
RESULT 789  
ID AAR45346 standard; protein; 462 AA.  
DE Thrombomodulin analogue 398-420X.  
PN WO9325675-A1.  
PD 23-DEC-1993.

PA (SCHD ) SCHERING AG. 10.8%; Score 69.5; DB 2; Length 462;  
Query Match 23.5%; Pred. No. 49;  
Best Local Similarity 23.5%; Pred. No. 49;  
RESULT 790  
ID AAR45344 standard; protein; 462 AA.  
DE Thrombomodulin analogue.  
PN WO9325675-A1.  
PD 23-DEC-1993.  
PA (SCHD ) SCHERING AG. 10.8%; Score 69.5; DB 2; Length 462;  
Query Match 23.5%; Pred. No. 49;  
Best Local Similarity 23.5%; Pred. No. 49;  
RESULT 791  
ID AAR45340 standard; protein; 463 AA.  
DE Thrombomodulin analogue 336-461X.  
PN WO9325675-A1.  
PD 23-DEC-1993.  
PA (SCHD ) SCHERING AG. 10.8%; Score 69.5; DB 2; Length 463;  
Query Match 23.5%; Pred. No. 49;  
Best Local Similarity 23.5%; Pred. No. 49;  
RESULT 792  
ID AAR22032 standard; protein; 475 AA.  
DE Truncated human urinary thrombomodulin.  
PN WO9200325-A.  
PD 09-JAN-1992.  
PA (MOCH ) MOCHIDA PHARM CO LTD. 10.8%; Score 69.5; DB 2; Length 475;  
Query Match 23.5%; Pred. No. 51;  
Best Local Similarity 23.5%; Pred. No. 51;  
RESULT 793  
ID AAR78725 standard; protein; 476 AA.  
DE Mature thrombomodulin.  
PN JP07165796-A.  
PD 27-JUN-1995.  
PA (KOWA ) KOWA CO LTD. 10.8%; Score 69.5; DB 2; Length 476;  
Query Match 23.5%; Pred. No. 51;  
Best Local Similarity 23.5%; Pred. No. 51;  
RESULT 794  
ID AAR86377 standard; protein; 476 AA.  
DE Modified thrombomodulin, lacking sialic acid.  
PN JP07224100-A.  
PD 22-AUG-1995.  
PA (KOWA ) KOWA CO LTD. 10.8%; Score 69.5; DB 2; Length 476;  
Query Match 23.5%; Pred. No. 51;  
Best Local Similarity 23.5%; Pred. No. 51;  
RESULT 795  
ID AAR86376 standard; protein; 476 AA.  
DE Modified thrombomodulin, GAG-UTM, lacking sialic acid.  
PN JP07224100-A.  
PD 22-AUG-1995.  
PA (KOWA ) KOWA CO LTD. 10.8%; Score 69.5; DB 2; Length 476;  
Query Match 23.5%; Pred. No. 51;  
Best Local Similarity 23.5%; Pred. No. 51;  
RESULT 796  
ID AAR22013 standard; protein; 480 AA.  
DE Truncated human thrombomodulin encoded by plasmid M13TMD3.  
PN EP474273-A.  
PD 11-MAR-1992.  
PA (ASAH ) ASAH KASEI KOGYO KK. 10.8%; Score 69.5; DB 2; Length 480;  
Query Match 23.5%; Pred. No. 51;  
Best Local Similarity 23.5%; Pred. No. 51;  
RESULT 797  
ID AAR13877 standard; protein; 486 AA.  
DE Thrombin-binding substances (A) and (B).  
PN EP445681-A.  
PD 11-SEP-1991.  
PA (KOWA ) KOWA CO LTD. 10.8%; Score 69.5; DB 2; Length 486;  
Query Match 23.5%; Pred. No. 52;  
Best Local Similarity 23.5%; Pred. No. 52;  
RESULT 798  
ID AAE17531 standard; protein; 490 AA.  
DE Human thrombomodulin (TW) deletion mutant, P490.  
PN WO200198352-A2.  
PD 27-DEC-2001.  
PA (SCHD ) SCHERING AG.

Query Match 10.8%; Score 69.5; DB 5; Length 490;  
Best Local Similarity 23.5%; Pred. No. 53;  
RESULT 799  
ID AAE23032 standard; protein; 490 AA.  
DE Human thrombomodulin deletion mutant #2.  
PN WO200217953-A2.  
PD 07-MAR-2002.  
PA (SCHD ) SCHERING AG.  
Query Match 10.8%; Score 69.5; DB 5; Length 490;  
Best Local Similarity 23.5%; Pred. No. 53;  
RESULT 800  
ID AAR24400 standard; protein; 494 AA.  
DE Recombinant thrombin-binding gene.  
PN EP488317-A2.  
PD 03-JUN-1992.  
PA (KOWA ) KOWA CO LTD.  
Query Match 10.8%; Score 69.5; DB 2; Length 494;  
Best Local Similarity 23.5%; Pred. No. 53;  
RESULT 801  
ID AAR78727 standard; protein; 494 AA.  
DE Thrombomodulin with non-native signal peptide.  
PN JP07165796-A.  
PD 27-JUN-1995.  
PA (KOWA ) KOWA CO LTD.  
Query Match 10.8%; Score 69.5; DB 2; Length 494;  
Best Local Similarity 23.5%; Pred. No. 53;  
RESULT 802  
ID AAR78726 standard; protein; 494 AA.  
DE Thrombomodulin with wild-type signal peptide.  
PN JP07165796-A.  
PD 27-JUN-1995.  
PA (KOWA ) KOWA CO LTD.  
Query Match 10.8%; Score 69.5; DB 2; Length 494;  
Best Local Similarity 23.5%; Pred. No. 53;  
RESULT 803  
ID AAV67401 standard; protein; 494 AA.  
DE Novel sugar chain-bonded thrombomodulin-like peptide #1.  
PN WO200000516-A1.  
PD 06-JAN-2000.  
PA (MOCH ) MOCHIDA PHARM CO LTD.  
Query Match 10.8%; Score 69.5; DB 3; Length 494;  
Best Local Similarity 23.5%; Pred. No. 53;  
RESULT 804  
ID AAR94607 standard; protein; 497 AA.  
DE Human recombinant soluble thrombomodulin for autoantibody detection.  
PN WO9610180-A1.  
PD 04-APR-1996.  
PA (OKLA-) OKLAHOMA MED RES FOUND.  
Query Match 10.8%; Score 69.5; DB 2; Length 497;  
Best Local Similarity 23.5%; Pred. No. 54;  
RESULT 805  
ID AAW69520 standard; protein; 497 AA.  
DE rSTM protein SEQ ID NO:4 from WO9829453 Claim 14.  
PN WO9829453-A1.  
PD 09-JUL-1998.  
PA (MOCH ) MOCHIDA PHARM CO LTD.  
Query Match 10.8%; Score 69.5; DB 2; Length 497;  
Best Local Similarity 23.5%; Pred. No. 54;  
RESULT 806  
ID AAR84185 standard; protein; 498 AA.  
DE Human derived thrombomodulin.  
PN WO9528953-A1.  
PD 02-NOV-1995.  
PA (ASAH ) ASAH KASEI KOGYO KK.  
Query Match 10.8%; Score 69.5; DB 2; Length 498;  
Best Local Similarity 23.5%; Pred. No. 54;  
RESULT 807  
ID AAW01600 standard; protein; 498 AA.  
DE Thrombomodulin TME456 protein.  
PN JP08283174-A.  
PD 29-OCT-1996.  
PA (ASAH ) ASAH KASEI KOGYO KK.  
Query Match 10.8%; Score 69.5; DB 2; Length 498;

Best Local Similarity 23.5%; Pred. No. 54;  
RESULT 808  
ID AAY67402 standard; protein; 498 AA.  
DE Novel sugar chain-bonded thrombomodulin-like peptide #2.  
PN WO200000516-A1.  
PD 06-JAN-2000.  
PA (MOCH ) MOCHIDA PHARM CO LTD.  
Query Match 10.8%; Score 69.5; DB 3; Length 498;  
Best Local Similarity 23.5%; Pred. No. 54;  
RESULT 809  
ID AAY69530 standard; protein; 500 AA.  
DE Human thrombomodulin variant, SEQ ID NO:4.  
PN JP11341990-A.  
PD 14-DEC-1999.  
PA (ASAH ) ASAH KASEI KOGYO KK.  
Query Match 10.8%; Score 69.5; DB 3; Length 500;  
Best Local Similarity 23.5%; Pred. No. 54;  
RESULT 810  
ID AEF31119 standard; protein; 505 AA.  
DE Solulin.  
PN WO2006005362-A1.  
PD 19-JAN-2006.  
PA (FRAU ) FRAUNHOFER GES FORDERUNG ANGEWANDTEN EV.  
PA (PAIO-) PAION DEUT GMBH.  
Query Match 10.8%; Score 69.5; DB 10; Length 505;  
Best Local Similarity 23.5%; Pred. No. 55;  
RESULT 811  
ID AAR10617 standard; protein; 515 AA.  
DE Soluble thrombomodulin deriv.  
PN EP412841-A.  
PD 13-FEB-1991.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 10.8%; Score 69.5; DB 2; Length 515;  
Best Local Similarity 23.5%; Pred. No. 56;  
RESULT 812  
ID AAR22017 standard; protein; 516 AA.  
DE Human thrombomodulin (1-516) with Asp367 substituted by Ala.  
PN EP474273-A.  
PD 11-MAR-1992.  
PA (ASAH ) ASAH KASEI KOGYO KK.  
Query Match 10.8%; Score 69.5; DB 2; Length 516;  
Best Local Similarity 23.5%; Pred. No. 56;  
RESULT 813  
ID AAR22016 standard; protein; 516 AA.  
DE Truncated human thrombomodulin encoded by plasmid pSV2TMD1.  
PN EP474273-A.  
PD 11-MAR-1992.  
PA (ASAH ) ASAH KASEI KOGYO KK.  
Query Match 10.8%; Score 69.5; DB 2; Length 516;  
Best Local Similarity 23.5%; Pred. No. 56;  
RESULT 814  
ID AAR22018 standard; protein; 516 AA.  
DE Human thrombomodulin (1-516) with Asp367 substituted by Glu.  
PN EP474273-A.  
PD 11-MAR-1992.  
PA (ASAH ) ASAH KASEI KOGYO KK.  
Query Match 10.8%; Score 69.5; DB 2; Length 516;  
Best Local Similarity 23.5%; Pred. No. 56;  
RESULT 815  
ID AAY09347 standard; protein; 516 AA.  
DE Human thrombomodulin SEQ ID NO:1.  
PN WO9918994-A1.  
PD 22-APR-1999.  
PA (ASAH ) ASAH KASEI KOGYO KK.  
Query Match 10.8%; Score 69.5; DB 2; Length 516;  
Best Local Similarity 23.5%; Pred. No. 56;  
RESULT 816  
ID AAY09348 standard; protein; 516 AA.  
DE Human thrombomodulin SEQ ID NO:2.  
PN WO9918994-A1.  
PD 22-APR-1999.  
PA (ASAH ) ASAH KASEI KOGYO KK.  
Query Match 10.8%; Score 69.5; DB 2; Length 516;





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ID AAE17596 standard; protein; 557 AA.
DE Human thrombomodulin (TM) mutant, L339A.
PN WO200198352-A2.
PD 27-DEC-2001.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 836
ID AAE17591 standard; protein; 557 AA.
DE Human thrombomodulin (TM) mutant, Y358A.
PN WO200198352-A2.
PD 27-DEC-2001.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 837
ID AAE17595 standard; protein; 557 AA.
DE Human thrombomodulin (TM) mutant, D338A.
PN WO200198352-A2.
PD 27-DEC-2001.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 838
ID AAE17597 standard; protein; 557 AA.
DE Human thrombomodulin (TM) mutant, D349A.
PN WO200198352-A2.
PD 27-DEC-2001.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 839
ID AAE17525 standard; protein; 557 AA.
DE Human thrombomodulin (TM) mutant, M388L.
PN WO200198352-A2.
PD 27-DEC-2001.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 840
ID AAE17529 standard; protein; 557 AA.
DE Human thrombomodulin (TM) mutant, D341A.
PN WO200198352-A2.
PD 27-DEC-2001.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 841
ID AAE17530 standard; protein; 557 AA.
DE Human thrombomodulin (TM) mutant, E343A.
PN WO200198352-A2.
PD 27-DEC-2001.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 842
ID AAE17598 standard; protein; 557 AA.
DE Human thrombomodulin (TM) mutant, E357A.
PN WO200198352-A2.
PD 27-DEC-2001.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 843
ID AAE17527 standard; protein; 557 AA.
DE Human thrombomodulin (TM) mutant, H457Q.
PN WO200198352-A2.
PD 27-DEC-2001.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 844
ID AAE23031 standard; protein; 557 AA.
DE Human thrombomodulin mutant, S474A.
PN WO200217953-A2.
PD 07-MAR-2002.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 845
ID AAE23029 standard; protein; 557 AA.
DE Human thrombomodulin mutant, R456G.
PN WO200217953-A2.
PD 07-MAR-2002.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 846
ID AAE23030 standard; protein; 557 AA.
DE Human thrombomodulin mutant, H457Q.
PN WO200217953-A2.
PD 07-MAR-2002.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 847
ID AAE23028 standard; protein; 557 AA.
DE Human thrombomodulin mutant, M388L.
PN WO200217953-A2.
PD 07-MAR-2002.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 848
ID AD065702 standard; protein; 557 AA.
DE Novel human protein sequence #675.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 10.8%; Score 69.5; DB 8; Length 557;
Best Local Similarity 23.5%; Pred. No. 61;
RESULT 849
ID AB078293 standard; protein; 568 AA.
DE Pseudomonas aeruginosa polypeptide #10468.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.8%; Score 69.5; DB 7; Length 568;
Best Local Similarity 28.8%; Pred. No. 63;
RESULT 850
ID AAP82070 standard; protein; 575 AA.
DE Human thrombomodulin encoded by plasmid p2.1.
PN WO8809811-A.
PD 15-DEC-1988.
PA (NOVO ) NOVO IND AS.
Query Match 10.8%; Score 69.5; DB 1; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 851
ID AAR11534 standard; protein; 575 AA.
DE Human thrombomodulin type II polypeptide.
PN WO9104276-A.
PD 04-APR-1991.
PA (ASAH ) ASahi Kasei Kogyo KK.
Query Match 10.8%; Score 69.5; DB 2; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 852
ID AAR14341 standard; protein; 575 AA.
DE Human thrombomodulin.
PN WO9115514-A.
PD 17-OCT-1991.
PA (SCHD ) SCHERING AG.
Query Match 10.8%; Score 69.5; DB 2; Length 575;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 853
ID AAR20639 standard; protein; 575 AA.
DE Human urinary thrombomodulin.
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PN WO9200325-A.  
PD 09-JAN-1992.  
PA (MOCH ) MOCHIDA PHARM CO LTD.  
Query Match 10.8%; Score 69.5; DB 2; Length 575;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 854  
ID AAR22189 standard; protein; 575 AA.  
DE Sequence of thrombomodulin.  
PN WO9203149-A.  
PD 05-MAR-1992.  
PA (BERL-) BERLEX LAB INC.  
Query Match 10.8%; Score 69.5; DB 2; Length 575;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 855  
ID AAR31572 standard; protein; 575 AA.  
DE Human thrombomodulin.  
PN WO9301282-A1.  
PD 21-JAN-1993.  
PA (BERL-) BERLEX LAB INC.  
Query Match 10.8%; Score 69.5; DB 2; Length 575;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 856  
ID AAR41806 standard; peptide; 575 AA.  
DE Thrombomodulin.  
PN JP05213998-A.  
PD 24-AUG-1993.  
PA (ASAH ) ASahi CHEM IND CO LTD.  
Query Match 10.8%; Score 69.5; DB 2; Length 575;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 857  
ID AAR43031 standard; protein; 575 AA.  
DE Human thrombomodulin.  
PN WO9322447-A1.  
PD 11-NOV-1993.  
PA (ASAH ) ASahi KASRI KOGYO KK.  
Query Match 10.8%; Score 69.5; DB 2; Length 575;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 858  
ID AAW73970 standard; protein; 575 AA.  
DE Human thrombomodulin protein sequence.  
PN US5863760-A.  
PD 26-JAN-1999.  
PA (SCHD ) SCHERING AG.  
Query Match 10.8%; Score 69.5; DB 2; Length 575;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 859  
ID AAE17521 standard; protein; 575 AA.  
DE Human full-length native thrombomodulin (TM).  
PN WO200198352-A2.  
PD 27-DEC-2001.  
PA (SCHD ) SCHERING AG.  
Query Match 10.8%; Score 69.5; DB 5; Length 575;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 860  
ID AAE23026 standard; protein; 575 AA.  
DE Human thrombomodulin protein.  
PN WO200217953-A2.  
PD 07-MAR-2002.  
PA (SCHD ) SCHERING AG.  
Query Match 10.8%; Score 69.5; DB 5; Length 575;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 861  
ID ABG72575 standard; protein; 575 AA.  
DE Human thrombomodulin protein #2 (CD141).  
PN WO200293172-A1.  
PD 21-NOV-2002.  
PA (MILT-) MILTENI BIOTEC INC.  
Query Match 10.8%; Score 69.5; DB 6; Length 575;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 862  
ID ABUS2408 standard; protein; 575 AA.  
DE Human GPCR related protein NOV44a.  
PN WO200279398-A2.

PD 10-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.8%; Score 69.5; DB 6; Length 575;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 863  
ID ABM78950 standard; protein; 575 AA.  
DE Breast cancer specific marker under-expressed in breast cancer.  
PN WO2003073911-A2.  
PD 12-SEP-2003.  
PA (GEOU ) UNIV GEORGETOWN.  
Query Match 10.8%; Score 69.5; DB 7; Length 575;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 864  
ID ADE54760 standard; protein; 575 AA.  
DE Human Protein P07204, SEQ ID NO 565.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 10.8%; Score 69.5; DB 7; Length 575;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 865  
ID ADD48168 standard; protein; 575 AA.  
DE Human Protein NP\_000352, SEQ ID NO 13866.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 10.8%; Score 69.5; DB 7; Length 575;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 866  
ID ADL24151 standard; protein; 575 AA.  
DE Human NOVX polypeptide #98.  
PN US2004002120-A1.  
PD 01-JAN-2004.  
PA (KEKU/) KEKUDA R.  
PA (TCHE/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (PATT/) PATTURAJAN M.  
PA (BURG/) BURGESS C E.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (GORM/) GORMAN L.  
PA (MALX/) MALYANKAR U M.  
PA (BOLD/) BOLDOG F L.  
PA (GUOX/) GUO X.  
PA (SHEN/) SHENOY S G.  
PA (PADI/) PADIGARU M.  
PA (TAUP/) TAUPIER R J.  
PA (MILL/) MILLER C E.  
PA (CASM/) CASHMAN S J.  
PA (PENA/) PENA C E A.  
PA (GANG/) GANGOLLI E A.  
PA (GUSE/) GUSEV V Y.  
PA (SMIT/) SMITHSON G.  
PA (ZERR/) ZERRHUSEN B D.  
PA (GERL/) GERLACH V.  
PA (POCH/) POCHART P F.  
PA (FERN/) FERNANDES E R.  
PA (SHIM/) SHIMKETS R A.  
PA (RASP/) RASTELLI L.  
PA (SPAD/) SPADERNA S K.  
PA (LARO/) LAROCHELLE W J.  
PA (ZHON/) ZHONG M.  
PA (KHRA/) KHRAMTSOV N V.  
PA (VOSS/) VOSS E Z.  
PA (HERR/) HERRMANN J L.  
Query Match 10.8%; Score 69.5; DB 8; Length 575;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 867  
ID ADN04006 standard; protein; 575 AA.  
DE Antipsoriatic protein sequence #198.

PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 69.5; DB 8; Length 575;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 868  
ID ADP12616 standard; protein; 575 AA.  
DE Protein encoded by mRNA of the invention #226.  
PN WO2004042346-A2.  
PD 21-MAY-2004.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Query Match 10.8%; Score 69.5; DB 8; Length 575;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 869  
ID ADO28681 standard; protein; 575 AA.  
DE Human thrombomodulin protein SEQ ID NO:110.  
PN WO2004044178-A2.  
PD 27-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 69.5; DB 8; Length 575;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 870  
ID ADP79506 standard; protein; 575 AA.  
DE Human thrombomodulin.  
PN WO2004050844-A2.  
PD 17-JUN-2004.  
PA (BIOV-) BIOVEC LLC.  
Query Match 10.8%; Score 69.5; DB 8; Length 575;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 871  
ID ADR32191 standard; protein; 575 AA.  
DE Human thrombomodulin SEQ ID NO:2.  
PN WO2004076635-A2.  
PD 10-SEP-2004.  
PA (BIOV-) BIOVEC BV.  
Query Match 10.8%; Score 69.5; DB 8; Length 575;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 872  
ID ADU06321 standard; protein; 575 AA.  
DE Novel bronchial cancer-associated human protein seqID545.  
PN DE10316701-A1.  
PD 04-NOV-2004.  
PA (HINZ/) HINZMANN B.  
PA (HERM/) HERMANN K.  
PA (CAST/) HEIDEN CASTANOS-VELEZ E.  
Query Match 10.8%; Score 69.5; DB 8; Length 575;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 873  
ID AEC90400 standard; protein; 575 AA.  
DE Human thrombomodulin SEQ ID NO 4.  
PN WO2005081926-A2.  
PD 09-SEP-2005.  
PA (UYEM-) UNIV EMORY.  
Query Match 10.8%; Score 69.5; DB 9; Length 575;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 874  
ID ABG72572 standard; protein; 631 AA.  
DE Human thrombomodulin protein #1 (CD141).  
PN WO200293172-A1.  
PD 21-NOV-2002.  
PA (MILT-) MILTENYI BIOTECH INC.  
Query Match 10.8%; Score 69.5; DB 6; Length 631;  
Best Local Similarity 23.5%; Pred. No. 71;  
RESULT 875  
ID ADN05602 standard; protein; 681 AA.  
DE Antipsoriatic protein sequence #966.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.8%; Score 69.5; DB 8; Length 681;  
Best Local Similarity 23.5%; Pred. No. 78;  
RESULT 876  
ID AAU33693 standard; protein; 200 AA.

DE Pseudomonas aeruginosa cellular proliferation protein #137.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 10.7%; Score 69; DB 4; Length 200;  
Best Local Similarity 25.8%; Pred. No. 21;  
RESULT 877  
ID ABU15655 standard; protein; 200 AA.  
DE Protein encoded by Prokaryotic essential gene #1182.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 10.7%; Score 69; DB 6; Length 200;  
Best Local Similarity 25.8%; Pred. No. 21;  
RESULT 878  
ID AAG23831 standard; protein; 214 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27282.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 10.7%; Score 69; DB 3; Length 214;  
Best Local Similarity 35.7%; Pred. No. 22;  
RESULT 879  
ID ABO76121 standard; protein; 229 AA.  
DE Pseudomonas aeruginosa polypeptide #8296.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.7%; Score 69; DB 7; Length 229;  
Best Local Similarity 25.8%; Pred. No. 24;  
RESULT 880  
ID ABG29324 standard; protein; 234 AA.  
DE Novel human diagnostic protein #29315.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.7%; Score 69; DB 4; Length 234;  
Best Local Similarity 29.1%; Pred. No. 25;  
RESULT 881  
ID ADC33348 standard; protein; 234 AA.  
DE Human novel contig-encoded polypeptide sequence, SEQ ID NO:3430.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.7%; Score 69; DB 7; Length 234;  
Best Local Similarity 29.1%; Pred. No. 25;  
RESULT 882  
ID AAG50626 standard; protein; 252 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64177.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 10.7%; Score 69; DB 3; Length 252;  
Best Local Similarity 35.7%; Pred. No. 27;  
RESULT 883  
ID ABO72740 standard; protein; 261 AA.  
DE Pseudomonas aeruginosa polypeptide #4915.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.7%; Score 69; DB 7; Length 261;  
Best Local Similarity 24.8%; Pred. No. 28;  
RESULT 884  
ID AAU72792 standard; protein; 271 AA.  
DE Human anticancer protein #5.  
PN CN1313298-A.  
PD 19-SEP-2001.  
PA (SHAN-) SHANGHAI INST ONCOLOGY.  
Query Match 10.7%; Score 69; DB 5; Length 271;  
Best Local Similarity 31.9%; Pred. No. 30;  
RESULT 885  
ID AAG50625 standard; protein; 293 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64176.  
PN EP1033405-A2.  
PD 06-SEP-2000.

Query Match  
Best Local Similarity 10.7%; Score 69; DB 3; Length 293;  
RESULT 886  
ID AAG21634 standard; protein; 299 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24260.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 10.7%; Score 69; DB 3; Length 299;  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 31.0%; Pred. No. 33;  
RESULT 887  
ID AAG50624 standard; protein; 299 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64175.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 10.7%; Score 69; DB 3; Length 299;  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 35.7%; Pred. No. 33;  
RESULT 888  
ID AAG50623 standard; protein; 400 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64173.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 10.7%; Score 69; DB 3; Length 400;  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 35.7%; Pred. No. 47;  
RESULT 889  
ID AAG21633 standard; protein; 400 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24259.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 10.7%; Score 69; DB 3; Length 400;  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 31.0%; Pred. No. 47;  
RESULT 890  
ID AAG21632 standard; protein; 418 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24258.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 10.7%; Score 69; DB 3; Length 418;  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 31.0%; Pred. No. 50;  
RESULT 891  
ID AAG50622 standard; protein; 418 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64172.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 10.7%; Score 69; DB 3; Length 418;  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 35.7%; Pred. No. 50;  
RESULT 892  
ID AAG50621 standard; protein; 420 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64171.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 10.7%; Score 69; DB 3; Length 420;  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 35.7%; Pred. No. 50;  
RESULT 893  
ID ADT55510 standard; protein; 430 AA.  
DE Plant polypeptide, SEQ ID 5587.  
PN US2004216190-A1.  
PD 28-OCT-2004.  
PA (KOVA/) KOVALIC D K.  
Query Match  
Best Local Similarity 10.7%; Score 69; DB 8; Length 430;  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 35.7%; Pred. No. 52;  
RESULT 894  
ID AED19037 standard; protein; 454 AA.  
DE Cherry salmon fatty acid desaturase gene, SEQ ID NO:2.  
PN WO2005094570-A1.  
PD 13-OCT-2005.  
PA (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.  
Query Match  
Best Local Similarity 10.7%; Score 69; DB 9; Length 454;  
PD 07-MAY-2003.  
Query Match  
Best Local Similarity 29.3%; Pred. No. 55;  
RESULT 895  
ID ADB64137 standard; protein; 1077 AA.  
DE Human protein encoded by clone CTONG20020950.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match  
Best Local Similarity 10.7%; Score 69; DB 7; Length 1077;  
PD 03-JUL-2003.  
Query Match  
Best Local Similarity 28.1%; Pred. No. 1.5e+02;  
RESULT 896  
ID ADD01192 standard; protein; 1081 AA.  
DE Human nucleic acid-associated protein NAAP-30 SEQ ID NO:30.  
PN WO2003054219-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 10.7%; Score 69; DB 7; Length 1081;  
PD 03-JUL-2003.  
Query Match  
Best Local Similarity 28.1%; Pred. No. 1.5e+02;  
RESULT 897  
ID ADX73027 standard; protein; 326 AA.  
DE Plant full length insert polypeptide seqid 42393.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match  
Best Local Similarity 10.6%; Score 68.5; DB 8; Length 326;  
PD 18-DEC-1997.  
Query Match  
Best Local Similarity 29.9%; Pred. No. 42;  
RESULT 898  
ID AAW37261 standard; protein; 356 AA.  
DE Rat vitamin D receptor isoform protein (VDR1).  
PN WO9747172-A1.  
PD 18-DEC-1997.  
PA (CHUS) CHUGAI SEIYAKU KK.  
Query Match  
Best Local Similarity 10.6%; Score 68.5; DB 2; Length 356;  
PD 17-DEC-1998.  
Query Match  
Best Local Similarity 30.1%; Pred. No. 47;  
RESULT 899  
ID AAW94622 standard; protein; 356 AA.  
DE Rat vitamin D receptor isoform protein VDR1.  
PN WO9856908-A1.  
PD 17-DEC-1998.  
PA (CHUS) CHUGAI SEIYAKU KK.  
Query Match  
Best Local Similarity 10.6%; Score 68.5; DB 2; Length 356;  
PD 17-DEC-1998.  
Query Match  
Best Local Similarity 30.1%; Pred. No. 47;  
RESULT 900  
ID AAB84255 standard; protein; 376 AA.  
DE Amino acid sequence of a human nuclear vitamin D receptor mutant.  
PN WO200138193-A1.  
PD 31-MAY-2001.  
PA (CNRS) CENT NAT RECH SCI.  
Query Match  
Best Local Similarity 10.6%; Score 68.5; DB 4; Length 376;  
PD 31-MAY-2001.  
Query Match  
Best Local Similarity 30.1%; Pred. No. 50;  
RESULT 901  
ID ADP05823 standard; protein; 422 AA.  
DE Mouse nuclear receptor protein SeqID197.  
PN WO2004045369-A2.  
PD 03-JUN-2004.  
PA (NURA-) NURA INC.  
Query Match  
Best Local Similarity 10.6%; Score 68.5; DB 8; Length 422;  
PD 03-JUN-2004.  
Query Match  
Best Local Similarity 30.1%; Pred. No. 58;  
RESULT 902  
ID AAW47509 standard; protein; 423 AA.  
DE Rat vitamin D receptor (VDR0).  
PN WO9747172-A1.  
PD 18-DEC-1997.  
PA (CHUS) CHUGAI SEIYAKU KK.  
Query Match  
Best Local Similarity 10.6%; Score 68.5; DB 2; Length 423;  
PD 18-DEC-1997.  
Query Match  
Best Local Similarity 30.1%; Pred. No. 58;  
RESULT 903  
ID AAW94623 standard; protein; 423 AA.  
DE Rat vitamin D receptor protein VDR0.  
PN WO9856908-A1.  
PD 17-DEC-1998.  
PA (CHUS) CHUGAI SEIYAKU KK.  
Query Match  
Best Local Similarity 10.6%; Score 68.5; DB 2; Length 423;  
PD 17-DEC-1998.  
Query Match  
Best Local Similarity 30.1%; Pred. No. 58;  
RESULT 904  
ID AAW94623 standard; protein; 423 AA.  
DE Rat vitamin D receptor protein VDR0.  
PN WO9856908-A1.  
PD 17-DEC-1998.  
PA (CHUS) CHUGAI SEIYAKU KK.  
Query Match  
Best Local Similarity 10.6%; Score 68.5; DB 2; Length 423;  
PD 17-DEC-1998.  
Query Match  
Best Local Similarity 30.1%; Pred. No. 58;  
RESULT 904

ID AAW68156 standard; protein; 427 AA.  
DE Human vitamin D receptor.  
PN WO9831835-A1.  
PD 23-JUL-1998.  
PA (UYNA-) UNIV MARYLAND BALTIMORE.  
PA (UYPI-) UNIV PITTSBURGH.  
Query Match 10.6%; Score 68.5; DB 2; Length 427;  
Best Local Similarity 30.1%; Pred. No. 58;  
RESULT 905  
ID AAY09064 standard; protein; 427 AA.  
DE Human vitamin D receptor (VDR) gene transcript 11 amino acid sequence.  
PN WO9916872-A1.  
PD 08-APR-1999.  
PA (GARV-) GARVAN INST MEDICAL RES.  
Query Match 10.6%; Score 68.5; DB 2; Length 427;  
Best Local Similarity 30.1%; Pred. No. 58;  
RESULT 906  
ID AAB84254 standard; protein; 427 AA.  
DE Amino acid sequence of a human nuclear vitamin D receptor (VDR).  
PN WO200138393-A1.  
PD 31-MAY-2001.  
PA (CNRS) CENT NAT RECH SCI.  
Query Match 10.6%; Score 68.5; DB 4; Length 427;  
Best Local Similarity 30.1%; Pred. No. 58;  
RESULT 907  
ID ADB99956 standard; protein; 427 AA.  
DE Human vitamin D nuclear receptor.  
PN WO2003041657-A2.  
PD 22-MAY-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 10.6%; Score 68.5; DB 7; Length 427;  
Best Local Similarity 30.1%; Pred. No. 58;  
RESULT 908  
ID ADL83243 standard; protein; 427 AA.  
DE Human PRO4854, SEQ ID 445.  
PN WO2004024097-A2.  
PD 25-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 10.6%; Score 68.5; DB 8; Length 427;  
Best Local Similarity 30.1%; Pred. No. 58;  
RESULT 909  
ID ADP05821 standard; protein; 427 AA.  
DE Human nuclear receptor protein SeqId195.  
PN WO2004045369-A2.  
PD 03-JUN-2004.  
PA (NURA-) NURA INC.  
Query Match 10.6%; Score 68.5; DB 8; Length 427;  
Best Local Similarity 30.1%; Pred. No. 58;  
RESULT 910  
ID ADP54492 standard; protein; 427 AA.  
DE Human PRO protein sequence SEQ ID NO:468.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 10.6%; Score 68.5; DB 8; Length 427;  
Best Local Similarity 30.1%; Pred. No. 58;  
RESULT 911  
ID ADX05510 standard; protein; 427 AA.  
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 75.  
PN WO2005012875-A2.  
PD 10-FEB-2005.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 10.6%; Score 68.5; DB 9; Length 427;  
Best Local Similarity 30.1%; Pred. No. 58;  
RESULT 912  
ID ADY15298 standard; protein; 427 AA.  
DE PRO polypeptide SEQ ID NO 1104.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH) GENENTECH INC.  
Query Match 10.6%; Score 68.5; DB 9; Length 427;  
Best Local Similarity 30.1%; Pred. No. 58;  
RESULT 913  
ID ADX77856 standard; protein; 849 AA.  
DE PRO polypeptide SEQ ID NO 1106.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH) GENENTECH INC.  
Query Match 10.6%; Score 68.5; DB 9; Length 427;  
Best Local Similarity 30.1%; Pred. No. 58;  
RESULT 914  
ID ADZ21386 standard; protein; 427 AA.  
DE Vitamin D receptor.  
PN WO2005033291-A2.  
PD 14-APR-2005.  
PA (UYRP) UNIV ROCHESTER.  
Query Match 10.6%; Score 68.5; DB 9; Length 427;  
Best Local Similarity 30.1%; Pred. No. 58;  
RESULT 915  
ID AEC92031 standard; protein; 427 AA.  
DE Human vitamin D3 receptor (VDR) protein, SEQ ID: 2.  
PN US2005202515-A1.  
PD 15-SEP-2005.  
PA (AMHP) WYETH.  
Query Match 10.6%; Score 68.5; DB 9; Length 427;  
Best Local Similarity 30.1%; Pred. No. 58;  
RESULT 916  
ID AED54296 standard; protein; 427 AA.  
DE Human VDR1 receptor polypeptide.  
PN WO2005101022-A2.  
PD 27-OCT-2005.  
PA (FARB) BAYER HEALTHCARE AG.  
Query Match 10.6%; Score 68.5; DB 9; Length 427;  
Best Local Similarity 30.1%; Pred. No. 58;  
RESULT 917  
ID AAY09036 standard; protein; 450 AA.  
DE Human vitamin D receptor (VDR) gene transcript 9 amino acid sequence.  
PN WO9916872-A1.  
PD 08-APR-1999.  
PA (GARV-) GARVAN INST MEDICAL RES.  
Query Match 10.6%; Score 68.5; DB 2; Length 450;  
Best Local Similarity 30.1%; Pred. No. 62;  
RESULT 918  
ID AAY09035 standard; protein; 477 AA.  
DE Human vitamin D receptor (VDR) gene transcript 6 amino acid sequence.  
PN WO9916872-A1.  
PD 08-APR-1999.  
PA (GARV-) GARVAN INST MEDICAL RES.  
Query Match 10.6%; Score 68.5; DB 2; Length 477;  
Best Local Similarity 30.1%; Pred. No. 67;  
RESULT 919  
ID ADJ33699 standard; protein; 213 AA.  
DE Protein of the invention SEQ ID NO:676.  
PN WO200187917-A1.  
PD 22-NOV-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.6%; Score 68; DB 5; Length 213;  
Best Local Similarity 24.4%; Pred. No. 29;  
RESULT 920  
ID ABO77058 standard; protein; 451 AA.  
DE Pseudomonas aeruginosa polypeptide #9233.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.6%; Score 68; DB 7; Length 451;  
Best Local Similarity 28.8%; Pred. No. 71;  
RESULT 921  
ID ABO73678 standard; protein; 613 AA.  
DE Pseudomonas aeruginosa polypeptide #5853.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.6%; Score 68; DB 7; Length 613;  
Best Local Similarity 31.0%; Pred. No. 1e+02;  
RESULT 922  
ID ADX77856 standard; protein; 849 AA.

DE Plant full length insert polypeptide seqid 47222.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOV/) CAO Y.  
Query Match 10.6%; Score 68; DB 8; Length 849;  
Best Local Similarity 25.0%; Pred. No. 1.5e+02;  
RESULT 923  
ID ABO73085 standard; protein; 863 AA.  
DE Pseudomonas aeruginosa polypeptide #5260.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.6%; Score 68; DB 7; Length 863;  
Best Local Similarity 27.1%; Pred. No. 1.5e+02;  
RESULT 924  
ID ADZ21348 standard; protein; 70 AA.  
DE Vitamin D receptor DNA binding domain.  
PN WO2005033291-A2.  
PD 14-APR-2005.  
PA (UYRP) UNIV ROCHESTER.  
Query Match 10.5%; Score 67.5; DB 9; Length 70;  
Best Local Similarity 32.3%; Pred. No. 8.8;  
RESULT 925  
ID ABO76684 standard; protein; 521 AA.  
DE Pseudomonas aeruginosa polypeptide #8859.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.5%; Score 67.5; DB 7; Length 521;  
Best Local Similarity 28.3%; Pred. No. 97;  
RESULT 926  
ID ABO67969 standard; protein; 690 AA.  
DE Pseudomonas aeruginosa polypeptide #144.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.5%; Score 67.5; DB 7; Length 690;  
Best Local Similarity 28.7%; Pred. No. 1.4e+02;  
RESULT 927  
ID ABM95053 standard; protein; 1076 AA.  
DE Rice abiotic stress responsive polypeptide SEQ ID NO:7299.  
PN WO2003008540-A2.  
PD 30-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 10.5%; Score 67.5; DB 7; Length 1076;  
Best Local Similarity 22.6%; Pred. No. 2.3e+02;  
RESULT 928  
ID ABO69387 standard; protein; 285 AA.  
DE Pseudomonas aeruginosa polypeptide #1562.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.4%; Score 67; DB 7; Length 285;  
Best Local Similarity 24.2%; Pred. No. 54;  
RESULT 929  
ID RAO16407 standard; protein; 426 AA.  
DE Human nucleic acid-associated protein (NAAP) - SEQ ID NO 4.  
PN WO200300864-A2.  
PD 03-JAN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 10.4%; Score 67; DB 6; Length 426;  
Best Local Similarity 26.8%; Pred. No. 87;  
RESULT 930  
ID ABE85564 standard; protein; 454 AA.  
DE PUGA pathway enzyme delta-5 desaturase SEQ ID NO 106.  
PN WO2005118814-A2.  
PD 15-DEC-2005.  
PA (FLUX-) FLUXOME SCI AS.

Query Match 10.4%; Score 67; DB 10; Length 454;  
Best Local Similarity 29.5%; Pred. No. 94;  
RESULT 931  
ID ADS44937 standard; protein; 475 AA.  
DE Bacterial polypeptide #23367.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOV/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 10.4%; Score 67; DB 8; Length 475;  
Best Local Similarity 22.5%; Pred. No. 99;  
RESULT 932  
ID AAU28084 standard; protein; 529 AA.  
DE Novel human secretory protein, Seq ID No 253.  
PN WO200166689-A2.  
PD 13-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.4%; Score 67; DB 4; Length 529;  
Best Local Similarity 26.8%; Pred. No. 1.1e+02;  
RESULT 933  
ID ABO73410 standard; protein; 209 AA.  
DE Pseudomonas aeruginosa polypeptide #5585.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.3%; Score 66.5; DB 7; Length 209;  
Best Local Similarity 31.6%; Pred. No. 42;  
RESULT 934  
ID ABO69685 standard; protein; 333 AA.  
DE Pseudomonas aeruginosa polypeptide #1860.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.3%; Score 66.5; DB 7; Length 333;  
Best Local Similarity 22.8%; Pred. No. 74;  
RESULT 935  
ID AAR07294 standard; protein; 418 AA.  
DE Chicken ovalbumin upstream promoter transcription factor.  
PN EP392691-A.  
PD 17-OCT-1990.  
PA (BAYU) BAYLOR COLLEGE MEDICINE.  
PA (OMAL/) OMALLEY B W.  
Query Match 10.3%; Score 66.5; DB 2; Length 418;  
Best Local Similarity 26.5%; Pred. No. 97;  
RESULT 936  
ID ADE62161 standard; protein; 419 AA.  
DE Rat Protein AAA83437, SEQ ID NO 8090.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 10.3%; Score 66.5; DB 7; Length 419;  
Best Local Similarity 26.5%; Pred. No. 97;  
RESULT 937  
ID ADE62157 standard; protein; 419 AA.  
DE Rat Protein AAA83437, SEQ ID NO 8086.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 10.3%; Score 66.5; DB 7; Length 419;  
Best Local Similarity 26.5%; Pred. No. 97;  
RESULT 938  
ID ADP05633 standard; protein; 422 AA.  
DE Mouse nuclear receptor protein SeqID7.  
PN WO2004045369-A2.  
PD 03-JUN-2004.  
PA (NURA-) NURA INC.  
Query Match 10.3%; Score 66.5; DB 8; Length 422;  
Best Local Similarity 26.5%; Pred. No. 98;

RESULT 939  
ID AAU84296 standard; protein; 423 AA.  
DE Human endometrial cancer related protein, NR2F1.  
PN WO200209573-A2.  
PD 07-FEB-2002.  
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match 10.3%; Score 66.5; DB 5; Length 423;  
Best Local Similarity 26.5%; Pred. No. 98;  
RESULT 940  
ID ADE62163 standard; protein; 423 AA.  
DE Human Protein NP\_005645, SEQ ID NO 8092.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 10.3%; Score 66.5; DB 7; Length 423;  
Best Local Similarity 26.5%; Pred. No. 98;  
RESULT 941  
ID ADE62159 standard; protein; 423 AA.  
DE Human Protein NP\_005645, SEQ ID NO 8088.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 10.3%; Score 66.5; DB 7; Length 423;  
Best Local Similarity 26.5%; Pred. No. 98;  
RESULT 942  
ID ADN95495 standard; protein; 423 AA.  
DE Human BEC/LEC-related protein sequence SeqID418.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW) LUDWIG INST CANCER RES.  
PA (LICN) LICENTIA LTD.  
Query Match 10.3%; Score 66.5; DB 7; Length 423;  
Best Local Similarity 26.5%; Pred. No. 98;  
RESULT 943  
ID ADP05631 standard; protein; 423 AA.  
DE Human nuclear receptor protein SeqIDS.  
PN WO2004045369-A2.  
PD 03-JUN-2004.  
PA (NURA) NURA INC.  
Query Match 10.3%; Score 66.5; DB 8; Length 423;  
Best Local Similarity 26.5%; Pred. No. 98;  
RESULT 944  
ID ADY34352 standard; protein; 423 AA.  
DE Human nuclear hormone receptor NR2F1.  
PN WO2005017112-A2.  
PD 24-FEB-2005.  
PA (IMMU) IMMUSOL INC.  
Query Match 10.3%; Score 66.5; DB 9; Length 423;  
Best Local Similarity 26.5%; Pred. No. 98;  
RESULT 945  
ID AD209795 standard; protein; 423 AA.  
DE Human breast cancer marker NR2F1 protein.  
PN EP1522594-A2.  
PD 13-APR-2005.  
PA (FARB) BAYER HEALTHCARE AG.  
Query Match 10.3%; Score 66.5; DB 9; Length 423;  
Best Local Similarity 26.5%; Pred. No. 98;  
RESULT 946  
ID AEC01577 standard; protein; 423 AA.  
DE Human nuclear receptor subfamily 2 group F member 1 protein, SEQ ID: 10.  
PN US2005176030-A1.  
PD 11-AUG-2005.  
PA (GANL) GAN L.  
PA (GONZ) GONZALEZ-ZULUETA M.  
PA (YESS) YE S.  
PA (URFE) URFER R.  
PA (NIKO) NIKOLICH K.  
Query Match 10.3%; Score 66.5; DB 9; Length 423;  
Best Local Similarity 26.5%; Pred. No. 98;  
RESULT 947  
ID AAU45310 standard; protein; 913 AA.

DE Propionibacterium acnes immunogenic protein #6206.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI) CORIXA CORP.  
Query Match 10.3%; Score 66.5; DB 4; Length 913;  
Best Local Similarity 28.4%; Pred. No. 2.5e+02;  
RESULT 948  
ID ABM41829 standard; protein; 913 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #6505.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI) CORIXA CORP.  
Query Match 10.3%; Score 66.5; DB 6; Length 913;  
Best Local Similarity 28.4%; Pred. No. 2.5e+02;  
RESULT 949  
ID AAP81770 standard; protein; 3210 AA.  
DE Deduced sequence encoded by middle reading frame of cDNA clone HIV-2  
SBL/ISV of HIV related retrovirus strain.  
PN WO8808449-A.  
PD 03-NOV-1988.  
PA (SBL) SBL STATENS BAKTERI.  
PA (STAT) STATENS BAKTERIOLOGISKA LAB.  
PA (STAT) STATENS BAKTERIOLOGISKA LAB.  
Query Match 10.3%; Score 66.5; DB 1; Length 3210;  
Best Local Similarity 26.4%; Pred. No. 1.1e+03;  
RESULT 950  
ID ADO29248 standard; protein; 3301 AA.  
DE Mouse GPCR CELSR3, SEQ ID NO:349.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM) PRIMAL INC.  
Query Match 10.3%; Score 66.5; DB 8; Length 3301;  
Best Local Similarity 26.8%; Pred. No. 1.1e+03;  
RESULT 951  
ID AAU48730 standard; protein; 162 AA.  
DE Propionibacterium acnes immunogenic protein #9626.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI) CORIXA CORP.  
Query Match 10.2%; Score 66; DB 4; Length 162;  
Best Local Similarity 35.1%; Pred. No. 36;  
RESULT 952  
ID ABM45249 standard; protein; 162 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #9925.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI) CORIXA CORP.  
Query Match 10.2%; Score 66; DB 6; Length 162;  
Best Local Similarity 35.1%; Pred. No. 36;  
RESULT 953  
ID AB083736 standard; protein; 178 AA.  
DE Pseudomonas aeruginosa polypeptide #15911.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO) GENOME THERAPEUTICS CORP.  
Query Match 10.2%; Score 66; DB 7; Length 178;  
Best Local Similarity 29.1%; Pred. No. 40;  
RESULT 954  
ID AB076457 standard; protein; 518 AA.  
DE Pseudomonas aeruginosa polypeptide #8632.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO) GENOME THERAPEUTICS CORP.  
Query Match 10.2%; Score 66; DB 7; Length 518;  
Best Local Similarity 24.8%; Pred. No. 1.4e+02;  
RESULT 955  
ID AAU13905 standard; protein; 1539 AA.  
DE Human SMCY protein.  
PN WO9710267-A1.  
PD 20-MAR-1997.  
PA (PROM) PROMEGA CORP.  
Query Match 10.2%; Score 66; DB 2; Length 1539;  
Best Local Similarity 26.7%; Pred. No. 5.2e+02;



RESULT 956  
ID ADM33397 standard; protein; 1539 AA.  
DE Human PRO71282 protein SEQ ID NO:14.  
PN WO2004028447-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 66; DB 8; Length 1539;  
Best Local Similarity 26.7%; Pred. No. 5.2e+02;  
RESULT 957  
ID ADP12536 standard; protein; 1539 AA.  
DE Protein encoded by mRNA of the invention #146.  
PN WO2004042346-A2.  
PD 21-MAY-2004.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Query Match 10.2%; Score 66; DB 8; Length 1539;  
Best Local Similarity 26.7%; Pred. No. 5.2e+02;  
RESULT 958  
ID ABA24048 standard; protein; 1539 AA.  
DE Human PRO polypeptide SEQ ID NO 590.  
PN WO2005051988-A2.  
PD 09-JUN-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 66; DB 9; Length 1539;  
Best Local Similarity 26.7%; Pred. No. 5.2e+02;  
RESULT 959  
ID AAO21341 standard; protein; 106 AA.  
DE Arabidopsis thaliana KCP-like protein, SEQ ID NO 96.  
PN WO200222821-A2.  
PD 21-MAR-2002.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 10.2%; Score 65.5; DB 5; Length 106;  
Best Local Similarity 21.2%; Pred. No. 25;  
RESULT 960  
ID ABO76562 standard; protein; 201 AA.  
DE Pseudomonas aeruginosa polypeptide #8737.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.2%; Score 65.5; DB 7; Length 201;  
Best Local Similarity 25.0%; Pred. No. 53;  
RESULT 961  
ID ABG29970 standard; protein; 222 AA.  
DE Novel human diagnostic protein #29961.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.2%; Score 65.5; DB 4; Length 222;  
Best Local Similarity 23.0%; Pred. No. 59;  
RESULT 962  
ID ABO76208 standard; protein; 279 AA.  
DE Pseudomonas aeruginosa polypeptide #8383.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.2%; Score 65.5; DB 7; Length 279;  
Best Local Similarity 28.0%; Pred. No. 78;  
RESULT 963  
ID ADX80612 standard; protein; 326 AA.  
DE Plant full length insert polypeptide seqid 49978.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOV/) CAO Y.  
Query Match 10.2%; Score 65.5; DB 8; Length 326;  
Best Local Similarity 28.7%; Pred. No. 94;  
RESULT 964  
ID ABO74508 standard; protein; 342 AA.  
DE Pseudomonas aeruginosa polypeptide #6683.  
PN US6551795-B1.

PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.2%; Score 65.5; DB 7; Length 342;  
Best Local Similarity 26.9%; Pred. No. 1e+02;  
RESULT 965  
ID ADQ96186 standard; protein; 420 AA.  
DE T cell activation associated protein #182.  
PN WO2004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH KASEI PHARMA CORP.  
Query Match 10.2%; Score 65.5; DB 8; Length 420;  
Best Local Similarity 25.0%; Pred. No. 1.3e+02;  
RESULT 966  
ID ADQ96188 standard; protein; 420 AA.  
DE T cell activation associated protein #183.  
PN WO2004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH KASEI PHARMA CORP.  
Query Match 10.2%; Score 65.5; DB 8; Length 420;  
Best Local Similarity 25.0%; Pred. No. 1.3e+02;  
RESULT 967  
ID RAY02383 standard; protein; 704 AA.  
DE Polypeptide identified by the signal sequence trap method.  
PN WO9918126-A1.  
PD 15-APR-1999.  
PA (ONOV ) ONO PHARM CO LTD.  
Query Match 10.2%; Score 65.5; DB 2; Length 704;  
Best Local Similarity 25.0%; Pred. No. 2.4e+02;  
RESULT 968  
ID AAY15223 standard; protein; 706 AA.  
DE Human receptor protein (HURP) 2 amino acid sequence.  
PN WO9941375-A2.  
PD 19-AUG-1999.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 10.2%; Score 65.5; DB 2; Length 706;  
Best Local Similarity 25.0%; Pred. No. 2.4e+02;  
RESULT 969  
ID ABUS6726 standard; protein; 706 AA.  
DE Lung cancer-associated polypeptide #319.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 10.2%; Score 65.5; DB 6; Length 706;  
Best Local Similarity 25.0%; Pred. No. 2.4e+02;  
RESULT 970  
ID ABUS5901 standard; protein; 706 AA.  
DE Human protein Frizzled-6.  
PN WO200277204-A2.  
PD 03-OCT-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match 10.2%; Score 65.5; DB 6; Length 706;  
Best Local Similarity 25.0%; Pred. No. 2.4e+02;  
RESULT 971  
ID AAE34055 standard; protein; 706 AA.  
DE FZD6 protein.  
PN WO200290992-A2.  
PD 14-NOV-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match 10.2%; Score 65.5; DB 6; Length 706;  
Best Local Similarity 25.0%; Pred. No. 2.4e+02;  
RESULT 972  
ID ADC86003 standard; protein; 706 AA.  
DE Human GPCR protein SEQ ID NO:456.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 10.2%; Score 65.5; DB 7; Length 706;  
Best Local Similarity 25.0%; Pred. No. 2.4e+02;  
RESULT 973  
ID ADG74267 standard; protein; 706 AA.  
DE Human frizzled protein, SEQ ID NO 52.  
PN WO200292635-A2.

PD 21-NOV-2002.  
PA (RECG ) UNIV CALIFORNIA.  
Query Match 10.2%; Score 65.5; DB 7; Length 706;  
Best Local Similarity 25.0%; Pred. No. 2.4e+02;  
RESULT 974  
ID ADN39178 standard; protein; 706 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:496.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 10.2%; Score 65.5; DB 7; Length 706;  
Best Local Similarity 25.0%; Pred. No. 2.4e+02;  
RESULT 975  
ID ADN40014 standard; protein; 706 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C384.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 10.2%; Score 65.5; DB 7; Length 706;  
Best Local Similarity 25.0%; Pred. No. 2.4e+02;  
RESULT 976  
ID ADO29335 standard; protein; 706 AA.  
DE Human GPCR FZD6, SEQ ID NO:436.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 10.2%; Score 65.5; DB 8; Length 706;  
Best Local Similarity 25.0%; Pred. No. 2.4e+02;  
RESULT 977  
ID ADO22262 standard; protein; 706 AA.  
DE Human FZD6 protein (homologue of Drosophila frizzled).  
PN WO2004042028-A2.  
PD 21-MAY-2004.  
PA (RECG ) UNIV CALIFORNIA.  
Query Match 10.2%; Score 65.5; DB 8; Length 706;  
Best Local Similarity 25.0%; Pred. No. 2.4e+02;  
RESULT 978  
ID ADQ96190 standard; protein; 706 AA.  
DE T cell activation associated protein #184.  
PN WO2004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH KASEI PHARMA CORP.  
Query Match 10.2%; Score 65.5; DB 8; Length 706;  
Best Local Similarity 25.0%; Pred. No. 2.4e+02;  
RESULT 979  
ID ADQ96192 standard; protein; 706 AA.  
DE T cell activation associated protein #185.  
PN WO2004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH KASEI PHARMA CORP.  
Query Match 10.2%; Score 65.5; DB 8; Length 706;  
Best Local Similarity 25.0%; Pred. No. 2.4e+02;  
RESULT 980  
ID ADY15220 standard; protein; 706 AA.  
DE PRO polypeptide SEQ ID NO 1026.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 65.5; DB 9; Length 706;  
Best Local Similarity 25.0%; Pred. No. 2.4e+02;  
RESULT 981  
ID ADY19746 standard; protein; 706 AA.  
DE PRO polypeptide SEQ ID NO 5552.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 65.5; DB 9; Length 706;  
Best Local Similarity 25.0%; Pred. No. 2.4e+02;  
RESULT 982  
ID AEA51354 standard; protein; 706 AA.  
DE Human protein expressed during angiogenesis, NOC8003L17.  
PN WO2005054426-A2.  
PD 16-JUN-2005.

PA (ANGI-) ANGIOGENETICS SWEDEN AB.  
Query Match 10.2%; Score 65.5; DB 9; Length 706;  
Best Local Similarity 25.0%; Pred. No. 2.4e+02;  
RESULT 983  
ID AEB28130 standard; protein; 706 AA.  
DE Human Fizzled receptor FZD6 protein.  
PN WO2005063966-A2.  
PD 14-JUL-2005.  
PA (AXAR-) AXARON BIOSCIENCE AG.  
Query Match 10.2%; Score 65.5; DB 9; Length 706;  
Best Local Similarity 25.0%; Pred. No. 2.4e+02;  
RESULT 984  
ID ABM69665 standard; protein; 137 AA.  
DE Photorhabdus luminescens protein sequence #2762.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 10.1%; Score 65; DB 6; Length 137;  
Best Local Similarity 24.3%; Pred. No. 38;  
RESULT 985  
ID AAB94570 standard; protein; 152 AA.  
DE Human protein sequence SEQ ID NO:15353.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 10.1%; Score 65; DB 4; Length 152;  
Best Local Similarity 29.2%; Pred. No. 43;  
RESULT 986  
ID ABO70303 standard; protein; 190 AA.  
DE Pseudomonas aeruginosa polypeptide #2478.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.1%; Score 65; DB 7; Length 190;  
Best Local Similarity 21.1%; Pred. No. 56;  
RESULT 987  
ID ABO70829 standard; protein; 274 AA.  
DE Pseudomonas aeruginosa polypeptide #3004.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.1%; Score 65; DB 7; Length 274;  
Best Local Similarity 28.9%; Pred. No. 87;  
RESULT 988  
ID AAB66685 standard; protein; 305 AA.  
DE ASH2 clone protein.  
PN WO200102828-A2.  
PD 11-JAN-2001.  
PA (TULA-) TULARIK INC.  
Query Match 10.1%; Score 65; DB 4; Length 305;  
Best Local Similarity 28.8%; Pred. No. 99;  
RESULT 989  
ID ABG28722 standard; protein; 321 AA.  
DE Novel human diagnostic protein #28713.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.1%; Score 65; DB 4; Length 321;  
Best Local Similarity 25.7%; Pred. No. 1.1e+02;  
RESULT 990  
ID AAY04998 standard; protein; 388 AA.  
DE Mycobacterium species protein sequence 50B.  
PN WO9909186-A2.  
PD 25-FEB-1999.  
PA (INSP ) INST PASTEUR.  
Query Match 10.1%; Score 65; DB 2; Length 388;  
Best Local Similarity 29.3%; Pred. No. 1.3e+02;  
RESULT 991  
ID ABO76986 standard; protein; 407 AA.  
DE Pseudomonas aeruginosa polypeptide #9161.  
PN US6551795-B1.  
PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.1%; Score 65; DB 7; Length 407;  
Best Local Similarity 28.6%; Pred. No. 1.4e+02;  
RESULT 992  
ID AAR11515 standard; protein; 440 AA.  
DE Soybean chlorotic mottle virus coat protein.  
PN AU9060867-A.  
PD 07-MAR-1991.  
PA (NAAG-) NAT INST AGROBIOL R.  
PA (TOFU) TONEN CORP.  
PA (NORQ) NORINSHO KK.  
PA (TOFU) TONEN CORP.  
Query Match 10.1%; Score 65; DB 2; Length 440;  
Best Local Similarity 20.0%; Pred. No. 1.5e+02;  
RESULT 993  
ID RAB03084 standard; protein; 501 AA.  
DE Human ASH2L2 protein.  
PN CN1247228-A.  
PD 15-MAR-2000.  
PA (BASI-) INST BASIC MEDICAL SCI CHINESE ACAD MEDI.  
Query Match 10.1%; Score 65; DB 3; Length 501;  
Best Local Similarity 28.8%; Pred. No. 1.8e+02;  
RESULT 994  
ID ABU03696 standard; protein; 501 AA.  
DE Human expressed protein tag (EPT) #362.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 10.1%; Score 65; DB 6; Length 501;  
Best Local Similarity 28.8%; Pred. No. 1.8e+02;  
RESULT 995  
ID ABU03701 standard; protein; 501 AA.  
DE Human expressed protein tag (EPT) #367.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 10.1%; Score 65; DB 6; Length 501;  
Best Local Similarity 28.8%; Pred. No. 1.8e+02;  
RESULT 996  
ID ABU03704 standard; protein; 501 AA.  
DE Human expressed protein tag (EPT) #370.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 10.1%; Score 65; DB 6; Length 501;  
Best Local Similarity 28.8%; Pred. No. 1.8e+02;  
RESULT 997  
ID ABU03706 standard; protein; 534 AA.  
DE Human expressed protein tag (EPT) #372.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 10.1%; Score 65; DB 6; Length 534;  
Best Local Similarity 28.8%; Pred. No. 1.9e+02;  
RESULT 998  
ID ABU03695 standard; protein; 534 AA.  
DE Human expressed protein tag (EPT) #361.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 10.1%; Score 65; DB 6; Length 534;  
Best Local Similarity 28.8%; Pred. No. 1.9e+02;  
RESULT 999  
ID ABG07273 standard; protein; 576 AA.  
DE Novel human diagnostic protein #7264.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.1%; Score 65; DB 4; Length 576;  
Best Local Similarity 28.8%; Pred. No. 2.1e+02;  
RESULT 1000  
ID ABG07275 standard; protein; 626 AA.  
DE Novel human diagnostic protein #7266.

PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.1%; Score 65; DB 4; Length 626;  
Best Local Similarity 28.8%; Pred. No. 2.3e+02;  
RESULT 1001  
ID -AAB03083 standard; protein; 628 AA.  
DE Human ASH2L1 protein.  
PN CN1247228-A.  
PD 15-MAR-2000.  
PA (BASI-) INST BASIC MEDICAL SCI CHINESE ACAD MEDI.  
Query Match 10.1%; Score 65; DB 3; Length 628;  
Best Local Similarity 28.8%; Pred. No. 2.3e+02;  
RESULT 1002  
ID AAB47150 standard; protein; 628 AA.  
DE CDIFF-11, Incyte ID No. 2848676CD1.  
PN WO200119860-A2.  
PD 22-MAR-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 10.1%; Score 65; DB 4; Length 628;  
Best Local Similarity 28.8%; Pred. No. 2.3e+02;  
RESULT 1003  
ID ABU03702 standard; protein; 628 AA.  
DE Human expressed protein tag (EPT) #368.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 10.1%; Score 65; DB 6; Length 628;  
Best Local Similarity 28.8%; Pred. No. 2.3e+02;  
RESULT 1004  
ID ABU03703 standard; protein; 628 AA.  
DE Human expressed protein tag (EPT) #369.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 10.1%; Score 65; DB 6; Length 628;  
Best Local Similarity 28.8%; Pred. No. 2.3e+02;  
RESULT 1005  
ID ABU03700 standard; protein; 628 AA.  
DE Human expressed protein tag (EPT) #366.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 10.1%; Score 65; DB 6; Length 628;  
Best Local Similarity 28.8%; Pred. No. 2.3e+02;  
RESULT 1006  
ID ABU03707 standard; protein; 628 AA.  
DE Human expressed protein tag (EPT) #373.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 10.1%; Score 65; DB 6; Length 628;  
Best Local Similarity 28.8%; Pred. No. 2.3e+02;  
RESULT 1007  
ID ABU03699 standard; protein; 628 AA.  
DE Human expressed protein tag (EPT) #365.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 10.1%; Score 65; DB 6; Length 628;  
Best Local Similarity 28.8%; Pred. No. 2.3e+02;  
RESULT 1008  
ID ABU03705 standard; protein; 628 AA.  
DE Human expressed protein tag (EPT) #371.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 10.1%; Score 65; DB 6; Length 628;  
Best Local Similarity 28.8%; Pred. No. 2.3e+02;  
RESULT 1009  
ID ABU03698 standard; protein; 628 AA.  
DE Human expressed protein tag (EPT) #364.  
PN WO200278524-A2.

PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 10.1%; Score 65; DB 6; Length 628;  
Best Local Similarity 28.8%; Pred. No. 2.3e+02;  
RESULT 1010  
ID ABU03697 standard; protein; 628 AA.  
DE Human expressed protein tag (EPT) #363.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 10.1%; Score 65; DB 6; Length 628;  
Best Local Similarity 28.8%; Pred. No. 2.3e+02;  
RESULT 1011  
ID AAB6688 standard; protein; 650 AA.  
DE ASH2 isoform 707 protein.  
PN WO200102828-A2.  
PD 11-JAN-2001.  
PA (TULA-) TULARIK INC.  
Query Match 10.1%; Score 65; DB 4; Length 650;  
Best Local Similarity 28.8%; Pred. No. 2.4e+02;  
RESULT 1012  
ID ABB6491 standard; protein; 678 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 20265.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 10.1%; Score 65; DB 4; Length 678;  
Best Local Similarity 33.3%; Pred. No. 2.6e+02;  
RESULT 1013  
ID ABR57269 standard; protein; 1099 AA.  
DE Human PHD finger protein 2 PHD\_finger\_2.  
PN WO2003040296-A2.  
PD 15-MAY-2003.  
PA (DEVE-) DEVELOGEN ENTWICKLUNGSMIOLOGISCHE FORSCH.  
PA (HAED-) HAEDER T.  
Query Match 10.1%; Score 65; DB 6; Length 1099;  
Best Local Similarity 26.7%; Pred. No. 4.6e+02;  
RESULT 1014  
ID ADX07391 standard; protein; 1099 AA.  
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 1956.  
PN WO2005012875-A2.  
PD 10-FEB-2005.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 10.1%; Score 65; DB 9; Length 1099;  
Best Local Similarity 26.7%; Pred. No. 4.6e+02;  
RESULT 1015  
ID AAU94346 standard; protein; 1798 AA.  
DE Protein LAMB2 differentially expressed in breast cancer tissue.  
PN WO200210436-A2.  
PD 07-FEB-2002.  
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.  
PA (BAAK/) BAAK J.  
Query Match 10.1%; Score 65; DB 5; Length 1798;  
Best Local Similarity 27.4%; Pred. No. 8.2e+02;  
RESULT 1016  
ID AAM50360 standard; protein; 1798 AA.  
DE Human laminin-15 beta 2 chain.  
PN WO200183516-A1.  
PD 08-NOV-2001.  
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.  
Query Match 10.1%; Score 65; DB 5; Length 1798;  
Best Local Similarity 27.4%; Pred. No. 8.2e+02;  
RESULT 1017  
ID AAU42676 standard; protein; 113 AA.  
DE Propionibacterium acnes immunogenic protein #3572.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 10.0%; Score 64.5; DB 4; Length 113;  
Best Local Similarity 25.0%; Pred. No. 35;  
RESULT 1018  
ID ABM39195 standard; protein; 113 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #3871.

PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 10.0%; Score 64.5; DB 6; Length 113;  
Best Local Similarity 25.0%; Pred. No. 35;  
RESULT 1019  
ID AD160152 standard; protein; 126 AA.  
DE Secreted polypeptide #36.  
PN WO2003025142-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.0%; Score 64.5; DB 7; Length 126;  
Best Local Similarity 27.7%; Pred. No. 39;  
RESULT 1020  
ID ADJ71800 standard; protein; 126 AA.  
DE Human prokineticin-like protein.  
PN WO2003040326-A2.  
PD 15-MAY-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.0%; Score 64.5; DB 7; Length 126;  
Best Local Similarity 27.7%; Pred. No. 39;  
RESULT 1021  
ID AAU42971 standard; protein; 154 AA.  
DE Propionibacterium acnes immunogenic protein #3867.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 10.0%; Score 64.5; DB 4; Length 154;  
Best Local Similarity 28.3%; Pred. No. 50;  
RESULT 1022  
ID ABM39490 standard; protein; 154 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #4166.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 10.0%; Score 64.5; DB 6; Length 154;  
Best Local Similarity 28.3%; Pred. No. 50;  
RESULT 1023  
ID ADE31234 standard; protein; 189 AA.  
DE Human diagnostic and therapeutic polypeptide (DITHP), SEQ ID NO 366.  
PN WO2003062376-A2.  
PD 31-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 10.0%; Score 64.5; DB 7; Length 189;  
Best Local Similarity 34.1%; Pred. No. 64;  
RESULT 1024  
ID AAM78612 standard; protein; 227 AA.  
DE Human protein SEQ ID NO 1274.  
PN WO200157150-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.0%; Score 64.5; DB 4; Length 227;  
Best Local Similarity 23.9%; Pred. No. 80;  
RESULT 1025  
ID AB053041 standard; protein; 227 AA.  
DE Human putative spliceosome associated protein (SAP) #17.  
PN US2003068803-A1.  
PD 10-APR-2003.  
PA (REED/) REED R.  
PA (ZHOU/) ZHOU Z.  
Query Match 10.0%; Score 64.5; DB 6; Length 227;  
Best Local Similarity 23.9%; Pred. No. 80;  
RESULT 1026  
ID ADJ68918 standard; protein; 227 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID724.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 10.0%; Score 64.5; DB 7; Length 227;  
Best Local Similarity 23.9%; Pred. No. 80;  
RESULT 1027  
ID AD225523 standard; protein; 227 AA.

DE Cytokine receptor activity increasing protein MP6 SEQ ID NO 51.  
PN WO2005030241-A2.  
PD 07-APR-2005.  
PA (MEYE-) MEYER PHARM LLC.  
Query Match 10.0%; Score 64.5; DB 9; Length 227;  
Best Local Similarity 23.9%; Pred. No. 80;  
RESULT 1028  
ID ADZ25511 standard; protein; 255 AA.  
DE Cytokine receptor activity increasing protein MP7 SEQ ID NO 39.  
PN WO2005030241-A2.  
PD 07-APR-2005.  
PA (MEYE-) MEYER PHARM LLC.  
Query Match 10.0%; Score 64.5; DB 9; Length 255;  
Best Local Similarity 23.9%; Pred. No. 92;  
RESULT 1029  
ID ADT87996 standard; protein; 264 AA.  
DE Human regulatory protein, NHRP-33.  
PN US2004203109-A1.  
PD 14-OCT-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 10.0%; Score 64.5; DB 8; Length 264;  
Best Local Similarity 23.9%; Pred. No. 95;  
RESULT 1030  
ID ABO80087 standard; protein; 382 AA.  
DE Pseudomonas aeruginosa polypeptide #12262.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.0%; Score 64.5; DB 7; Length 382;  
Best Local Similarity 26.8%; Pred. No. 1.5e+02;  
RESULT 1031  
ID ABB11193 standard; peptide; 431 AA.  
DE Human Zn finger protein homologue, SEQ ID NO:1563.  
PN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.0%; Score 64.5; DB 4; Length 431;  
Best Local Similarity 30.8%; Pred. No. 1.7e+02;  
RESULT 1032  
ID ABO68760 standard; protein; 525 AA.  
DE Pseudomonas aeruginosa polypeptide #935.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.0%; Score 64.5; DB 7; Length 525;  
Best Local Similarity 31.1%; Pred. No. 2.2e+02;  
RESULT 1033  
ID AAB21042 standard; protein; 534 AA.  
DE Human nucleic acid-binding protein, NUABP-46.  
PN WO200044900-A2.  
PD 03-AUG-2000.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 10.0%; Score 64.5; DB 3; Length 534;  
Best Local Similarity 30.8%; Pred. No. 2.2e+02;  
RESULT 1034  
ID ABO82315 standard; protein; 593 AA.  
DE Pseudomonas aeruginosa polypeptide #14490.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.0%; Score 64.5; DB 7; Length 593;  
Best Local Similarity 30.2%; Pred. No. 2.5e+02;  
RESULT 1035  
ID ABO68758 standard; protein; 921 AA.  
DE Pseudomonas aeruginosa polypeptide #933.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.0%; Score 64.5; DB 7; Length 921;  
Best Local Similarity 26.1%; Pred. No. 4.2e+02;  
RESULT 1036  
ID ADG84161 standard; protein; 1161 AA.  
DE Human TMD0841 protein SeqID99.

PN WO2003089583-A2.  
PD 30-OCT-2003.  
PA (ORIG-) ORIGENE TECHNOLOGIES INC.  
Query Match 10.0%; Score 64.5; DB 7; Length 1161;  
Best Local Similarity 26.5%; Pred. No. 5.6e+02;  
RESULT 1037  
ID AAR80843 standard; protein; 145 AA.  
DE Cross-reactive allergen CRAL51 partial sequence.  
PN WO9519437-A1.  
PD 20-JUL-1995.  
PA (UYMA-) UNIV MANITOBA.  
Query Match 9.9%; Score 64; DB 2; Length 145;  
Best Local Similarity 31.4%; Pred. No. 53;  
RESULT 1038  
ID ADT55674 standard; protein; 182 AA.  
DE Plant polypeptide, SEQ ID 5751.  
PN US2004216190-A1.  
PD 28-OCT-2004.  
PA (KOVA/) KOVALIC D K.  
Query Match 9.9%; Score 64; DB 8; Length 182;  
Best Local Similarity 22.8%; Pred. No. 70;  
RESULT 1039  
ID ABB09175 standard; protein; 214 AA.  
DE Leptin-VEGF-165-C-terminal-His tag fusion protein SEQ ID NO:1.  
PN WO200226779-A2.  
PD 04-APR-2002.  
PA (BAXT) BAXTER AG.  
PA (BAXT) BAXTER INT INC.  
Query Match 9.9%; Score 64; DB 5; Length 214;  
Best Local Similarity 29.1%; Pred. No. 85;  
RESULT 1040  
ID ABUI0041 standard; protein; 214 AA.  
DE Leptin-VEGF165-His tag fusion protein.  
PN US2003044405-A1.  
PD 06-MAR-2003.  
PA (REDL/) REDL H.  
PA (FUER/) FUERST W.  
PA (KNEI/) KNEIDINGER R.  
PA (HELG/) HELGERSON S L.  
PA (LOOK/) LOOKER D.  
PA (INMA/) INMAN E M.  
PA (RICH/) RICHARDS J P.  
PA (WONG/) WONG C.  
Query Match 9.9%; Score 64; DB 6; Length 214;  
Best Local Similarity 29.1%; Pred. No. 85;  
RESULT 1041  
ID ADS00679 standard; protein; 214 AA.  
DE Leptin-VEGF165 C-terminal-His tag fusion protein.  
PN US2004191261-A1.  
PD 30-SEP-2004.  
PA (BAXT) BAXTER AG.  
PA (BAXT) BAXTER INT INC.  
Query Match 9.9%; Score 64; DB 8; Length 214;  
Best Local Similarity 29.1%; Pred. No. 85;  
RESULT 1042  
ID AAB73602 standard; protein; 220 AA.  
DE Human zinc finger protein ZNFp71 fragment (residues 67-286).  
PN WO200130840-A1.  
PD 03-MAY-2001.  
PA (SHAN-) SHANGHAI BIO ROAD GENE DEV LTD.  
Query Match 9.9%; Score 64; DB 4; Length 220;  
Best Local Similarity 28.8%; Pred. No. 88;  
RESULT 1043  
ID ADQ20492 standard; protein; 227 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3312.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 9.9%; Score 64; DB 8; Length 227;  
Best Local Similarity 28.8%; Pred. No. 91;  
RESULT 1044  
ID ABO74758 standard; protein; 366 AA.  
DE Pseudomonas aeruginosa polypeptide #6933.

PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.9%; Score 64; DB 7; Length 366;  
Best Local Similarity 30.2%; Pred. No. 1.6e+02;  
RESULT 1045  
ID AAY21803 standard; protein; 1855 AA.  
DE B. subtilis rib operon protein translated from reading frame 3.  
PN US5925538-A.  
PD 20-JUL-1999.  
PA (HOFF) ROCHE VITAMINS INC.  
Query Match 9.9%; Score 64; DB 2; Length 1855;  
Best Local Similarity 28.3%; Pred. No. 1.1e+03;  
RESULT 1046  
ID AAY83271 standard; protein; 1855 AA.  
DE Polypeptide encoded by rib operon of Bacillus subtilis.  
PN EP1001026-A2.  
PD 17-MAY-2000.  
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
Query Match 9.9%; Score 64; DB 3; Length 1855;  
Best Local Similarity 28.3%; Pred. No. 1.1e+03;  
RESULT 1047  
ID AAO21324 standard; protein; 106 AA.  
DE Arabidopsis thaliana KCP-like protein, SEQ ID NO 79.  
PN WO200222821-A2.  
PD 21-MAR-2002.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 9.9%; Score 63.5; DB 5; Length 106;  
Best Local Similarity 21.2%; Pred. No. 42;  
RESULT 1048  
ID AAU51371 standard; protein; 129 AA.  
DE Propionibacterium acnes immunogenic protein #12267.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 9.9%; Score 63.5; DB 4; Length 129;  
Best Local Similarity 28.4%; Pred. No. 53;  
RESULT 1049  
ID ABM47890 standard; protein; 129 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #12566.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 9.9%; Score 63.5; DB 6; Length 129;  
Best Local Similarity 28.4%; Pred. No. 53;  
RESULT 1050  
ID ABO69906 standard; protein; 148 AA.  
DE Pseudomonas aeruginosa polypeptide #2081.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.9%; Score 63.5; DB 7; Length 148;  
Best Local Similarity 32.9%; Pred. No. 62;  
RESULT 1051  
ID ADY25230 standard; protein; 199 AA.  
DE Plant full length insert polypeptide seqid 73014.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 9.9%; Score 63.5; DB 8; Length 199;  
Best Local Similarity 27.3%; Pred. No. 89;  
RESULT 1052  
ID ADM04665 standard; protein; 215 AA.  
DE Human protein of the invention SEQ ID NO:3350.  
PN EP1347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.9%; Score 63.5; DB 7; Length 215;  
Best Local Similarity 32.8%; Pred. No. 98;  
RESULT 1053  
ID AEC87595 standard; protein; 215 AA.  
DE Human cDNA clone protein FEBRA20211710, SEQ ID 3350.  
PN EP1580263-A1.  
PD 28-SEP-2005.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.9%; Score 63.5; DB 9; Length 215;  
Best Local Similarity 32.8%; Pred. No. 98;  
RESULT 1054  
ID ABO00623 standard; protein; 260 AA.  
DE Novel human polypeptide #210.  
PN WO2003023013-A2.  
PD 20-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.9%; Score 63.5; DB 6; Length 260;  
Best Local Similarity 43.9%; Pred. No. 1.2e+02;  
RESULT 1055  
ID ADY07390 standard; protein; 261 AA.  
DE Plant full length insert polypeptide seqid 63205.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 9.9%; Score 63.5; DB 8; Length 261;  
Best Local Similarity 31.7%; Pred. No. 1.2e+02;  
RESULT 1056  
ID ADU02419 standard; protein; 338 AA.  
DE Novel human polypeptide seqid 886.  
PN WO2004093804-A2.  
PD 04-NOV-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 9.9%; Score 63.5; DB 8; Length 338;  
Best Local Similarity 43.9%; Pred. No. 1.7e+02;  
RESULT 1057  
ID ADX91872 standard; protein; 367 AA.  
DE Plant full length insert polypeptide seqid 54536.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 9.9%; Score 63.5; DB 8; Length 367;  
Best Local Similarity 21.6%; Pred. No. 1.8e+02;  
RESULT 1058  
ID ABG60058 standard; protein; 375 AA.  
DE Human D1THP polypeptide #116.  
PN WO200220754-A2.  
PD 14-MAR-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.9%; Score 63.5; DB 5; Length 375;  
Best Local Similarity 35.2%; Pred. No. 1.9e+02;  
RESULT 1059  
ID ABG26874 standard; protein; 392 AA.  
DE Novel human diagnostic protein #26865.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.9%; Score 63.5; DB 4; Length 392;  
Best Local Similarity 24.0%; Pred. No. 2e+02;  
RESULT 1060  
ID ABG27718 standard; protein; 435 AA.  
DE Novel human diagnostic protein #27709.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.

Query Match  
Best Local Similarity 9.9%; Score 63.5; DB 4; Length 435;  
RESULT 1061  
ID AAB94169 standard; protein; 464 AA.  
DE Human protein sequence SEQ ID NO:14472.  
PN EPI074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match  
Best Local Similarity 9.9%; Score 63.5; DB 4; Length 464;  
RESULT 1062  
ID ABA00452 standard; protein; 786 AA.  
DE Human KRC zinc finger-acidic domain structures (ZAS) domain.  
PN WO2005042726-A2.  
PD 12-MAY-2005.  
PA (HARD ) HARVARD COLLEGE.  
Query Match  
Best Local Similarity 9.9%; Score 63.5; DB 9; Length 786;  
RESULT 1063  
ID ABP69375 standard; protein; 1708 AA.  
DE Human polypeptide SEQ ID NO 1422.  
PN WO200270539-A2.  
PD 12-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 9.9%; Score 63.5; DB 5; Length 1708;  
RESULT 1064  
ID ABB82733 standard; protein; 2406 AA.  
DE Human KRC protein.  
PN WO200290595-A1.  
PD 14-NOV-2002.  
PA (HARD ) HARVARD COLLEGE.  
Query Match  
Best Local Similarity 9.9%; Score 63.5; DB 6; Length 2406;  
RESULT 1065  
ID ADJ69698 standard; protein; 2406 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID1504.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match  
Best Local Similarity 9.9%; Score 63.5; DB 7; Length 2406;  
RESULT 1066  
ID ADQ97930 standard; protein; 2406 AA.  
DE Human cancer associated sequence HPI1-024, SEQ ID 907.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match  
Best Local Similarity 9.9%; Score 63.5; DB 8; Length 2406;  
RESULT 1067  
ID AEA00446 standard; protein; 2406 AA.  
DE Human kappa recognition component (KRC) polypeptide.  
PN WO2005042726-A2.  
PD 12-MAY-2005.  
PA (HARD ) HARVARD COLLEGE.  
Query Match  
Best Local Similarity 9.9%; Score 63.5; DB 9; Length 2406;  
RESULT 1068  
ID AAU47558 standard; protein; 123 AA.  
DE Propionibacterium acnes immunogenic protein #8454.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 9.8%; Score 63; DB 4; Length 123;  
RESULT 1069  
ID ABM44077 standard; protein; 123 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #8753.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.

Query Match  
Best Local Similarity 9.8%; Score 63; DB 6; Length 123;  
RESULT 1070  
ID ADX79085 standard; protein; 127 AA.  
DE Plant full length insert polypeptide seqid 48451.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ-) LIU J.  
PA (ZHOU-) ZHOU Y.  
PA (KOVA-) KOVALIC D K.  
PA (SCRE-) SCREEN S E.  
PA (TABA-) TABASKA J E.  
PA (CAOY-) CAO Y.  
Query Match  
Best Local Similarity 9.8%; Score 63; DB 8; Length 127;  
RESULT 1071  
ID ABG00364 standard; protein; 160 AA.  
DE Novel human diagnostic protein #355.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 9.8%; Score 63; DB 4; Length 160;  
RESULT 1072  
ID AAU55928 standard; protein; 172 AA.  
DE Propionibacterium acnes immunogenic protein #16924.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 9.8%; Score 63; DB 4; Length 172;  
RESULT 1073  
ID ABM52447 standard; protein; 172 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #17123.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 9.8%; Score 63; DB 6; Length 172;  
RESULT 1074  
ID AAU55408 standard; protein; 190 AA.  
DE Propionibacterium acnes immunogenic protein #16304.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 9.8%; Score 63; DB 4; Length 190;  
RESULT 1075  
ID ABM51927 standard; protein; 190 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #16603.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 9.8%; Score 63; DB 6; Length 190;  
RESULT 1076  
ID ABG14052 standard; protein; 198 AA.  
DE Novel human diagnostic protein #14043.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 9.8%; Score 63; DB 4; Length 198;  
RESULT 1077  
ID ABO74665 standard; protein; 267 AA.  
DE Pseudomonas aeruginosa polypeptide #6840.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 9.8%; Score 63; DB 7; Length 267;  
RESULT 1078  
ID ADY05166 standard; protein; 295 AA.

DE Plant full length insert polypeptide seqid 60981.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match  
Best Local Similarity 9.8%; Score 63; DB 8; Length 295;  
Best Local Similarity 25.0%; Pred. No. 1.6e+02;  
RESULT 1079  
ID ABO76978 standard; protein; 302 AA.  
DE Pseudomonas aeruginosa polypeptide #9153.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 9.8%; Score 63; DB 7; Length 302;  
Best Local Similarity 25.5%; Pred. No. 1.7e+02;  
RESULT 1080  
ID ADQ19814 standard; protein; 332 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2633.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match  
Best Local Similarity 9.8%; Score 63; DB 8; Length 332;  
Best Local Similarity 25.8%; Pred. No. 1.9e+02;  
RESULT 1081  
ID ABG23967 standard; protein; 343 AA.  
DE Novel human diagnostic protein #23958.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEE INC.  
Query Match  
Best Local Similarity 9.8%; Score 63; DB 4; Length 343;  
Best Local Similarity 27.4%; Pred. No. 1.9e+02;  
RESULT 1082  
ID AM93267 standard; protein; 447 AA.  
DE Human polypeptide, SEQ ID NO: 2729.  
PN EP130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Query Match  
Best Local Similarity 9.8%; Score 63; DB 4; Length 447;  
Best Local Similarity 24.5%; Pred. No. 2.7e+02;  
RESULT 1083  
ID ADL30696 standard; protein; 447 AA.  
DE Human protein encoded by a full length cDNA clone seqid 2729.  
PN EP1396543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match  
Best Local Similarity 9.8%; Score 63; DB 8; Length 447;  
Best Local Similarity 24.5%; Pred. No. 2.7e+02;  
RESULT 1084  
ID ADU02730 standard; protein; 492 AA.  
DE Novel human polypeptide seqid 1197.  
PN WO2004093804-A2.  
PD 04-NOV-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match  
Best Local Similarity 9.8%; Score 63; DB 8; Length 492;  
Best Local Similarity 27.3%; Pred. No. 3e+02;  
RESULT 1085  
ID ADM29286 standard; protein; 1787 AA.  
DE Human novel protein NOV4b.  
PN WO2003064628-A2.  
PD 07-AUG-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 9.8%; Score 63; DB 7; Length 1787;  
Best Local Similarity 20.8%; Pred. No. 1.4e+03;  
RESULT 1086  
ID ADQ97927 standard; protein; 2353 AA.  
DE Mouse cancer associated sequence MP11-024, SEQ ID 904.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match  
Best Local Similarity 9.8%; Score 63; DB 8; Length 2353;  
Best Local Similarity 25.2%; Pred. No. 1.9e+03;  
RESULT 1087  
ID AAU40478 standard; protein; 69 AA.  
DE Propionibacterium acnes immunogenic protein #1374.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 4; Length 69;  
Best Local Similarity 29.0%; Pred. No. 33;  
RESULT 1088  
ID ABM36997 standard; protein; 69 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #1673.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 6; Length 69;  
Best Local Similarity 29.0%; Pred. No. 33;  
RESULT 1089  
ID ABE69709 standard; protein; 77 AA.  
DE Human papillomavirus protein #279.  
PN WO2005115458-A2.  
PD 08-DEC-2005.  
PA (UABR-) UAB RES FOUND.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 10; Length 77;  
Best Local Similarity 24.6%; Pred. No. 37;  
RESULT 1090  
ID AAY44192 standard; protein; 156 AA.  
DE Human keratinocyte-derived RNase-like protein.  
PN EP943679-A1.  
PD 22-SEP-1999.  
PA (INNO-) INNOGENETICS NV.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 2; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1091  
ID AAB10601 standard; protein; 156 AA.  
DE Human SAP-2 pre-protein.  
PN WO200046245-A2.  
PD 10-AUG-2000.  
PA (SCHD) SCHERING AG.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 3; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1092  
ID AAB66270 standard; protein; 156 AA.  
DE Human TANGO 295 SEQ ID NO: 23.  
PN WO200100673-A1.  
PD 04-JAN-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 4; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1093  
ID AAB50934 standard; protein; 156 AA.  
DE Human PRO6006 protein.  
PN WO200073452-A2.  
PD 07-DEC-2000.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 4; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1094  
ID ABB84987 standard; protein; 156 AA.  
DE Human PRO6006 protein sequence SEQ ID NO:342.  
PN WO2002006590-A2.  
PD 03-JAN-2002.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 5; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1095  
ID ABG34059 standard; protein; 156 AA.  
DE Human Pro peptide #30.  
PN WO200224888-A2.  
PD 28-MAR-2002.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 5; Length 156;



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Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1096
ID ABB95593 standard; protein; 156 AA.
DE Human angiogenesis related protein PRO6006 SEQ ID NO: 342.
PN W0200208284-A2.
PD 31-JAN-2002.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 5; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1097
ID ADA01328 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003086779-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 6; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1098
ID ADA43757 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 6; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1099
ID ADA43525 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 6; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1100
ID ADA01200 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 6; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1101
ID ADA01084 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1102
ID ADA43641 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1103
ID ADA06903 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1104
ID ADA08391 standard; protein; 156 AA.
DE Novel human secreted and transmembrane protein PRO6006.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1105
ID ADB99684 standard; protein; 156 AA.
DE Human PRO polypeptide SEQ ID 60.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1106
ID ADB86967 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1107
ID ADB66122 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1108
ID ADB99800 standard; protein; 156 AA.
DE Human PRO polypeptide SEQ ID 60.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1109
ID ADB99455 standard; protein; 156 AA.
DE Novel human secreted and transmembrane protein PRO6006.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1110
ID ADB66006 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1111
ID ADC23404 standard; protein; 156 AA.
DE Human transmembrane PRO polypeptide (SeqID 60).
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 7; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1112
ID ADC26097 standard; protein; 156 AA.
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DE Human PRO6006 protein.  
PN US2003073194-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.7%; Score 62.5; DB 7; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1113  
ID ADD10631 standard; protein; 156 AA.  
DE Human secreted/transmembrane PRO polypeptide #171.  
PN US2003105011-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.7%; Score 62.5; DB 7; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1114  
ID ADD11591 standard; protein; 156 AA.  
DE Human secreted/transmembrane PRO polypeptide #171.  
PN US2003105013-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.7%; Score 62.5; DB 7; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1115  
ID ADD37384 standard; protein; 156 AA.  
DE Human secreted/transmembrane PRO polypeptide #171.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.7%; Score 62.5; DB 7; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1116  
ID ADE04924 standard; protein; 156 AA.  
DE Human PRO polypeptide #30.  
PN US2003068778-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.7%; Score 62.5; DB 7; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1117  
ID ADE11230 standard; protein; 156 AA.  
DE Human PRO polypeptide #30.  
PN US2003073191-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.7%; Score 62.5; DB 7; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1118  
ID ADD88161 standard; protein; 156 AA.  
DE Human PRO polypeptide #30.  
PN US2003082733-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.7%; Score 62.5; DB 7; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1119  
ID ADD95456 standard; protein; 156 AA.  
DE Human secreted/transmembrane polypeptide PRO6006.  
PN US2003064473-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.7%; Score 62.5; DB 7; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1120  
ID ADE06386 standard; protein; 156 AA.  
DE Human PRO polypeptide #30.  
PN US2003073195-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.7%; Score 62.5; DB 7; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1121  
ID ADE38161 standard; protein; 156 AA.  
DE Human PRO polypeptide #30.

PN US2003119120-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.7%; Score 62.5; DB 7; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1122  
ID ADD88277 standard; protein; 156 AA.  
DE Human PRO polypeptide #30.  
PN US2003073189-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.7%; Score 62.5; DB 7; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1123  
ID ADD90858 standard; protein; 156 AA.  
DE Human secreted/transmembrane polypeptide PRO6006.  
PN US2003073188-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.7%; Score 62.5; DB 7; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1124  
ID ADF99413 standard; protein; 156 AA.  
DE Human secreted/transmembrane polypeptide PRO6006.  
PN US2003078401-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.7%; Score 62.5; DB 7; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1125  
ID ADG06506 standard; protein; 156 AA.  
DE Human PRO polypeptide #30.  
PN US2003077742-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.7%; Score 62.5; DB 7; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1126  
ID ADG05457 standard; protein; 156 AA.  
DE Human PRO polypeptide #30.  
PN US2003077741-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.7%; Score 62.5; DB 7; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1127  
ID ADG82458 standard; protein; 156 AA.  
DE Human PRO polypeptide #30.  
PN US2003077744-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.7%; Score 62.5; DB 7; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1128  
ID ADE51711 standard; protein; 156 AA.  
DE Human secreted/transmembrane polypeptide PRO6006.  
PN US2003104560-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.7%; Score 62.5; DB 8; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1129  
ID ADE51827 standard; protein; 156 AA.  
DE Human secreted/transmembrane polypeptide PRO6006.  
PN US2003104561-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.7%; Score 62.5; DB 8; Length 156;  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1130  
ID ADE37685 standard; protein; 156 AA.  
DE Human secreted/transmembrane polypeptide PRO6006.  
PN US2003104564-A1.

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PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1131
ID ADE37569 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1132
ID ADD95340 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1133
ID ADE38040 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1134
ID ADE76129 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1135
ID ADE39452 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1136
ID ADE04256 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1137
ID ADE39853 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1138
ID ADE19718 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1139
ID ADE77296 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003124666-A1.
PD 03-JUL-2003.

PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1140
ID ADE65404 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1141
ID ADE76013 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1142
ID ADE37924 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1143
ID ADE64534 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1144
ID ADE41592 standard; protein; 156 AA.
DE Human secreted/transmembrane PRO polypeptide #171.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1145
ID ADE38869 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1146
ID ADE51943 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1147
ID ADD90974 standard; protein; 156 AA.
DE Human secreted/transmembrane polypeptide PRO6006.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 62.5; DB 8; Length 156;
Best Local Similarity 23.2%; Pred. No. 87;
RESULT 1148
ID ADE38753 standard; protein; 156 AA.
DE Human PRO polypeptide #30.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
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Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;  
RESULT 1149  
ID ADE37453 standard; protein; 156 AA.  
DE Human secreted/transmembrane polypeptide PRO6006.  
PN US2003104563-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;  
RESULT 1150  
ID ADE06270 standard; protein; 156 AA.  
DE Human PRO polypeptide #30.  
PN US2003138898-A1.  
PD 24-JUL-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;  
RESULT 1151  
ID ADD90129 standard; protein; 156 AA.  
DE Human secreted/transmembrane polypeptide PRO6006.  
PN US2003138904-A1.  
PD 24-JUL-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;  
RESULT 1152  
ID ADE38637 standard; protein; 156 AA.  
DE Human PRO polypeptide #30.  
PN US2003119086-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;  
RESULT 1153  
ID ADE39568 standard; protein; 156 AA.  
DE Human PRO polypeptide #30.  
PN US2003119118-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;  
RESULT 1154  
ID ADD89173 standard; protein; 156 AA.  
DE Human PRO polypeptide #30.  
PN US2003138897-A1.  
PD 24-JUL-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;  
RESULT 1155  
ID ADD88940 standard; protein; 156 AA.  
DE Human PRO polypeptide #30.  
PN US2003138899-A1.  
PD 24-JUL-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;  
RESULT 1156  
ID ADE19834 standard; protein; 156 AA.  
DE Human PRO polypeptide #30.  
PN US2003138900-A1.  
PD 24-JUL-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;  
RESULT 1157  
ID ADE77412 standard; protein; 156 AA.  
DE Human secreted/transmembrane polypeptide PRO6006.  
PN US2003124667-A1.  
PD 03-JUL-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;  
RESULT 1158  
ID ADE56288 standard; protein; 156 AA.  
DE Human PRO polypeptide #30.  
PN US2003119113-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;  
RESULT 1159  
ID ADE39336 standard; protein; 156 AA.  
DE Human PRO polypeptide #30.  
PN US2003119115-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;  
RESULT 1160  
ID ADE38521 standard; protein; 156 AA.  
DE Human secreted/transmembrane polypeptide PRO6006.  
PN US2003104559-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;  
RESULT 1161  
ID ADG11074 standard; protein; 156 AA.  
DE Human secreted/transmembrane polypeptide PRO6006.  
PN US2003170809-A1.  
PD 11-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;  
RESULT 1162  
ID ADG10958 standard; protein; 156 AA.  
DE Human secreted/transmembrane polypeptide PRO6006.  
PN US2003077743-A1.  
PD 24-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;  
RESULT 1163  
ID ADH31486 standard; protein; 156 AA.  
DE Human PRO polypeptide #30.  
PN US2003119139-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;  
RESULT 1164  
ID ADH38734 standard; protein; 156 AA.  
DE Human secreted/transmembrane polypeptide PRO6006.  
PN US2003119140-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;  
RESULT 1165  
ID ADH29369 standard; protein; 156 AA.  
DE Human secreted/transmembrane polypeptide PRO6006.  
PN US2003119137-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;  
RESULT 1166  
ID ADH23672 standard; protein; 156 AA.  
DE Human secreted/transmembrane polypeptide PRO6006.  
PN US2003119143-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;  
RESULT 1167  
ID ADE77412 standard; protein; 156 AA.  
DE Human secreted/transmembrane polypeptide PRO6006.  
PN US2003124667-A1.  
PD 03-JUL-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 9.7%; Score 62.5; DB 8; Length 156;



DE Novel human secreted and transmembrane protein PRO6006.  
PN US2003119122-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC. 9.7%; Score 62.5; DB 8; Length 156;  
Query Match  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1186  
ID ADI13569 standard; protein; 156 AA.  
DE Novel human secreted and transmembrane protein PRO6006.  
PN US2003119131-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC. 9.7%; Score 62.5; DB 8; Length 156;  
Query Match  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1187  
ID ADK00825 standard; protein; 156 AA.  
DE Human PRO polypeptide #30.  
PN US2003186373-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC. 9.7%; Score 62.5; DB 8; Length 156;  
Query Match  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1188  
ID ADL08566 standard; protein; 156 AA.  
DE Human secreted/transmembrane polypeptide PRO6006.  
PN US2003186372-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC. 9.7%; Score 62.5; DB 8; Length 156;  
Query Match  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1189  
ID ADR83120 standard; protein; 156 AA.  
DE Human PRO polypeptide #171.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC. 9.7%; Score 62.5; DB 8; Length 156;  
Query Match  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1190  
ID ADN05526 standard; protein; 156 AA.  
DE Antiposoriatic protein sequence #929.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC. 9.7%; Score 62.5; DB 8; Length 156;  
Query Match  
Best Local Similarity 23.2%; Pred. No. 87;  
RESULT 1191  
ID AAY44194 standard; peptide; 164 AA.  
DE Hexa-His tagged human keratinocyte-derived RNase-like protein.  
PN EP943679-A1.  
PD 22-SEP-1999.  
PA (INNO-) INNOGENETICS NV. 9.7%; Score 62.5; DB 2; Length 164;  
Query Match  
Best Local Similarity 23.2%; Pred. No. 92;  
RESULT 1192  
ID ADM17825 standard; protein; 323 AA.  
DE Pirus radiata transcription factor protein SBP family Seq 1601.  
PN WO200501050-A2.  
PD 06-JAN-2005.  
PA (ARBO-) ARBORGEN LLC. 9.7%; Score 62.5; DB 9; Length 323;  
Query Match  
Best Local Similarity 30.7%; Pred. No. 2.1e+02;  
RESULT 1193  
ID ABP73597 standard; protein; 328 AA.  
DE Candida albicans essential protein SEQ ID NO 7434.  
PN WO200253728-A2.  
PD 11-JUL-2002.  
PA (ELIT-) ELITRA PHARM INC. 9.7%; Score 62.5; DB 5; Length 328;  
Query Match  
Best Local Similarity 24.4%; Pred. No. 2.1e+02;  
RESULT 1194  
ID AAY47239 standard; protein; 414 AA.  
DE Human apolipoprotein AI regulatory protein-1.

PN US5721096-A.  
PD 24-FEB-1998.  
PA (CHIL-) CHILDRENS MEDICAL CENT. 9.7%; Score 62.5; DB 2; Length 414;  
Query Match  
Best Local Similarity 25.3%; Pred. No. 2.8e+02;  
RESULT 1195  
ID ABB57372 standard; protein; 414 AA.  
DE Mouse ischaemic condition related protein sequence SEQ ID NO:1055.  
PN WO200188188-A2.  
PD 22-NOV-2001.  
PA (UTNI-) UNIV NIHON SCHOOL JURIDICAL PERSON. 9.7%; Score 62.5; DB 5; Length 414;  
Query Match  
Best Local Similarity 25.3%; Pred. No. 2.8e+02;  
RESULT 1196  
ID ADE60663 standard; protein; 414 AA.  
DE Rat Protein O09018, SEQ ID NO 6575.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP. 9.7%; Score 62.5; DB 7; Length 414;  
PA (FARB ) BAYER AG.  
Query Match  
Best Local Similarity 25.3%; Pred. No. 2.8e+02;  
RESULT 1197  
ID ADE60665 standard; protein; 414 AA.  
DE Human Protein P24468, SEQ ID NO 6577.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP. 9.7%; Score 62.5; DB 7; Length 414;  
PA (FARB ) BAYER AG.  
Query Match  
Best Local Similarity 25.3%; Pred. No. 2.8e+02;  
RESULT 1198  
ID ADP05637 standard; protein; 414 AA.  
DE Mouse nuclear receptor protein SeqID11.  
PN WO2004045369-A2.  
PD 03-JUN-2004.  
PA (NURA-) NURA INC. 9.7%; Score 62.5; DB 8; Length 414;  
Query Match  
Best Local Similarity 25.3%; Pred. No. 2.8e+02;  
RESULT 1199  
ID ADP05635 standard; protein; 414 AA.  
DE Human nuclear receptor protein SeqID9.  
PN WO2004045369-A2.  
PD 03-JUN-2004.  
PA (NURA-) NURA INC. 9.7%; Score 62.5; DB 8; Length 414;  
Query Match  
Best Local Similarity 25.3%; Pred. No. 2.8e+02;  
RESULT 1200  
ID ADX07466 standard; protein; 414 AA.  
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 2031.  
PN WO2005012875-A2.  
PD 10-FEB-2005.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO. 9.7%; Score 62.5; DB 9; Length 414;  
Query Match  
Best Local Similarity 25.3%; Pred. No. 2.8e+02;  
RESULT 1201  
ID ADC31143 standard; protein; 516 AA.  
DE Human novel polypeptide sequence, SEQ ID NO:1225.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC. 9.7%; Score 62.5; DB 7; Length 516;  
Query Match  
Best Local Similarity 30.8%; Pred. No. 3.6e+02;  
RESULT 1202  
ID ABU96691 standard; protein; 569 AA.  
DE Human nucleic acid-associated protein (NAAP) #20.  
PN WO2003023003-A2.  
PD 20-MAR-2003.  
PA (INCY-) INCYTE GENOMICS INC. 9.7%; Score 62.5; DB 6; Length 569;  
Query Match  
Best Local Similarity 29.0%; Pred. No. 4.1e+02;  
RESULT 1203  
ID ABM65727 standard; protein; 751 AA.

DE Propionibacterium acnes immunogenic polypeptide #30403.  
PN WO2003033515-A1.  
PD 24-APR-2003  
PA (CORI-) CORIXA CORP.  
Query Match 9.7%; Score 62.5; DB 6; Length 751;  
Best Local Similarity 29.0%; Pred. No. 5.7e+02;  
RESULT 1204  
ID ADA55031 standard; protein; 752 AA.  
DE Human protein, SEQ ID 2599.  
PN EP1293569-A2.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.7%; Score 62.5; DB 6; Length 752;  
Best Local Similarity 29.0%; Pred. No. 5.7e+02;  
RESULT 1205  
ID AAU72900 standard; protein; 1094 AA.  
DE Human metalloprotease partial protein sequence #12.  
PN WO200183782-A2.  
PD 08-NOV-2001.  
PA (SUG-) SUGEN INC.  
Query Match 9.7%; Score 62.5; DB 5; Length 1094;  
Best Local Similarity 24.1%; Pred. No. 8.9e+02;  
RESULT 1206  
ID ABP01721 standard; protein; 70 AA.  
DE Human ORFX protein sequence SEQ ID NO:3424.  
PN WO200192523-A2.  
PD 06-DEC-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.6%; Score 62; DB 5; Length 70;  
Best Local Similarity 31.1%; Pred. No. 38;  
RESULT 1207  
ID AAY44195 standard; peptide; 136 AA.  
DE Hexa-His tagged human keratinocyte-derived RNase-like mature protein.  
PN EP943679-A1.  
PD 22-SEP-1999.  
PA (INNO-) INNOGENETICS NV.  
Query Match 9.6%; Score 62; DB 2; Length 136;  
Best Local Similarity 22.8%; Pred. No. 84;  
RESULT 1208  
ID ABO68420 standard; protein; 151 AA.  
DE Pseudomonas aeruginosa polypeptide #595.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.8%; Score 62; DB 7; Length 151;  
Best Local Similarity 22.2%; Pred. No. 95;  
RESULT 1209  
ID ADE08357 standard; protein; 166 AA.  
DE Novel protein (useful for identifying genetic disorders) #512.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.6%; Score 62; DB 7; Length 166;  
Best Local Similarity 24.6%; Pred. No. 1.1e+02;  
RESULT 1210  
ID ADY04755 standard; protein; 182 AA.  
DE Plant full length insert polypeptide seqid 60570.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABAJ/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 9.6%; Score 62; DB 8; Length 182;  
Best Local Similarity 25.9%; Pred. No. 1.2e+02;  
RESULT 1211  
ID ABB78817 standard; protein; 218 AA.  
DE Human NOV8 protein sequence SEQ ID NO:24.  
PN WO200230974-A2.  
PD 18-APR-2002.

PA (CURA-) CURAGEN CORP.  
PA (MILL/) MILLET I.  
Query Match 9.6%; Score 62; DB 5; Length 218;  
Best Local Similarity 26.6%; Pred. No. 1.5e+02;  
RESULT 1212  
ID AAU18157 standard; protein; 303 AA.  
DE Novel human DNA-binding protein #4.  
PN WO200155162-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 62; DB 4; Length 303;  
Best Local Similarity 25.0%; Pred. No. 2.2e+02;  
RESULT 1213  
ID ABG92578 standard; protein; 303 AA.  
DE Human DNA-binding protein #4.  
PN US2002102638-A1.  
PD 01-AUG-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.6%; Score 62; DB 5; Length 303;  
Best Local Similarity 25.0%; Pred. No. 2.2e+02;  
RESULT 1214  
ID ADC25295 standard; protein; 303 AA.  
DE Human extracellular matrix protein from gene 4.  
PN US2003049650-A1.  
PD 13-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 62; DB 7; Length 303;  
Best Local Similarity 25.0%; Pred. No. 2.2e+02;  
RESULT 1215  
ID ABR53477 standard; protein; 371 AA.  
DE Protein sequence #SEQ ID 1819.  
PN EP1258494-A1.  
PD 20-NOV-2002.  
PA (CELL-) CELLZOME AG.  
Query Match 9.6%; Score 62; DB 6; Length 371;  
Best Local Similarity 23.8%; Pred. No. 2.8e+02;  
RESULT 1216  
ID ADK64574 standard; protein; 371 AA.  
DE Disease treating protein complex-derived protein #1088.  
PN EP1338608-A2.  
PD 27-AUG-2003.  
PA (CELL-) CELLZOME AG.  
Query Match 9.6%; Score 62; DB 7; Length 371;  
Best Local Similarity 23.8%; Pred. No. 2.8e+02;  
RESULT 1217  
ID ABO58806 standard; protein; 412 AA.  
DE Human genome derived single exon protein #5040.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 9.6%; Score 62; DB 8; Length 412;  
Best Local Similarity 28.0%; Pred. No. 3.2e+02;  
RESULT 1218  
ID ADB84071 standard; protein; 577 AA.  
DE Frog NURR1-related protein sequence, SEQ ID 84.  
PN WO2003012040-A2.  
PD 13-FEB-2003.  
PA (BAYU) BAYLOR COLLEGE MEDICINE.  
Query Match 9.6%; Score 62; DB 7; Length 577;  
Best Local Similarity 31.7%; Pred. No. 4.7e+02;  
RESULT 1219  
ID ADL22717 standard; protein; 705 AA.  
DE Human disease detection and treatment (MDDT) protein - SEQ ID 166.  
PN WO2003062379-A2.  
PD 31-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.6%; Score 62; DB 7; Length 705;  
Best Local Similarity 31.9%; Pred. No. 6e+02;  
RESULT 1220

ID ABB65602 standard; protein; 954 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 23598.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY. 9.6%; Score 62; DB 4; Length 954;  
Best Local Similarity 24.1%; Pred. No. 8.6e+02;  
Query Match 9.6%; Score 62; DB 8; Length 1642;  
Best Local Similarity 25.7%; Pred. No. 1.6e+03;  
RESULT 1221  
ID ABO73001 standard; protein; 959 AA.  
DE Pseudomonas aeruginosa polypeptide #5176.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.6%; Score 62; DB 7; Length 959;  
Best Local Similarity 27.1%; Pred. No. 8.7e+02;  
RESULT 1222  
ID ABB62516 standard; protein; 1162 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 14340.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY. 9.6%; Score 62; DB 4; Length 1162;  
Best Local Similarity 31.2%; Pred. No. 1.1e+03;  
RESULT 1223  
ID ADK67911 standard; protein; 1270 AA.  
DE Human extracellular messenger (EXMES) polypeptide.  
PN WO2004013292-A2.  
PD 12-FEB-2004.  
PA (INCY-) INCYTE CORP. 9.6%; Score 62; DB 8; Length 1270;  
Best Local Similarity 28.1%; Pred. No. 1.2e+03;  
RESULT 1224  
ID ADQ14315 standard; protein; 1424 AA.  
DE Human collagen type IV alpha 3 (Goodpasture antigen).  
PN WO2004060262-A2.  
PD 22-JUL-2004.  
PA (LORA-) LORANTIS LTD. 9.6%; Score 62; DB 8; Length 1424;  
Best Local Similarity 25.7%; Pred. No. 1.4e+03;  
RESULT 1225  
ID ADR41697 standard; protein; 1424 AA.  
DE Human collagen (aa sequence), type IV, alpha 3 (Goodpasture antigen).  
PN WO2004064863-A1.  
PD 05-AUG-2004.  
PA (LORA-) LORANTIS LTD. 9.6%; Score 62; DB 8; Length 1424;  
Best Local Similarity 25.7%; Pred. No. 1.4e+03;  
RESULT 1226  
ID ADU06693 standard; protein; 1424 AA.  
DE Novel bronchial cancer-associated human protein SeqID919.  
PN DE10316701-A1.  
PD 04-NOV-2004.  
PA (HINZ/) HINZMANN B. 9.6%; Score 62; DB 8; Length 1424;  
PA (HERM/) HERMANN K. 9.6%; Score 62; DB 8; Length 1424;  
PA (CAST/) HEIDEN CASTANOS-VELEZ E. 9.6%; Score 62; DB 8; Length 1424;  
Best Local Similarity 25.7%; Pred. No. 1.4e+03;  
RESULT 1227  
ID AEB77777 standard; protein; 1424 AA.  
DE Human Goodpasture antigen, collagen, type IV, alpha 3.  
PN WO2005073250-A2.  
PD 11-AUG-2005.  
PA (LORA-) LORANTIS LTD. 9.6%; Score 62; DB 9; Length 1424;  
Best Local Similarity 25.7%; Pred. No. 1.4e+03;  
RESULT 1228  
ID ABM84483 standard; protein; 1611 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4732.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP. 9.6%; Score 62; DB 8; Length 1611;  
Best Local Similarity 25.7%; Pred. No. 1.6e+03;  
RESULT 1229  
ID ABA64562 standard; protein; 1642 AA.  
DE Human lupus-related protein #10.  
PN WO2004076639-A2.  
PD 10-SEP-2004.  
PA (AMHP ) WYETH. 9.6%; Score 62; DB 8; Length 1642;  
PA (OTOO/) O'TOOLE M M. 9.6%; Score 62; DB 8; Length 1642;  
PA (WEIL/) WEI L. 9.6%; Score 62; DB 8; Length 1642;  
Best Local Similarity 25.7%; Pred. No. 1.6e+03;  
RESULT 1230  
ID ADD47063 standard; protein; 1670 AA.  
DE Human Protein NP\_000082, SEQ ID NO 12751.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP. 9.6%; Score 62; DB 7; Length 1670;  
PA (FARB ) BAYER AG. 9.6%; Score 62; DB 7; Length 1670;  
Best Local Similarity 25.7%; Pred. No. 1.7e+03;  
RESULT 1231  
ID ABA64561 standard; protein; 1670 AA.  
DE Human lupus-related protein #9.  
PN WO2004076639-A2.  
PD 10-SEP-2004.  
PA (AMHP ) WYETH. 9.6%; Score 62; DB 8; Length 1670;  
PA (OTOO/) O'TOOLE M M. 9.6%; Score 62; DB 8; Length 1670;  
PA (WEIL/) WEI L. 9.6%; Score 62; DB 8; Length 1670;  
Best Local Similarity 25.7%; Pred. No. 1.7e+03;  
RESULT 1232  
ID AAB33149 standard; protein; 112 AA.  
DE Pinus radiata transcription factor protein sequence #266.  
PN WO200053724-A2.  
PD 14-SEP-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD. 9.5%; Score 61.5; DB 3; Length 112;  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD. 9.5%; Score 61.5; DB 3; Length 112;  
Best Local Similarity 27.1%; Pred. No. 76;  
RESULT 1233  
ID AAG00283 standard; protein; 121 AA.  
DE Human secreted protein, SEQ ID NO: 4364.  
PN EP1033401-A2.  
PD 06-SEP-2000.  
PA (GEST ) GENSET. 9.5%; Score 61.5; DB 3; Length 121;  
Best Local Similarity 22.3%; Pred. No. 84;  
RESULT 1234  
ID ABU03604 standard; protein; 121 AA.  
DE Human expressed protein tag (EPT) #270.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCO INC. 9.5%; Score 61.5; DB 6; Length 121;  
Best Local Similarity 22.3%; Pred. No. 84;  
RESULT 1235  
ID ABO78982 standard; protein; 226 AA.  
DE Pseudomonas aeruginosa polypeptide #11157.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP. 9.5%; Score 61.5; DB 7; Length 226;  
Best Local Similarity 29.5%; Pred. No. 1.8e+02;  
RESULT 1236  
ID ABO81392 standard; protein; 244 AA.  
DE Pseudomonas aeruginosa polypeptide #13567.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP. 9.5%; Score 61.5; DB 7; Length 244;  
Best Local Similarity 26.9%; Pred. No. 1.9e+02;  
RESULT 1237  
ID ABO83546 standard; protein; 249 AA.  
DE Pseudomonas aeruginosa polypeptide #15721.



PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.5%; Score 61.5; DB 7; Length 249;  
Best Local Similarity 24.7%; Pred. No. 2e+02;  
RESULT 1238  
ID AAR47150 standard; protein; 252 AA.  
DE IL-2 receptor gamma chain.  
PN EP578932-A2.  
PD 19-JAN-1994.  
PA (AJIN) AJINOMOTO KK.  
PA (SUGA/) SUGAMURA K.  
Query Match 9.5%; Score 61.5; DB 2; Length 252;  
Best Local Similarity 22.3%; Pred. No. 2e+02;  
RESULT 1239  
ID ABU03606 standard; protein; 252 AA.  
DE Human expressed protein tag (EPT) #272.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 9.5%; Score 61.5; DB 6; Length 252;  
Best Local Similarity 22.3%; Pred. No. 2e+02;  
RESULT 1240  
ID ABO77598 standard; protein; 269 AA.  
DE Pseudomonas aeruginosa polypeptide #9773.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.5%; Score 61.5; DB 7; Length 269;  
Best Local Similarity 31.5%; Pred. No. 2.2e+02;  
RESULT 1241  
ID ABB97515 standard; protein; 277 AA.  
DE Novel human protein SEQ ID NO: 783.  
PN WO200228660-A2.  
PD 21-MAR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.5%; Score 61.5; DB 5; Length 277;  
Best Local Similarity 20.9%; Pred. No. 2.2e+02;  
RESULT 1242  
ID ADP2440 standard; protein; 301 AA.  
DE Sea-squirt (Ciona intestinalis) zinc finger protein #7.  
PN JP2004057126-A.  
PD 26-FEB-2004.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Query Match 9.5%; Score 61.5; DB 8; Length 301;  
Best Local Similarity 33.3%; Pred. No. 2.5e+02;  
RESULT 1243  
ID ABR61610 standard; peptide; 341 AA.  
DE IL-2 common gamma chain (cgammac) fragment (residues 1-341).  
PN WO2003087374-A1.  
PD 23-OCT-2003.  
PA (YEDA) YEDA RES & DEV CO LTD.  
Query Match 9.5%; Score 61.5; DB 7; Length 341;  
Best Local Similarity 22.3%; Pred. No. 2.9e+02;  
RESULT 1244  
ID ABR61609 standard; peptide; 357 AA.  
DE IL-2 common gamma chain (cgammac) fragment (residues 1-357).  
PN WO2003087374-A1.  
PD 23-OCT-2003.  
PA (YEDA) YEDA RES & DEV CO LTD.  
Query Match 9.5%; Score 61.5; DB 7; Length 357;  
Best Local Similarity 22.3%; Pred. No. 3e+02;  
RESULT 1245  
ID ABM87580 standard; protein; 359 AA.  
DE Rice abiotic stress responsive polypeptide SEQ ID NO:5826.  
PN WO2003008540-A2.  
PD 30-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 9.5%; Score 61.5; DB 7; Length 359;  
Best Local Similarity 23.9%; Pred. No. 3.1e+02;  
RESULT 1246  
ID AAE13734 standard; protein; 360 AA.  
DE Human soluble IL-2Rgamma/kappa light chain chimeric DNA construct.

PN WO200177171-A2.  
PD 18-OCT-2001.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 9.5%; Score 61.5; DB 5; Length 360;  
Best Local Similarity 22.3%; Pred. No. 3.1e+02;  
RESULT 1247  
ID AAR47148 standard; protein; 369 AA.  
DE IL-2 receptor gamma chain.  
PN EP578932-A2.  
PD 19-JAN-1994.  
PA (AJIN) AJINOMOTO KK.  
PA (SUGA/) SUGAMURA K.  
Query Match 9.5%; Score 61.5; DB 2; Length 369;  
Best Local Similarity 22.3%; Pred. No. 3.2e+02;  
RESULT 1248  
ID AAU96932 standard; protein; 369 AA.  
DE Human cytokine receptor common gamma chain.  
PN US6372898-B1.  
PD 16-APR-2002.  
PA (SCHE) SCHERING CORP.  
Query Match 9.5%; Score 61.5; DB 5; Length 369;  
Best Local Similarity 22.3%; Pred. No. 3.2e+02;  
RESULT 1249  
ID ABU03612 standard; protein; 369 AA.  
DE Human expressed protein tag (EPT) #278.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 9.5%; Score 61.5; DB 6; Length 369;  
Best Local Similarity 22.3%; Pred. No. 3.2e+02;  
RESULT 1250  
ID ABU03613 standard; protein; 369 AA.  
DE Human expressed protein tag (EPT) #279.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 9.5%; Score 61.5; DB 6; Length 369;  
Best Local Similarity 22.3%; Pred. No. 3.2e+02;  
RESULT 1251  
ID ABU03602 standard; protein; 369 AA.  
DE Human expressed protein tag (EPT) #268.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 9.5%; Score 61.5; DB 6; Length 369;  
Best Local Similarity 22.3%; Pred. No. 3.2e+02;  
RESULT 1252  
ID ABU03603 standard; protein; 369 AA.  
DE Human expressed protein tag (EPT) #269.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 9.5%; Score 61.5; DB 6; Length 369;  
Best Local Similarity 22.3%; Pred. No. 3.2e+02;  
RESULT 1253  
ID ABU03605 standard; protein; 369 AA.  
DE Human expressed protein tag (EPT) #271.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 9.5%; Score 61.5; DB 6; Length 369;  
Best Local Similarity 22.3%; Pred. No. 3.2e+02;  
RESULT 1254  
ID ABU03600 standard; protein; 369 AA.  
DE Human expressed protein tag (EPT) #266.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 9.5%; Score 61.5; DB 6; Length 369;  
Best Local Similarity 22.3%; Pred. No. 3.2e+02;  
RESULT 1255  
ID ABU03601 standard; protein; 369 AA.  
DE Human expressed protein tag (EPT) #267.

PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 9.5%; Score 61.5; DB 6; Length 369;  
Best Local Similarity 22.3%; Pred. No. 3.2e+02;  
RESULT 1256  
ID ADP65163 standard; protein; 369 AA.  
DE Human interleukin 2 receptor, gamma chain, precursor, Interleukin-2.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 9.5%; Score 61.5; DB 7; Length 369;  
Best Local Similarity 22.3%; Pred. No. 3.2e+02;  
RESULT 1257  
ID ADP12957 standard; protein; 369 AA.  
DE Protein encoding reference mRNA sequence #42.  
PN WO2004042346-A2.  
PD 21-MAY-2004.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Query Match 9.5%; Score 61.5; DB 8; Length 369;  
Best Local Similarity 22.3%; Pred. No. 3.2e+02;  
RESULT 1258  
ID ADU07285 standard; protein; 369 AA.  
DE Human IL-9R gamma chain.  
PN WO2004091519-A2.  
PD 28-OCT-2004.  
PA (MEDI-) MEDIMMUNE INC.  
Query Match 9.5%; Score 61.5; DB 8; Length 369;  
Best Local Similarity 22.3%; Pred. No. 3.2e+02;  
RESULT 1259  
ID ADT88352 standard; protein; 369 AA.  
DE Human IL-19R gamma subunit isoform seqid 60.  
PN WO2004091510-A2.  
PD 28-OCT-2004.  
PA (MEDI-) MEDIMMUNE INC.  
Query Match 9.5%; Score 61.5; DB 8; Length 369;  
Best Local Similarity 22.3%; Pred. No. 3.2e+02;  
RESULT 1260  
ID ADY19463 standard; protein; 369 AA.  
DE PRO polypeptide SEQ ID NO 5269.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH) GENENTECH INC.  
Query Match 9.5%; Score 61.5; DB 9; Length 369;  
Best Local Similarity 22.3%; Pred. No. 3.2e+02;  
RESULT 1261  
ID AED66944 standard; protein; 369 AA.  
DE Human interleukin-9 receptor (IL-9R) gamma chain protein, SEQ ID: 60.  
PN US2005260204-A1.  
PD 24-NOV-2005.  
PA (MEDI-) MEDIMMUNE INC.  
Query Match 9.5%; Score 61.5; DB 9; Length 369;  
Best Local Similarity 22.3%; Pred. No. 3.2e+02;  
RESULT 1262  
ID ADX95163 standard; protein; 415 AA.  
DE Plant full length insert polypeptide seqid 57827.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 9.5%; Score 61.5; DB 8; Length 415;  
Best Local Similarity 22.2%; Pred. No. 3.6e+02;  
RESULT 1263  
ID ADY09233 standard; protein; 420 AA.  
DE Plant full length insert polypeptide seqid 65048.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.

PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 9.5%; Score 61.5; DB 8; Length 420;  
Best Local Similarity 22.2%; Pred. No. 3.7e+02;  
RESULT 1264  
ID AEF32726 standard; protein; 444 AA.  
DE Human coronavirus HKU1 amino acid sequence SEQ ID NO:1312.  
PN US2006018923-A1.  
PD 26-JAN-2006.  
PA (YUEN/) YUEN K Y.  
PA (WOOC/) WOO C Y P.  
PA (LAUK/) LAU K P S.  
PA (CHAN/) CHAN K H.  
PA (POON/) POON L M.  
PA (PEIR/) PEIRIS J S M.  
PA (GUAN/) GUAN Y.  
Query Match 9.5%; Score 61.5; DB 10; Length 444;  
Best Local Similarity 32.1%; Pred. No. 3.9e+02;  
RESULT 1265  
ID AAW31646 standard; protein; 482 AA.  
DE Human cytokine receptor gc chain-Ig fusion protein.  
PN WO9743416-A1.  
PD 20-NOV-1997.  
PA (BIOJ) BIOGEN INC.  
Query Match 9.5%; Score 61.5; DB 2; Length 482;  
Best Local Similarity 22.3%; Pred. No. 4.4e+02;  
RESULT 1266  
ID ABU03608 standard; protein; 482 AA.  
DE Human expressed protein tag (EPT) #274.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 9.5%; Score 61.5; DB 6; Length 482;  
Best Local Similarity 22.3%; Pred. No. 4.4e+02;  
RESULT 1267  
ID AAB73600 standard; protein; 513 AA.  
DE Zinc finger protein 57.  
PN WO200130840-A1.  
PD 03-MAY-2001.  
PA (SHAN-) SHANGHAI BIO ROAD GENE DEV LTD.  
Query Match 9.5%; Score 61.5; DB 4; Length 513;  
Best Local Similarity 20.9%; Pred. No. 4.7e+02;  
RESULT 1268  
ID ADM87387 standard; protein; 545 AA.  
DE Human protein SEQ ID NO:480.  
PN WO2004009834-A2.  
PD 29-JAN-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 9.5%; Score 61.5; DB 8; Length 545;  
Best Local Similarity 20.9%; Pred. No. 5e+02;  
RESULT 1269  
ID ADP04927 standard; protein; 573 AA.  
DE Sea squirt protein with tissue specific expression in development Seq522.  
PN JP2004057129-A.  
PD 26-FEB-2004.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Query Match 9.5%; Score 61.5; DB 8; Length 573;  
Best Local Similarity 28.6%; Pred. No. 5.3e+02;  
RESULT 1270  
ID AAB85509 standard; protein; 629 AA.  
DE Human protein kinase SGK214.  
PN WO200155356-A2.  
PD 02-AUG-2001.  
PA (SUGE-) SUGEN INC.  
Query Match 9.5%; Score 61.5; DB 4; Length 629;  
Best Local Similarity 30.8%; Pred. No. 6e+02;  
RESULT 1271  
ID AAY92202 standard; protein; 691 AA.  
DE Fusion polypeptide 603, IL-4 trap.  
PN WO200018932-A2.  
PD 06-APR-2000.

PA (REGE-) REGENERON PHARM INC.  
Query Match 9.5%; Score 61.5; DB 3; Length 691;  
Best Local Similarity 22.3%; Pred. No. 6.7e+02;  
RESULT 1272  
ID ABU03610 standard; protein; 691 AA.  
DE Human expressed protein tag (EPT) #276.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 9.5%; Score 61.5; DB 6; Length 691;  
Best Local Similarity 22.3%; Pred. No. 6.7e+02;  
RESULT 1273  
ID ABW02175 standard; protein; 691 AA.  
DE Human cytokine trap-603 protein.  
PN US2003143697-A1.  
PD 31-JUL-2003.  
PA (STAH/ ) STAHL N.  
PA (YANC/ ) YANCOPOULOS G D.  
Query Match 9.5%; Score 61.5; DB 7; Length 691;  
Best Local Similarity 22.3%; Pred. No. 6.7e+02;  
RESULT 1274  
ID AAY92201 standard; protein; 694 AA.  
DE Fusion polypeptide 424, IL-4 trap.  
PN WO200018932-A2.  
PD 06-APR-2000.  
PA (REGE-) REGENERON PHARM INC.  
Query Match 9.5%; Score 61.5; DB 3; Length 694;  
Best Local Similarity 22.3%; Pred. No. 6.7e+02;  
RESULT 1275  
ID AAY92203 standard; protein; 694 AA.  
DE Fusion polypeptide 622, IL-4 trap.  
PN WO200018932-A2.  
PD 06-APR-2000.  
PA (REGE-) REGENERON PHARM INC.  
Query Match 9.5%; Score 61.5; DB 3; Length 694;  
Best Local Similarity 22.3%; Pred. No. 6.7e+02;  
RESULT 1276  
ID ABU03611 standard; protein; 694 AA.  
DE Human expressed protein tag (EPT) #277.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 9.5%; Score 61.5; DB 6; Length 694;  
Best Local Similarity 22.3%; Pred. No. 6.7e+02;  
RESULT 1277  
ID ABU03609 standard; protein; 694 AA.  
DE Human expressed protein tag (EPT) #275.  
PN WO200278524-A2.  
PD 10-OCT-2002.  
PA (ZYCO-) ZYCOS INC.  
Query Match 9.5%; Score 61.5; DB 6; Length 694;  
Best Local Similarity 22.3%; Pred. No. 6.7e+02;  
RESULT 1278  
ID ABW02174 standard; protein; 694 AA.  
DE Human cytokine trap-424 protein.  
PN US2003143697-A1.  
PD 31-JUL-2003.  
PA (STAH/ ) STAHL N.  
PA (YANC/ ) YANCOPOULOS G D.  
Query Match 9.5%; Score 61.5; DB 7; Length 694;  
Best Local Similarity 22.3%; Pred. No. 6.7e+02;  
RESULT 1279  
ID ABW02176 standard; protein; 694 AA.  
DE Human cytokine trap-622 protein.  
PN US2003143697-A1.  
PD 31-JUL-2003.  
PA (STAH/ ) STAHL N.  
PA (YANC/ ) YANCOPOULOS G D.  
Query Match 9.5%; Score 61.5; DB 7; Length 694;  
Best Local Similarity 22.3%; Pred. No. 6.7e+02;  
RESULT 1280  
ID ABB65096 standard; protein; 707 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 22080.

PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 9.5%; Score 61.5; DB 4; Length 707;  
Best Local Similarity 24.2%; Pred. No. 6.9e+02;  
RESULT 1281  
ID ABU19352 standard; protein; 1247 AA.  
DE NOVX related protein SEQ ID NO 70.  
PN WO200299062-A2.  
PD 12-DEC-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.5%; Score 61.5; DB 6; Length 1247;  
Best Local Similarity 33.3%; Pred. No. 1.4e+03;  
RESULT 1282  
ID ADO41704 standard; protein; 1247 AA.  
DE Novel human polypeptide NOV26a.  
PN US2004018555-A1.  
PD 29-JAN-2004.  
PA (ANDE/ ) ANDERSON D W.  
PA (ZERR/ ) ZERRHUSEN B D.  
PA (LILL/ ) LI L.  
PA (ZHON/ ) ZHONG M.  
PA (CASM/ ) CASMAN S J.  
PA (GERL/ ) GERLACH V.  
PA (SHIM/ ) SHIMKETS R A.  
PA (GORM/ ) GORMAN L.  
PA (PENA/ ) PENA C E A.  
PA (KEKU/ ) KEKUDA R.  
PA (PATT/ ) PATTURAJAN M.  
PA (SPYT/ ) SPYTEK K A.  
PA (LEIT/ ) LEITE M W.  
PA (RAST/ ) RASTELLI L.  
PA (MACD/ ) MACDOUGALL J R.  
PA (TAUP/ ) TAUPIER R J.  
PA (GUOX/ ) GUO X S.  
PA (MILL/ ) MILLER C E.  
PA (SHEN/ ) SHENOY S G.  
PA (HJAL/ ) HJALT T.  
PA (VOSS/ ) VOSS E Z.  
PA (BOLD/ ) BOLDOG F L.  
PA (MALY/ ) MALYANKAR U M.  
PA (PADI/ ) PADIGARU M.  
PA (JIWW/ ) JI W.  
PA (SMIT/ ) SMITHSON G.  
PA (EDIN/ ) EDINGER S R.  
PA (MILL/ ) MILLET I.  
PA (ELLE/ ) ELLERMAN K.  
Query Match 9.5%; Score 61.5; DB 8; Length 1247;  
Best Local Similarity 33.3%; Pred. No. 1.4e+03;  
RESULT 1283  
ID ABP76680 standard; protein; 19938 AA.  
DE Streptomyces viridochromogenes Avi gene cluster polypeptide frame 4.  
PN WO200268436-A1.  
PD 06-SEP-2002.  
PA (COMB-) COMBINATURE BIOPHARM AG.  
Query Match 9.5%; Score 61.5; DB 6; Length 19938;  
Best Local Similarity 25.0%; Pred. No. 3.7e+04;  
RESULT 1284  
ID AAY48277 standard; protein; 66 AA.  
DE Human prostate cancer-associated protein 63.  
PN DE19811193-A1.  
PD 16-SEP-1999.  
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
Query Match 9.5%; Score 61; DB 2; Length 66;  
Best Local Similarity 33.3%; Pred. No. 46;  
RESULT 1285  
ID ABB88631 standard; peptide; 71 AA.  
DE Conus magus I-superfamily conotoxin peptide sequence SEQ:125.  
PN WO200202590-A2.  
PD 10-JAN-2002.  
PA (UTAH ) UNIV UTAH RES FOUND.  
PA (COGN-) COGNETIX INC.  
Query Match 9.5%; Score 61; DB 5; Length 71;

Best Local Similarity 38.9%; Pred. No. 51;  
RESULT 1286  
ID AAU60927 standard; protein; 76 AA.  
DE Propionibacterium acnes immunogenic protein #21823.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 9.5%; Score 61; DB 4; Length 76;  
Best Local Similarity 27.1%; Pred. No. 55;  
RESULT 1287  
ID ABM57446 standard; protein; 76 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #22122.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 9.5%; Score 61; DB 6; Length 76;  
Best Local Similarity 27.1%; Pred. No. 55;  
RESULT 1288  
ID AAU40354 standard; protein; 130 AA.  
DE Propionibacterium acnes immunogenic protein #1250.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 9.5%; Score 61; DB 4; Length 130;  
Best Local Similarity 24.2%; Pred. No. 1e+02;  
RESULT 1289  
ID ABM36873 standard; protein; 130 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #1549.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 9.5%; Score 61; DB 6; Length 130;  
Best Local Similarity 24.2%; Pred. No. 1e+02;  
RESULT 1290  
ID AAU62706 standard; protein; 133 AA.  
DE Propionibacterium acnes immunogenic protein #23602.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 9.5%; Score 61; DB 4; Length 133;  
Best Local Similarity 29.8%; Pred. No. 1.1e+02;  
RESULT 1291  
ID ABM59225 standard; protein; 133 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #23901.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 9.5%; Score 61; DB 6; Length 133;  
Best Local Similarity 29.8%; Pred. No. 1.1e+02;  
RESULT 1292  
ID AAG03763 standard; protein; 136 AA.  
DE Human secreted protein, SEQ ID NO: 7844.  
PN EP1033401-A2.  
PD 06-SEP-2000.  
PA (GEST) GENSET.  
Query Match 9.5%; Score 61; DB 3; Length 136;  
Best Local Similarity 24.7%; Pred. No. 1.1e+02;  
RESULT 1293  
ID AA30384 standard; protein; 138 AA.  
DE Arabidopsis thaliana G2347 protein.  
PN WO20027185-A2.  
PD 03-OCT-2002.  
PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
Query Match 9.5%; Score 61; DB 6; Length 138;  
Best Local Similarity 25.8%; Pred. No. 1.1e+02;  
RESULT 1294  
ID ABG21912 standard; protein; 140 AA.  
DE Novel human diagnostic protein #21903.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HVSE-) HVSEQ INC.  
Query Match 9.5%; Score 61; DB 4; Length 140;  
Best Local Similarity 31.6%; Pred. No. 1.1e+02;

RESULT 1295  
ID AAU55085 standard; protein; 146 AA.  
DE Propionibacterium acnes immunogenic protein #15981.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 9.5%; Score 61; DB 4; Length 146;  
Best Local Similarity 28.6%; Pred. No. 1.2e+02;  
RESULT 1296  
ID ABM51604 standard; protein; 146 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #16280.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 9.5%; Score 61; DB 6; Length 146;  
Best Local Similarity 28.6%; Pred. No. 1.2e+02;  
RESULT 1297  
ID AA325383 standard; protein; 155 AA.  
DE Human NZMS-7 protein.  
PN WO200246385-A2.  
PD 13-JUN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.5%; Score 61; DB 5; Length 155;  
Best Local Similarity 26.0%; Pred. No. 1.3e+02;  
RESULT 1298  
ID AAG41559 standard; protein; 156 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51722.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 9.5%; Score 61; DB 3; Length 156;  
Best Local Similarity 25.8%; Pred. No. 1.3e+02;  
RESULT 1299  
ID AB081277 standard; protein; 161 AA.  
DE Pseudomonas aeruginosa polypeptide #13452.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.5%; Score 61; DB 7; Length 161;  
Best Local Similarity 24.8%; Pred. No. 1.3e+02;  
RESULT 1300  
ID AAM95503 standard; protein; 167 AA.  
DE Human reproductive system related antigen SEQ ID NO: 4161.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.5%; Score 61; DB 4; Length 167;  
Best Local Similarity 30.9%; Pred. No. 1.4e+02;  
RESULT 1301  
ID AB96186 standard; protein; 167 AA.  
DE Human testicular antigen SEQ ID NO: 1570.  
PN WO200155317-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.5%; Score 61; DB 4; Length 167;  
Best Local Similarity 30.9%; Pred. No. 1.4e+02;  
RESULT 1302  
ID AAU18158 standard; protein; 167 AA.  
DE Novel human DNA-binding protein #5.  
PN WO200155162-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.5%; Score 61; DB 4; Length 167;  
Best Local Similarity 30.9%; Pred. No. 1.4e+02;  
RESULT 1303  
ID ABG92579 standard; protein; 167 AA.  
DE Human DNA-binding protein #5.  
PN US2002102638-A1.  
PD 01-AUG-2002.  
PA (ROSE/) ROSEN C A.  
PD (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.5%; Score 61; DB 5; Length 167;  
Best Local Similarity 30.9%; Pred. No. 1.4e+02;

RESULT 1304  
ID ADC25296 standard; protein; 167 AA.  
DE Human extracellular matrix protein from gene 5.  
PN US2003049650-A1.  
PD 13-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.5%; Score 61; DB 7; Length 167;  
Best Local Similarity 30.9%; Pred. No. 1.4e+02;  
RESULT 1305  
ID RAY70953 standard; protein; 181 AA.  
DE Arabidopsis SERK interacting protein #2 from clone 3B39.  
PN WO200024914-A2.  
PD 04-MAY-2000.  
PA (NOVS) NOVARTIS AG.  
Query Match 9.5%; Score 61; DB 3; Length 181;  
Best Local Similarity 25.8%; Pred. No. 1.5e+02;  
RESULT 1306  
ID AAG41557 standard; protein; 181 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51721.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 9.5%; Score 61; DB 3; Length 181;  
Best Local Similarity 25.8%; Pred. No. 1.5e+02;  
RESULT 1307  
ID AAU93175 standard; protein; 181 AA.  
DE Arabidopsis transcription factor #213.  
PN WO200215675-A1.  
PD 28-FEB-2002.  
PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
PA (PILG/) PILGRIM M.  
PA (CREE/) CREELMAN R.  
PA (DUBE/) DUBELL A J.  
PA (HEAR/) HEARD J E.  
PA (JIAN/) JIANG C.  
PA (KEDD/) KEDDIE J.  
PA (ADAM/) ADAM L.  
PA (RATC/) RATCLIFF O.  
PA (REUB/) REUBER J L.  
PA (RIEC/) RIECHMANN J L.  
PA (YUGG/) YU G.  
PA (PINE/) PINEDA O.  
Query Match 9.5%; Score 61; DB 5; Length 181;  
Best Local Similarity 25.8%; Pred. No. 1.5e+02;  
RESULT 1308  
ID ADD31087 standard; protein; 181 AA.  
DE Plant yield-related protein from clone G2347.  
PN WO2003013227-A2.  
PD 20-FEB-2003.  
PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
Query Match 9.5%; Score 61; DB 7; Length 181;  
Best Local Similarity 25.8%; Pred. No. 1.5e+02;  
RESULT 1309  
ID ADI41969 standard; protein; 181 AA.  
DE Plant transcription factor #216.  
PN US2004019927-A1.  
PD 29-JAN-2004.  
PA (SHER/) SHERMAN B K.  
PA (RIEC/) RIECHMANN J L.  
PA (JIAN/) JIANG C.  
PA (HEAR/) HEARD J E.  
PA (HAAK/) HAAKE V.  
PA (CREE/) CREELMAN R A.  
PA (RATC/) RATCLIFFE O.  
PA (ADAM/) ADAM L J.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J.  
PA (BROU/) BROUN P E.  
PA (PILG/) PILGRIM M L.  
PA (DUBE/) DUBELL A N.  
PA (PINE/) PINEDA O.  
PA (YUGG/) YU G.  
Query Match 9.5%; Score 61; DB 8; Length 181;  
Best Local Similarity 25.8%; Pred. No. 1.5e+02;  
RESULT 1310  
ID ADO2545 standard; protein; 181 AA.  
DE Thalecress transcription factor protein #479.  
PN US2004045049-A1.  
PD 04-MAR-2004.  
PA (ZHAN/) ZHANG J.  
PA (FROM/) FROMM M E.  
PA (HEAR/) HEARD J E.  
PA (RIEC/) RIECHMANN J L.  
PA (ADAM/) ADAM L J.  
PA (BROU/) BROUN P E.  
PA (PINE/) PINEDA O.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J S.  
PA (YUGG/) YU G.  
PA (JIAN/) JIANG C.  
PA (SAMA/) SAMAH R S.  
PA (PILG/) PILGRIM M L.  
PA (CREE/) CREELMAN R A.  
PA (DUBE/) DUBELL A N.  
PA (RATC/) RATCLIFFE O.  
PA (KUMI/) KUMIMOTO R.  
PA (SHER/) SHERMAN B K.  
Query Match 9.5%; Score 61; DB 8; Length 181;  
Best Local Similarity 25.8%; Pred. No. 1.5e+02;  
RESULT 1311  
ID ADO03499 standard; protein; 181 AA.  
DE Thalecress transcription factor protein #581.  
PN US2004045049-A1.  
PD 04-MAR-2004.  
PA (ZHAN/) ZHANG J.  
PA (FROM/) FROMM M E.  
PA (HEAR/) HEARD J E.  
PA (RIEC/) RIECHMANN J L.  
PA (ADAM/) ADAM L J.  
PA (BROU/) BROUN P E.  
PA (PINE/) PINEDA O.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J S.  
PA (YUGG/) YU G.  
PA (JIAN/) JIANG C.  
PA (SAMA/) SAMAH R S.  
PA (PILG/) PILGRIM M L.  
PA (CREE/) CREELMAN R A.  
PA (DUBE/) DUBELL A N.  
PA (RATC/) RATCLIFFE O.  
PA (KUMI/) KUMIMOTO R.  
PA (SHER/) SHERMAN B K.  
Query Match 9.5%; Score 61; DB 8; Length 181;  
Best Local Similarity 25.8%; Pred. No. 1.5e+02;  
RESULT 1312  
ID ABB70680 standard; protein; 184 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 38832.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 9.5%; Score 61; DB 4; Length 184;  
Best Local Similarity 24.1%; Pred. No. 1.6e+02;  
RESULT 1313  
ID ADK34471 standard; protein; 191 AA.  
DE Novel human polypeptide SeqID6553.  
PN WO200216439-A2.  
PD 28-FEB-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.5%; Score 61; DB 5; Length 191;  
Best Local Similarity 29.9%; Pred. No. 1.6e+02;  
RESULT 1314  
ID AAG41557 standard; protein; 211 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51720.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 9.5%; Score 61; DB 3; Length 211;  
Best Local Similarity 25.8%; Pred. No. 1.5e+02;

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Best Local Similarity 25.8%; Pred. No. 1.9e+02;
RESULT 1315
ID AAU32776 standard; protein; 219 AA.
DE Novel human secreted protein #3267.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.5%; Score 61; DB 4; Length 219;
Best Local Similarity 27.6%; Pred. No. 1.9e+02;
RESULT 1316
ID AAU30328 standard; protein; 239 AA.
DE Novel human secreted protein #819.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.5%; Score 61; DB 4; Length 239;
Best Local Similarity 30.7%; Pred. No. 2.2e+02;
RESULT 1317
ID ADY25086 standard; protein; 240 AA.
DE Plant full length insert polypeptide seqid 72870.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 9.5%; Score 61; DB 8; Length 240;
Best Local Similarity 25.8%; Pred. No. 2.2e+02;
RESULT 1318
ID AAM95499 standard; protein; 253 AA.
DE Human reproductive system related antigen SEQ ID NO: 4157.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.5%; Score 61; DB 4; Length 253;
Best Local Similarity 25.5%; Pred. No. 2.3e+02;
RESULT 1319
ID ABB96182 standard; protein; 253 AA.
DE Human testicular antigen SEQ ID NO: 1566.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.5%; Score 61; DB 4; Length 253;
Best Local Similarity 25.5%; Pred. No. 2.3e+02;
RESULT 1320
ID AAU18236 standard; protein; 253 AA.
DE Novel human DNA-binding protein #83.
PN WO200155162-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.5%; Score 61; DB 4; Length 253;
Best Local Similarity 25.5%; Pred. No. 2.3e+02;
RESULT 1321
ID ABG92657 standard; protein; 253 AA.
DE Human DNA-binding protein #83.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 9.5%; Score 61; DB 5; Length 253;
Best Local Similarity 25.5%; Pred. No. 2.3e+02;
RESULT 1322
ID ADC25374 standard; protein; 253 AA.
DE Human extracellular matrix protein from gene 83.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.5%; Score 61; DB 7; Length 253;
Best Local Similarity 25.5%; Pred. No. 2.3e+02;
RESULT 1323
ID ABB71139 standard; protein; 456 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40209.
ID ABG05679 standard; protein; 261 AA.
DE Novel human diagnostic protein #5670.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.5%; Score 61; DB 4; Length 261;
Best Local Similarity 27.0%; Pred. No. 2.4e+02;
RESULT 1324
ID ABG18016 standard; protein; 325 AA.
DE Novel human diagnostic protein #18007.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.5%; Score 61; DB 4; Length 325;
Best Local Similarity 33.3%; Pred. No. 3.1e+02;
RESULT 1325
ID AAB25524 standard; protein; 339 AA.
DE Pinus radiata cell signalling involved protein SEQ ID NO:899.
PN WO200042171-A1.
PD 20-JUL-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 9.5%; Score 61; DB 3; Length 339;
Best Local Similarity 24.6%; Pred. No. 3.3e+02;
RESULT 1326
ID ABO59777 standard; protein; 374 AA.
DE Human genome derived single exon protein #6011.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 9.5%; Score 61; DB 8; Length 374;
Best Local Similarity 22.3%; Pred. No. 3.7e+02;
RESULT 1327
ID ABG08725 standard; protein; 397 AA.
DE Novel human diagnostic protein #8716.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.5%; Score 61; DB 4; Length 397;
Best Local Similarity 30.9%; Pred. No. 3.9e+02;
RESULT 1328
ID ADI24784 standard; protein; 399 AA.
DE Plant full length insert polypeptide seqid 72568.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 9.5%; Score 61; DB 8; Length 399;
Best Local Similarity 32.5%; Pred. No. 4e+02;
RESULT 1329
ID ABO77209 standard; protein; 428 AA.
DE Pseudomonas aeruginosa polypeptide #9384.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 9.5%; Score 61; DB 7; Length 428;
Best Local Similarity 25.6%; Pred. No. 4.3e+02;
RESULT 1330
ID ADC37583 standard; protein; 429 AA.
DE Human nucleic acid associated protein, NAAP-50.
PN WO2003046151-A2.
PD 05-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 9.5%; Score 61; DB 7; Length 429;
Best Local Similarity 22.3%; Pred. No. 4.3e+02;
RESULT 1331
ID ABB71139 standard; protein; 456 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40209.
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PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 9.5%; Score 61; DB 4; Length 456;  
Best Local Similarity 22.7%; Pred. No. 4.7e+02;  
RESULT 1332  
ID ABB06048 standard; protein; 468 AA.  
DE Human NS protein sequence SEQ ID NO:140.  
PN WO200206315-A2.  
PD 24-JAN-2002.  
PA (COMP-) COMPUGEN LTD.  
Query Match 9.5%; Score 61; DB 5; Length 468;  
Best Local Similarity 27.6%; Pred. No. 4.8e+02;  
RESULT 1333  
ID ADF32357 standard; protein; 491 AA.  
DE T365 protein.  
PN CN1394957-A.  
PD 05-FEB-2003.  
PA (GENE-) INST GENETICS CHINESE ACAD SCI.  
Query Match 9.5%; Score 61; DB 7; Length 491;  
Best Local Similarity 32.5%; Pred. No. 5.1e+02;  
RESULT 1334  
ID ABM89271 standard; protein; 498 AA.  
DE Rice abiotic stress responsive polypeptide SEQ ID NO:7517.  
PN WO2003008540-A2.  
PD 30-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 9.5%; Score 61; DB 7; Length 498;  
Best Local Similarity 25.0%; Pred. No. 5.2e+02;  
RESULT 1335  
ID ADX66627 standard; protein; 513 AA.  
DE Plant full length insert polypeptide seqid 37470.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABR/) TABASKA J E.  
PA (CAOX/) CAO Y.  
Query Match 9.5%; Score 61; DB 8; Length 513;  
Best Local Similarity 32.5%; Pred. No. 5.4e+02;  
RESULT 1336  
ID ABM89036 standard; protein; 516 AA.  
DE Rice abiotic stress responsive polypeptide SEQ ID NO:7282.  
PN WO2003008540-A2.  
PD 30-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 9.5%; Score 61; DB 7; Length 516;  
Best Local Similarity 28.8%; Pred. No. 5.4e+02;  
RESULT 1337  
ID ABP62937 standard; protein; 558 AA.  
DE Human polypeptide SEQ ID NO 374.  
PN WO200218424-A2.  
PD 07-MAR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.5%; Score 61; DB 5; Length 558;  
Best Local Similarity 22.3%; Pred. No. 5.9e+02;  
RESULT 1338  
ID ABB61808 standard; protein; 681 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 12216.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 9.5%; Score 61; DB 4; Length 681;  
Best Local Similarity 23.9%; Pred. No. 7.5e+02;  
RESULT 1339  
ID ABB60096 standard; protein; 961 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 7080.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 9.5%; Score 61; DB 4; Length 961;

Best Local Similarity 22.7%; Pred. No. 1.1e+03;  
RESULT 1340  
ID AAU80188 standard; protein; 961 AA.  
DE Human TSP1 domain containing protein encoded by cDNA FGO6969.  
PN JP2002085059-A.  
PD 26-MAR-2002.  
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.  
PA (YOSH ) YOSHITOMI PHARM IND KK.  
Query Match 9.5%; Score 61; DB 5; Length 961;  
Best Local Similarity 26.4%; Pred. No. 1.1e+03;  
RESULT 1341  
ID AAY79165 standard; protein; 1014 AA.  
DE Pneumocystis carinii major surface glycoprotein HMSGp1.  
PN WO200009760-A1.  
PD 24-FEB-2000.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 9.5%; Score 61; DB 3; Length 1014;  
Best Local Similarity 21.7%; Pred. No. 1.2e+03;  
RESULT 1342  
ID ABB61135 standard; protein; 1014 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 10197.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 9.5%; Score 61; DB 4; Length 1014;  
Best Local Similarity 32.3%; Pred. No. 1.2e+03;  
RESULT 1343  
ID ABG11821 standard; protein; 1049 AA.  
DE Novel human diagnostic protein #11812.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.5%; Score 61; DB 4; Length 1049;  
Best Local Similarity 28.8%; Pred. No. 1.3e+03;  
RESULT 1344  
ID ADI82537 standard; protein; 1064 AA.  
DE Human modifier of p21 (MP21) protein sequence SeqID103.  
PN WO2004005486-A2.  
PD 15-JAN-2004.  
PA (EXEL-) EXELIXIS INC.  
Query Match 9.5%; Score 61; DB 8; Length 1064;  
Best Local Similarity 24.0%; Pred. No. 1.3e+03;  
RESULT 1345  
ID ABM80078 standard; protein; 1064 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO60298, SEQ:203.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 9.5%; Score 61; DB 8; Length 1064;  
Best Local Similarity 24.0%; Pred. No. 1.3e+03;  
RESULT 1346  
ID ABB66149 standard; protein; 1320 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 25239.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 9.5%; Score 61; DB 4; Length 1320;  
Best Local Similarity 24.5%; Pred. No. 1.7e+03;  
RESULT 1347  
ID ABG11841 standard; protein; 1492 AA.  
DE Novel human diagnostic protein #11832.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.5%; Score 61; DB 4; Length 1492;  
Best Local Similarity 28.8%; Pred. No. 1.9e+03;  
RESULT 1348  
ID AAB59827 standard; protein; 1592 AA.  
DE Protein #4 encoded by TctD/E gene.  
PN WO200072650-A2.  
PD 07-DEC-2000.  
PA (UYOH-) UNIV OHIO.  
Query Match 9.5%; Score 61; DB 4; Length 1592;

Best Local Similarity 31.1%; Pred. No. 2.1e+03;  
RESULT 1349  
ID ADS17495 standard; protein; 1799 AA.  
DE Amino acid sequence of murine laminin beta-2.  
PN WO2004079007-A2.  
PD 16-SEP-2004.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
Query Match 9.5%; Score 61; DB 8; Length 1799;  
Best Local Similarity 27.9%; Pred. No. 2.4e+03;  
RESULT 1350  
ID ADR97664 standard; protein; 1799 AA.  
DE Murine laminin beta 2 chain protein, an actin acting substance SeqID 8.  
PN WO2004079332-A2.  
PD 16-SEP-2004.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
Query Match 9.5%; Score 61; DB 8; Length 1799;  
Best Local Similarity 27.9%; Pred. No. 2.4e+03;  
RESULT 1351  
ID ADM44476 standard; protein; 1799 AA.  
DE Murine laminin beta 2.  
PN WO2005001090-A1.  
PD 06-JAN-2005.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
Query Match 9.5%; Score 61; DB 9; Length 1799;  
Best Local Similarity 27.9%; Pred. No. 2.4e+03;  
RESULT 1352  
ID ADY5710 standard; protein; 1799 AA.  
DE Mouse laminin-2 beta chain protein.  
PN WO2005021744-A1.  
PD 10-WAR-2005.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
Query Match 9.5%; Score 61; DB 9; Length 1799;  
Best Local Similarity 27.9%; Pred. No. 2.4e+03;  
RESULT 1353  
ID ADV32464 standard; protein; 1799 AA.  
DE Mouse laminin beta chain protein.  
PN WO2005052050-A.  
PD 03-WAR-2005.  
PA (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.  
Query Match 9.5%; Score 61; DB 9; Length 1799;  
Best Local Similarity 27.9%; Pred. No. 2.4e+03;  
RESULT 1354  
ID AEB56264 standard; protein; 1799 AA.  
DE Event sequencer related protein SEQ ID NO 8.  
PN WO2005073890-A1.  
PD 11-AUG-2005.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
Query Match 9.5%; Score 61; DB 9; Length 1799;  
Best Local Similarity 27.9%; Pred. No. 2.4e+03;  
RESULT 1355  
ID AEF19266 standard; protein; 1799 AA.  
DE Mouse laminin-2 beta chain.  
PN WO2006001396-A1.  
PD 05-JAN-2006.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
Query Match 9.5%; Score 61; DB 10; Length 1799;  
Best Local Similarity 27.9%; Pred. No. 2.4e+03;  
RESULT 1356  
ID AEP16759 standard; protein; 1799 AA.  
DE Mouse laminin-2 beta chain.  
PN WO2006001397-A1.  
PD 05-JAN-2006.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
Query Match 9.5%; Score 61; DB 10; Length 1799;  
Best Local Similarity 27.9%; Pred. No. 2.4e+03;  
RESULT 1357  
ID ADO62867 standard; protein; 2068 AA.  
DE Transcription factor G2990 orthologous sequence, SEQ ID 1334.  
PN WO2004031349-A2.  
PD 15-APR-2004.  
PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
Query Match 9.5%; Score 61; DB 8; Length 2068;  
Best Local Similarity 34.2%; Pred. No. 2.8e+03;

RESULT 1358  
ID ABO79997 standard; protein; 90 AA.  
DE Pseudomonas aeruginosa polypeptide #12172.  
PN US551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.4%; Score 60.5; DB 7; Length 90;  
Best Local Similarity 32.8%; Pred. No. 77;  
RESULT 1359  
ID AAG18562 standard; protein; 106 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 20021.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 9.4%; Score 60.5; DB 3; Length 106;  
Best Local Similarity 21.2%; Pred. No. 93;  
RESULT 1360  
ID AAO21323 standard; protein; 106 AA.  
DE Arabidopsis thaliana KCP-like protein, SEQ ID NO 78.  
PN WO200222821-A2.  
PD 21-WAR-2002.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 9.4%; Score 60.5; DB 5; Length 106;  
Best Local Similarity 21.2%; Pred. No. 93;  
RESULT 1361  
ID ABM64904 standard; protein; 106 AA.  
DE Propionibacterium acnes immunogenic polypeptide #29580.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 9.4%; Score 60.5; DB 6; Length 106;  
Best Local Similarity 29.6%; Pred. No. 93;  
RESULT 1362  
ID ADG74890 standard; protein; 106 AA.  
DE Plant developmental pathway modulation-related RKS/ELS ligand protein 11.  
PN EP1382682-A2.  
PD 21-JAN-2004.  
PA (EXPR-) EXPRESSIVE RES BV.  
Query Match 9.4%; Score 60.5; DB 8; Length 106;  
Best Local Similarity 21.2%; Pred. No. 93;  
RESULT 1363  
ID AAU60791 standard; protein; 109 AA.  
DE Propionibacterium acnes immunogenic protein #21687.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 9.4%; Score 60.5; DB 4; Length 109;  
Best Local Similarity 26.5%; Pred. No. 96;  
RESULT 1364  
ID ABM57310 standard; protein; 109 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #21986.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 9.4%; Score 60.5; DB 6; Length 109;  
Best Local Similarity 26.5%; Pred. No. 96;  
RESULT 1365  
ID ADX66981 standard; protein; 112 AA.  
DE Plant full length insert polypeptide seqid 37824.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 9.4%; Score 60.5; DB 8; Length 112;  
Best Local Similarity 21.2%; Pred. No. 1e+02;  
RESULT 1366  
ID AAU53785 standard; protein; 118 AA.  
DE Propionibacterium acnes immunogenic protein #14681.  
PN WO200181581-A2.  
PD 01-NOV-2001.



PA (CORI-) CORIXA CORP.  
Query Match 9.4%; Score 60.5; DB 4; Length 118;  
Best Local Similarity 26.4%; Pred. No. 1.1e+02;  
RESULT 1367  
ID ABM50304 standard; protein; 118 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #14980.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 9.4%; Score 60.5; DB 6; Length 118;  
Best Local Similarity 26.4%; Pred. No. 1.1e+02;  
RESULT 1368  
ID AAU67602 standard; protein; 122 AA.  
DE Propionibacterium acnes immunogenic protein #28498.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 9.4%; Score 60.5; DB 4; Length 122;  
Best Local Similarity 29.6%; Pred. No. 1.1e+02;  
RESULT 1369  
ID ABM64121 standard; protein; 122 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #28797.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 9.4%; Score 60.5; DB 6; Length 122;  
Best Local Similarity 29.6%; Pred. No. 1.1e+02;  
RESULT 1370  
ID AAR78693 standard; protein; 162 AA.  
DE Rat skeletal muscle stress protein, p20.  
PN JP07181180-A.  
PD 21-JUL-1995.  
PA (KATO/) KATO K.  
PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.  
Query Match 9.4%; Score 60.5; DB 2; Length 162;  
Best Local Similarity 23.4%; Pred. No. 1.5e+02;  
RESULT 1371  
ID ABG93942 standard; protein; 162 AA.  
DE Rat polypeptide orthologous to DACC-9.  
PN WO200264623-A1.  
PD 22-AUG-2002.  
PA (ADPP-) ADP PHARM PTY LTD.  
PA (UNSY) UNIV SYDNEY.  
Query Match 9.4%; Score 60.5; DB 5; Length 162;  
Best Local Similarity 23.4%; Pred. No. 1.5e+02;  
RESULT 1372  
ID ADA34307 standard; protein; 162 AA.  
DE Acinetobacter baumannii protein #1468.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.4%; Score 60.5; DB 6; Length 162;  
Best Local Similarity 23.1%; Pred. No. 1.5e+02;  
RESULT 1373  
ID ADE56085 standard; protein; 162 AA.  
DE Rat Protein P97541, SEQ ID NO 1926.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 9.4%; Score 60.5; DB 7; Length 162;  
Best Local Similarity 23.4%; Pred. No. 1.5e+02;  
RESULT 1374  
ID AAU49482 standard; protein; 175 AA.  
DE Propionibacterium acnes immunogenic protein #10378.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 9.4%; Score 60.5; DB 4; Length 175;  
Best Local Similarity 27.1%; Pred. No. 1.7e+02;  
RESULT 1375  
ID ABM46001 standard; protein; 175 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #10677.

PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 9.4%; Score 60.5; DB 6; Length 175;  
Best Local Similarity 27.1%; Pred. No. 1.7e+02;  
RESULT 1376  
ID ADQ66278 standard; protein; 180 AA.  
DE Novel human protein sequence #1251.  
PN EP1440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.4%; Score 60.5; DB 8; Length 180;  
Best Local Similarity 39.6%; Pred. No. 1.8e+02;  
RESULT 1377  
ID ABO73633 standard; protein; 188 AA.  
DE Pseudomonas aeruginosa polypeptide #5808.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.4%; Score 60.5; DB 7; Length 188;  
Best Local Similarity 36.0%; Pred. No. 1.8e+02;  
RESULT 1378  
ID ADX68391 standard; protein; 194 AA.  
DE Plant full length insert polypeptide seqid 39234.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 9.4%; Score 60.5; DB 8; Length 194;  
Best Local Similarity 26.0%; Pred. No. 1.9e+02;  
RESULT 1379  
ID AAW40101 standard; protein; 210 AA.  
DE Human herpesvirus 8 (HHV-8) dihydrofolate reductase.  
PN WO9804284-A1.  
PD 05-FEB-1998.  
PA (UYJO) UNIV JOHNS HOPKINS.  
Query Match 9.4%; Score 60.5; DB 2; Length 210;  
Best Local Similarity 25.7%; Pred. No. 2.1e+02;  
RESULT 1380  
ID AAM82437 standard; protein; 210 AA.  
DE KSHV DHER protein encoded by ORF 2.  
PN US5849584-A.  
PD 15-DEC-1998.  
PA (UYCO) UNIV COLUMBIA NEW YORK.  
Query Match 9.4%; Score 60.5; DB 2; Length 210;  
Best Local Similarity 25.7%; Pred. No. 2.1e+02;  
RESULT 1381  
ID AAB93909 standard; protein; 217 AA.  
DE Human protein sequence SEQ ID NO:13873.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 9.4%; Score 60.5; DB 4; Length 217;  
Best Local Similarity 23.7%; Pred. No. 2.2e+02;  
RESULT 1382  
ID ABB70904 standard; protein; 231 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 39504.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 9.4%; Score 60.5; DB 4; Length 231;  
Best Local Similarity 40.6%; Pred. No. 2.4e+02;  
RESULT 1383  
ID ADY13434 standard; protein; 259 AA.  
DE Plant full length insert polypeptide seqid 69249.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIU/) LIU J.  
PA (ZHOU/) ZHOU Y.

PA (KOVA//) KOVALIC D K.  
PA (SCRE//) SCREEN S E.  
PA (TAB//) TABASKA J E.  
PA (CAOY//) CAO Y.  
Query Match 9.4%; Score 60.5; DB 8; Length 259;  
Best Local Similarity 23.1%; Pred. No. 2.7e+02;  
RESULT 1384  
ID AAM41811 standard; protein; 272 AA.  
DE Human polypeptide SEQ ID NO 6742.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.4%; Score 60.5; DB 4; Length 272;  
Best Local Similarity 23.7%; Pred. No. 2.9e+02;  
RESULT 1385  
ID AAM41810 standard; protein; 272 AA.  
DE Human polypeptide SEQ ID NO 6741.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.4%; Score 60.5; DB 4; Length 272;  
Best Local Similarity 23.7%; Pred. No. 2.9e+02;  
RESULT 1386  
ID ADX72922 standard; protein; 275 AA.  
DE Plant full length insert polypeptide seqid 42288.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ//) LIU J.  
PA (ZHOU//) ZHOU Y.  
PA (KOVA//) KOVALIC D K.  
PA (SCRE//) SCREEN S E.  
PA (TAB//) TABASKA J E.  
PA (CAOY//) CAO Y.  
Query Match 9.4%; Score 60.5; DB 8; Length 275;  
Best Local Similarity 28.7%; Pred. No. 2.9e+02;  
RESULT 1387  
ID ABO72046 standard; protein; 278 AA.  
DE Pseudomonas aeruginosa polypeptide #4221.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.4%; Score 60.5; DB 7; Length 278;  
Best Local Similarity 42.9%; Pred. No. 2.9e+02;  
RESULT 1388  
ID ABM89392 standard; protein; 278 AA.  
DE Rice abiotic stress responsive polypeptide SEQ ID NO:7638.  
PN WO2003008540-A2.  
PD 30-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 9.4%; Score 60.5; DB 7; Length 278;  
Best Local Similarity 32.3%; Pred. No. 2.9e+02;  
RESULT 1389  
ID ABO69424 standard; protein; 297 AA.  
DE Pseudomonas aeruginosa polypeptide #1599.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.4%; Score 60.5; DB 7; Length 297;  
Best Local Similarity 29.7%; Pred. No. 3.2e+02;  
RESULT 1390  
ID ADS29625 standard; protein; 322 AA.  
DE Bacterial polypeptide #18650.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY//) CAO Y.  
PA (HINK//) HINKLE G J.  
PA (SLAT//) SLATER S C.  
PA (CHEN//) CHEN X.  
PA (GOLD//) GOLDMAN B S.  
Query Match 9.4%; Score 60.5; DB 8; Length 322;  
Best Local Similarity 20.3%; Pred. No. 3.5e+02;  
RESULT 1391  
ID ADY22680 standard; protein; 324 AA.  
DE Plant full length insert polypeptide seqid 70464.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ//) LIU J.  
PA (ZHOU//) ZHOU Y.  
PA (KOVA//) KOVALIC D K.  
PA (SCRE//) SCREEN S E.  
PA (TAB//) TABASKA J E.  
PA (CAOY//) CAO Y.  
Query Match 9.4%; Score 60.5; DB 8; Length 324;  
Best Local Similarity 31.1%; Pred. No. 3.5e+02;  
RESULT 1392  
ID AAB93734 standard; protein; 325 AA.  
DE Human protein sequence SEQ ID NO:13380.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 9.4%; Score 60.5; DB 4; Length 325;  
Best Local Similarity 23.7%; Pred. No. 3.6e+02;  
RESULT 1393  
ID ADR44482 standard; protein; 325 AA.  
DE Human G protein beta subunit-like protein.  
PN WO2004074448-A2.  
PD 02-SEP-2004.  
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
Query Match 9.4%; Score 60.5; DB 8; Length 325;  
Best Local Similarity 23.7%; Pred. No. 3.6e+02;  
RESULT 1394  
ID ADR44461 standard; protein; 326 AA.  
DE Human G protein beta subunit-like protein.  
PN WO2004074448-A2.  
PD 02-SEP-2004.  
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
Query Match 9.4%; Score 60.5; DB 8; Length 326;  
Best Local Similarity 23.7%; Pred. No. 3.6e+02;  
RESULT 1395  
ID ADR44439 standard; protein; 327 AA.  
DE Human G protein beta subunit-like protein SEQ ID NO:6.  
PN WO2004074448-A2.  
PD 02-SEP-2004.  
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
Query Match 9.4%; Score 60.5; DB 8; Length 327;  
Best Local Similarity 23.7%; Pred. No. 3.6e+02;  
RESULT 1396  
ID ADX17736 standard; protein; 327 AA.  
DE PRO polypeptide SEQ ID NO 3542.  
PN WO2005016952-A2.  
PD 24-FEB-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 9.4%; Score 60.5; DB 9; Length 327;  
Best Local Similarity 23.7%; Pred. No. 3.6e+02;  
RESULT 1397  
ID AAB41611 standard; protein; 332 AA.  
DE Human OREF ORF1375 polypeptide sequence SEQ ID NO:2750.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.4%; Score 60.5; DB 3; Length 332;  
Best Local Similarity 23.7%; Pred. No. 3.6e+02;  
RESULT 1398  
ID AAM40024 standard; protein; 332 AA.  
DE Human polypeptide SEQ ID NO 3169.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.4%; Score 60.5; DB 4; Length 332;  
Best Local Similarity 23.7%; Pred. No. 3.6e+02;  
RESULT 1399  
ID AAM40025 standard; protein; 360 AA.  
DE Human polypeptide SEQ ID NO 3170.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.

Query Match 9.4%; Score 60.5; DB 4; Length 360;  
Best Local Similarity 23.7%; Pred. No. 4e+02;  
RESULT 1400  
ID AAO19957 standard; protein; 396 AA.  
DE C elegans LMW-1 protein.  
PN WO2003000861-A2.  
PD 03-JAN-2003.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 9.4%; Score 60.5; DB 6; Length 396;  
Best Local Similarity 20.4%; Pred. No. 4.5e+02;  
RESULT 1401  
ID ABB70903 standard; protein; 410 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 39501.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 9.4%; Score 60.5; DB 4; Length 410;  
Best Local Similarity 40.6%; Pred. No. 4.7e+02;  
RESULT 1402  
ID AAG39792 standard; protein; 452 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 49288.  
PN EP1033485-A2.  
PD 06-SEP-2000.  
Query Match 9.4%; Score 60.5; DB 3; Length 452;  
Best Local Similarity 26.5%; Pred. No. 5.3e+02;  
RESULT 1403  
ID ABO71664 standard; protein; 462 AA.  
DE Pseudomonas aeruginosa polypeptide #3839.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.4%; Score 60.5; DB 7; Length 462;  
Best Local Similarity 29.8%; Pred. No. 5.4e+02;  
RESULT 1404  
ID ABO70874 standard; protein; 471 AA.  
DE Pseudomonas aeruginosa polypeptide #3049.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.4%; Score 60.5; DB 7; Length 471;  
Best Local Similarity 25.5%; Pred. No. 5.5e+02;  
RESULT 1405  
ID AAB80627 standard; protein; 473 AA.  
DE Environmental stress tolerant protein SEQ ID 40.  
PN WO200106006-A1.  
PD 25-JAN-2001.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
Query Match 9.4%; Score 60.5; DB 4; Length 473;  
Best Local Similarity 23.8%; Pred. No. 5.6e+02;  
RESULT 1406  
ID ABO80372 standard; protein; 487 AA.  
DE Pseudomonas aeruginosa polypeptide #12547.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.4%; Score 60.5; DB 7; Length 487;  
Best Local Similarity 29.1%; Pred. No. 5.8e+02;  
RESULT 1407  
ID ADM20100 standard; protein; 502 AA.  
DE Protein encoded by novel human channel/transporter gene #174 clone 2.  
PN WO200154472-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.4%; Score 60.5; DB 4; Length 502;  
Best Local Similarity 23.7%; Pred. No. 6e+02;  
RESULT 1408  
ID ABO83526 standard; protein; 504 AA.  
DE Pseudomonas aeruginosa polypeptide #15701.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.4%; Score 60.5; DB 7; Length 504;  
Best Local Similarity 24.5%; Pred. No. 6e+02;

RESULT 1409  
ID ABO79664 standard; protein; 535 AA.  
DE Pseudomonas aeruginosa polypeptide #11839.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.4%; Score 60.5; DB 7; Length 535;  
Best Local Similarity 22.3%; Pred. No. 6.4e+02;  
RESULT 1410  
ID ABO68460 standard; protein; 541 AA.  
DE Pseudomonas aeruginosa polypeptide #635.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.4%; Score 60.5; DB 7; Length 541;  
Best Local Similarity 27.3%; Pred. No. 6.5e+02;  
RESULT 1411  
ID AAB84687 standard; protein; 622 AA.  
DE Amino acid sequence of a Drosophila hexosaminidase-2.  
PN WO200142492-A1.  
PD 14-JUN-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
PA (UTEM ) UNIV TEMPLE.  
PA (UYWY-) UNIV WYOMING.  
Query Match 9.4%; Score 60.5; DB 4; Length 622;  
Best Local Similarity 21.2%; Pred. No. 7.7e+02;  
RESULT 1412  
ID ABB58485 standard; protein; 622 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 2247.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 9.4%; Score 60.5; DB 4; Length 622;  
Best Local Similarity 21.2%; Pred. No. 7.7e+02;  
RESULT 1413  
ID AAE25828 standard; protein; 622 AA.  
DE Fruit fly hexosaminidase-2 (Hex-2).  
PN US2002065404-A1.  
PD 30-MAY-2002.  
PA (BETE/) BETENBAUGH M J.  
PA (PALT/) PALTER K.  
Query Match 9.4%; Score 60.5; DB 5; Length 622;  
Best Local Similarity 21.2%; Pred. No. 7.7e+02;  
RESULT 1414  
ID ADJ49709 standard; protein; 626 AA.  
DE Oil-associated gene related protein #1209.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDEAUX J R.  
PA (ROGE/) ROGERS J A.  
Query Match 9.4%; Score 60.5; DB 8; Length 626;  
Best Local Similarity 25.3%; Pred. No. 7.8e+02;  
RESULT 1415  
ID ADJ71063 standard; protein; 731 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID2869.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 9.4%; Score 60.5; DB 7; Length 731;  
Best Local Similarity 24.0%; Pred. No. 9.3e+02;  
RESULT 1416  
ID ABB63043 standard; protein; 855 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 15921.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 9.4%; Score 60.5; DB 4; Length 855;  
Best Local Similarity 18.5%; Pred. No. 1.1e+03;

RESULT 1417  
ID ABO1651 standard; protein; 894 AA.  
DE Pseudomonas aeruginosa polypeptide #13826.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.4%; Score 60.5; DB 7; Length 894;  
Best Local Similarity 23.9%; Pred. No. 1.2e+03;  
RESULT 1418  
ID AAW43394 standard; protein; 1019 AA.  
DE Singapore horseshoe crab factor C proenzyme (CrPC 21).  
PN SG42456-A1.  
PD 15-AUG-1997.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 9.4%; Score 60.5; DB 2; Length 1019;  
Best Local Similarity 24.8%; Pred. No. 1.4e+03;  
RESULT 1419  
ID AAY05750 standard; protein; 1019 AA.  
DE Horseshoe crab Factor C.  
PN WO9915676-A1.  
PD 01-APR-1999.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 9.4%; Score 60.5; DB 2; Length 1019;  
Best Local Similarity 24.8%; Pred. No. 1.4e+03;  
RESULT 1420  
ID AAW94302 standard; protein; 1019 AA.  
DE Horseshoe crab Factor C protein #2.  
PN US5858706-A.  
PD 12-JAN-1999.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 9.4%; Score 60.5; DB 2; Length 1019;  
Best Local Similarity 24.8%; Pred. No. 1.4e+03;  
RESULT 1421  
ID AAY42490 standard; protein; 1019 AA.  
DE Recombinant N-terminally truncated Horseshoe crab Factor C protein.  
PN US5985590-A.  
PD 16-NOV-1999.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 9.4%; Score 60.5; DB 3; Length 1019;  
Best Local Similarity 24.8%; Pred. No. 1.4e+03;  
RESULT 1422  
ID AAB60935 standard; protein; 1019 AA.  
DE Horseshoe crab recombinant Factor C #2.  
PN WO200127289-A2.  
PD 19-APR-2001.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 9.4%; Score 60.5; DB 4; Length 1019;  
Best Local Similarity 24.8%; Pred. No. 1.4e+03;  
RESULT 1423  
ID ABP72334 standard; protein; 1019 AA.  
DE Horseshoe crab Factor C.  
PN WO200302976-A2.  
PD 09-JAN-2003.  
PA (WHLK ) BIOWHITTAKER INC.  
Query Match 9.4%; Score 60.5; DB 6; Length 1019;  
Best Local Similarity 24.8%; Pred. No. 1.4e+03;  
RESULT 1424  
ID ADM39099 standard; protein; 1019 AA.  
DE Southeast Asian horseshoe crab Factor C.  
PN WO2005003163-A1.  
PD 13-JAN-2005.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 9.4%; Score 60.5; DB 9; Length 1019;  
Best Local Similarity 24.8%; Pred. No. 1.4e+03;  
RESULT 1425  
ID ABG07191 standard; protein; 2506 AA.  
DE Novel human diagnostic protein #7182.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.4%; Score 60.5; DB 4; Length 2506;  
Best Local Similarity 24.6%; Pred. No. 4.1e+03;  
RESULT 1426  
ID ABG30064 standard; protein; 2506 AA.  
DE Novel human diagnostic protein #30055.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.4%; Score 60.5; DB 4; Length 2506;  
Best Local Similarity 24.6%; Pred. No. 4.1e+03;  
RESULT 1427  
ID ADN73145 standard; protein; 5155 AA.  
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 1040.  
PN WO2004035798-A2.  
PD 29-APR-2004.  
PA (CROP-) CROPDESIGN NV.  
Query Match 9.4%; Score 60.5; DB 8; Length 5155;  
Best Local Similarity 36.8%; Pred. No. 9.6e+03;  
RESULT 1428  
ID AAU48414 standard; protein; 51 AA.  
DE Propionibacterium acnes immunogenic protein #9310.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 9.3%; Score 60; DB 4; Length 51;  
Best Local Similarity 35.8%; Pred. No. 45;  
RESULT 1429  
ID ABM44933 standard; protein; 51 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #9609.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 9.3%; Score 60; DB 6; Length 51;  
Best Local Similarity 35.8%; Pred. No. 45;  
RESULT 1430  
ID AAU29306 standard; protein; 89 AA.  
DE Human PRO polypeptide sequence #283.  
PN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 9.3%; Score 60; DB 4; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1431  
ID ABU58682 standard; protein; 89 AA.  
DE Human PRO polypeptide #283.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1432  
ID ABU88230 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO19680.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1433  
ID ABU84545 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #283.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1434  
ID ABR66419 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.  
PN US2003027278-A1.  
PD 06-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1435  
ID ABR65809 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.  
PN US2003031519-A1.  
PD 20-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;

Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1436  
ID ABU99749 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #283.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1437  
ID ABU82988 standard; protein; 89 AA.  
DE Human PRO polypeptide #283.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1438  
ID ABU90109 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO19680.  
PN US2003036147-A1.  
PD 20-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1439  
ID ABR68358 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1440  
ID ABU96411 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO19680.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1441  
ID ABU92842 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #283.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1442  
ID ABO08919 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #283.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1443  
ID ABO02971 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #283.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1444  
ID ABR75125 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1445  
ID ABR94887 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1446  
ID ABU85860 standard; protein; 89 AA.

DE Human PRO polypeptide #283.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1447  
ID ABU99020 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO19680.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1448  
ID ABU98235 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO19680.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1449  
ID ABU91941 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO19680.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1450  
ID ABU99634 standard; protein; 89 AA.  
DE Human PRO polypeptide #283.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1451  
ID ABU86475 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #283.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1452  
ID ABU67688 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #283.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1453  
ID ABU80716 standard; protein; 89 AA.  
DE Human PRO protein #283.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1454  
ID ABR99634 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1455  
ID ABR99024 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.  
PN US2003040084-A1.  
PD 27-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1456

ID ABO16547 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #283.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1457  
ID ABR92447 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1458  
ID ABO19088 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #283.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1459  
ID ABR78509 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1460  
ID ABU95245 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO19680.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1461  
ID ABO00384 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO19680.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1462  
ID ABO11716 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #283.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1463  
ID ABO02361 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #283.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1464  
ID ABU8935 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO19680.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1465  
ID ABU83630 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #283.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1466  
ID ABO06431 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO19680.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1467  
ID ABR59467 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1468  
ID ABO09529 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #283.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1469  
ID ABO19393 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO19680.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1470  
ID ABO11411 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #283.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1471  
ID ABR67029 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1472  
ID ABO16242 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #283.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1473  
ID ABO13948 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #283.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1474  
ID ABU65851 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein, SEQ ID 566.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1475  
ID ABO07699 standard; protein; 89 AA.  
DE Human PRO polypeptide #283.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1476  
ID ABO03886 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #283.  
PN US2003036128-A1.  
PD 20-FEB-2003.

Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1477  
ID ABR67334 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1478  
ID ABO15937 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #283.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1479  
ID ABR56218 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein, PRO19680.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1480  
ID ABR65546 standard; protein; 89 AA.  
DE Human PRO polypeptide #283.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1481  
ID ABR95491 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO19680.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1482  
ID ABR71394 standard; protein; 89 AA.  
DE Human PRO19680 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1483  
ID ABO08004 standard; protein; 89 AA.  
DE Human PRO polypeptide #283.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1484  
ID ABR70245 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1485  
ID ABR69578 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1486  
ID ABO01719 standard; protein; 89 AA.  
DE Human PRO polypeptide #283.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.

Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1487  
ID ABR81521 standard; protein; 89 AA.  
DE Human PRO polypeptide #283.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1488  
ID ABR60318 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1489  
ID ABR68053 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1490  
ID ABR65441 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1491  
ID ABR68663 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1492  
ID ABR72075 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1493  
ID ABR85555 standard; protein; 89 AA.  
DE Human PRO polypeptide #283.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1494  
ID ABR89245 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #283.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1495  
ID ABR83325 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #283.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1496  
ID ABR95181 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO19680.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;

RESULT 1497  
ID ABU90729 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO19680.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1498  
ID ABU84240 standard; protein; 89 AA.  
DE Human secreted/transmembrane protein (PRO) #283.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1499  
ID ABU93891 standard; protein; 89 AA.  
DE Novel human secreted and transmembrane protein PRO19680.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;  
RESULT 1500  
ID ABR65136 standard; protein; 89 AA.  
DE Human secreted polypeptide PRO19680, SEQ ID NO:566.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 9.3%; Score 60; DB 6; Length 89;  
Best Local Similarity 40.5%; Pred. No. 87;



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OM protein - protein search, using sw model

Run on: August 3, 2006, 09:56:18 ; Search time 16 Seconds  
(without alignments)  
715.612 Million cell updates/sec

Title: US-10-015-967-2

Perfect score: 644

Sequence: 1 MKVLISLLLLPLMLMSV.....SRACQQLKQCQLRSPALPL 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR 80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77.5	12.0	477	2 T19801	hypothetical prote
2	77	12.0	2669	1 JQ1750	genome polyprotein
3	74.5	11.6	448	2 I50451	vitamin D receptor
4	73.5	11.4	70	2 A60912	vitamin D receptor
5	71.5	11.1	108	2 G84522	similar to gibbere
6	71	11.0	411	2 S35333	steroid receptor p
7	71	11.0	2662	2 S16664	large protein L -
8	71	11.0	3190	2 T13828	CREB-binding prote
9	70.5	10.9	1283	2 T49804	hypothetical prote
10	70	10.9	543	2 A32693	steroid receptor p
11	70	10.9	746	2 B32693	steroid receptor p
12	70	10.9	1095	2 T24061	hypothetical prote
13	70	10.9	1620	2 T27283	hypothetical prote
14	69.5	10.8	221	2 C34768	ORF2 protein - Orf
15	69.5	10.8	575	1 THHUB	thrombomodulin pre
16	69	10.7	200	2 C83086	hypothetical prote
17	68.5	10.6	381	2 A46358	steroid/thyroid ho
18	68.5	10.6	422	2 PC4019	vitamin D receptor
19	68.5	10.6	423	2 A31761	1,25-dihydroxyvita
20	68.5	10.6	427	2 S24174	vitamin D receptor
21	68.5	10.6	427	2 A28200	vitamin D receptor
22	68.5	10.6	647	2 S36557	B1 protein - human
23	68.5	10.6	1006	2 S74992	hypothetical prote
24	68	10.6	283	2 S42393	G-box-binding prot
25	67	10.4	376	2 T48950	cysteine proteinase
26	67	10.4	475	2 E69643	histidine permease
27	67	10.4	1062	2 T14151	Inv protein - mous
28	67	10.4	1062	2 T30255	inversin - mouse
29	66.5	10.3	103	2 A72713	hypothetical prote

30	66.5	10.3	419	2 A57000	orphan receptor CO
31	66.5	10.3	422	2 I48305	gene COUP-TF1 prot
32	66.5	10.3	423	2 S02710	transcription fact
33	66	10.2	339	2 T36061	hypothetical prote
34	65.5	10.2	106	2 S60232	giberellin-regula
35	65.5	10.2	397	2 S26617	transcription fact
36	65.5	10.2	413	2 H82270	hypothetical prote
37	65.5	10.2	425	2 JC7230	vitamin D receptor
38	65.5	10.2	646	2 S36586	B1 protein - human
39	65.5	10.2	706	2 JE0164	frizzled-6 protein
40	65	10.1	363	2 JC4748	polygalacturonase
41	65	10.1	440	2 JS0374	hypothetical 51.6K
42	65	10.1	1797	2 A55677	laminin beta-2 ch
43	64.5	10.0	359	2 B29960	Balbani ring 2 ch
44	64.5	10.0	622	2 I48733	protein kinase rck
45	64	9.9	227	2 I39313	zinc-finger protei
46	64	9.9	334	2 T03556	probable D-ribose-
47	64	9.9	1798	2 S53869	laminin beta-2 cha
48	63.5	9.9	233	2 T09788	probable superoxid
49	63.5	9.9	262	2 T19323	hypothetical prote
50	63	9.8	160	2 I61899	eosinophil cationi
51	63	9.8	330	2 S74255	homeotic protein s
52	63	9.8	371	1 S53442	DNA repair protein
53	63	9.8	462	2 T04437	hypothetical prote
54	62.5	9.7	410	2 I50689	orphan receptor CO
55	62.5	9.7	414	2 I48975	apolipoprotein A-I
56	62.5	9.7	414	2 A37133	apolipoprotein A-I
57	62.5	9.7	419	2 G82192	PqIA family protei
58	62.5	9.7	420	2 JC7229	vitamin D receptor
59	62.5	9.7	767	2 S41479	DNA-binding protei
60	62.5	9.7	840	2 T21333	hypothetical prote
61	62.5	9.7	282	2 T42717	DNA-binding protei
62	62	9.6	235	2 T16916	hypothetical prote
63	62	9.6	346	2 B90620	NADH dehydrogenase
64	62	9.6	371	1 R6BYM7	ribosomal protein
65	62	9.6	577	2 S33763	hormone receptor N
66	62	9.6	728	2 A48830	probable transcrip
67	62	9.6	1453	2 G96613	hypothetical prote
68	62	9.6	1670	1 CGHU3B	collagen alpha 3(I
69	62	9.6	3026	2 T28431	variant surface pr
70	61.5	9.5	94	2 JH0787	transcription fact
71	61.5	9.5	369	2 A42565	interleukin-2 rece
72	61.5	9.5	403	2 S35334	steroid receptor p
73	61	9.5	138	2 T52567	squamosa promoter
74	61	9.5	181	2 T52607	squamosa promoter
75	61	9.5	183	2 A49905	protein secretion
76	61	9.5	346	2 T11168	NADH2 dehydrogenas
77	61	9.5	398	2 C91063	hypothetical prote
78	61	9.5	795	2 T34468	hypothetical prote
79	61	9.5	926	2 S58936	meiotic recombinat
80	61	9.5	1014	2 T30545	major surface glyc
81	61	9.5	1560	2 I54361	SMCX protein - hum
82	60.5	9.4	106	2 T49958	GAS4 - Arabidopsi
83	60.5	9.4	162	2 A53814	p20 protein - rat
84	60.5	9.4	256	2 F83194	polyamine transpor
85	60.5	9.4	322	2 F84343	pyruvate dehydroge
86	60.5	9.4	385	2 E96669	protein FLN19.19 f
87	60.5	9.4	393	2 A55859	regulatory protein
88	60.5	9.4	396	2 T27172	hypothetical prote
89	60.5	9.4	627	2 S76462	hypothetical prote
90	60.5	9.4	640	2 S47865	regulatory protein
91	60.5	9.4	808	2 F64914	dimethylsulfoxide
92	60.5	9.4	808	2 F90915	probable oxidoredu
93	60.5	9.4	5138	2 B96695	hypothetical prote
94	60	9.3	67	2 B69830	hypothetical prote
95	60	9.3	346	2 S25423	NADH2 dehydrogenas
96	60	9.3	346	2 B90626	NADH dehydrogenase
97	60	9.3	363	2 JC4049	polygalacturonase
98	60	9.3	548	2 A70780	probable membrane
99	60	9.3	614	2 G81721	hypothetical prote
100	60	9.3	825	2 JC4163	DNA-binding protei
101	60	9.3	1033	2 I48775	Smcx protein (esca
102	60	9.3	1869	2 A59290	class V chitin syn

103	60	9.3	3161	2	T30342	protein HMP1 - Ye	176	58	9.0	998	2	I58351	receptor protein-t
104	59.5	9.2	104	1	R5PM25	ribosomal protein	177	58	9.0	998	2	JC5672	receptor tyrosine
105	59.5	9.2	160	2	B53814	p20 protein - huma	178	58	9.0	1639	1	MMFFB2	laminin gamma-1 ch
106	59.5	9.2	183	1	R5BY32	ribosomal protein	179	58	9.0	5376	2	T42215	zonadhesin - mouse
107	59.5	9.2	208	2	C89697	protein K02B9.4 [i	180	57.5	8.9	110	2	H86408	F3H9.8 precursor - A
108	59.5	9.2	210	2	BQIC2	Balbani ring-2 ch	181	57.5	8.9	111	2	JG0177	LEP precursor - Ko
109	59.5	9.2	226	2	T23233	hypothetical prote	182	57.5	8.9	134	2	T08710	hypothetical prote
110	59.5	9.2	343	2	S51392	hypothetical prote	183	57.5	8.9	274	2	S75320	hypothetical prote
111	59.5	9.2	359	2	A22891	fix2 protein - Rhi	184	57.5	8.9	279	2	S7583	hypothetical prote
112	59.5	9.2	422	2	T10655	hypothetical prote	185	57.5	8.9	323	2	S38887	2S albumin - commo
113	59.5	9.2	427	2	JN0785	Carbon catabolite	186	57.5	8.9	339	2	G88444	protein C36E6.11 [
114	59.5	9.2	447	2	T12544	hypothetical prote	187	57.5	8.9	411	2	D84642	hypothetical prote
115	59.5	9.2	564	2	I48776	spermatogenesis re	188	57.5	8.9	433	2	D84335	hypothetical prote
116	59.5	9.2	633	2	F83028	DNA mismatch repai	189	57.5	8.9	475	2	I38597	zinc finger protei
117	59.5	9.2	946	2	S71168	Ca2+-transporting	190	57.5	8.9	535	2	A60531	probable estrase
118	59.5	9.2	1020	2	D86402	protein envelope C	191	57.5	8.9	535	2	S34576	D2 protein precurs
119	59.5	9.2	1020	2	T51926	Ca2+-transporting	192	57.5	8.9	1112	2	T40382	dna repair protein
120	59.5	9.2	1364	2	T00250	MEGF2 protein - hu	193	57.5	8.9	1216	2	T26104	hypothetical prote
121	59.5	9.2	2178	2	S29237	calcium channel pr	194	57.5	8.9	1417	2	P96613	hypothetical prote
122	59.5	9.2	2222	2	A37490	voltage-dependent	195	57	8.9	1417	2	H87383	hypothetical prote
123	59.5	9.2	2251	2	B54972	voltage-dependent	196	57	8.9	225	2	T49759	hypothetical prote
124	59.5	9.2	2259	2	S29236	calcium channel pr	197	57	8.9	305	2	A46476	B cell-associated
125	59.5	9.2	2270	2	A54972	voltage-dependent	198	57	8.9	313	2	E72371	oligopeptide ABC t
126	59.5	9.2	2272	2	C54972	voltage-dependent	199	57	8.9	333	2	S61849	hrpV protein - Pae
127	59.5	9.2	3034	2	T14119	seven-pass transme	200	57	8.9	346	2	T12384	NADH2 dehydrogenas
128	59	9.2	157	2	T24380	hypothetical prote	201	57	8.9	362	2	T20573	hypothetical prote
129	59	9.2	160	2	I61896	eosinophil cationi	202	57	8.9	368	2	G84769	regulatory protein
130	59	9.2	162	2	JL0106	eosinophil cationi	203	57	8.9	416	2	A41694	hypothetical prote
131	59	9.2	346	2	B90616	NADH dehydrogenase	204	57	8.9	433	2	T19632	hypothetical prote
132	59	9.2	346	2	B90622	NADH dehydrogenase	205	57	8.9	480	2	T20154	hypothetical prote
133	59	9.2	361	2	I50505	gene wnt8 protein	206	57	8.9	514	2	B96986	sugar ABC-transpor
134	59	9.2	402	2	S70703	carbon catabolite	207	57	8.9	531	2	E95358	probable L-sorbose
135	59	9.2	412	2	C86177	hypothetical prote	208	57	8.9	564	2	S59776	protein kinase DPF
136	59	9.2	437	2	T30897	hypothetical prote	209	57	8.9	592	2	JC7709	testis-specific ki
137	59	9.2	603	2	S22402	2-aminobenzoate-Co	210	57	8.9	692	2	S56849	probable membrane
138	59	9.2	716	2	S28185	phenylalanine ammo	211	57	8.9	754	2	S62561	ATP dependent RNA
139	59	9.2	730	2	B83951	translation initia	212	57	8.9	976	2	A36355	protein-tyrosine k
140	59	9.2	802	1	S48529	NAB3 protein - yea	213	57	8.9	1451	2	T33083	hypothetical prote
141	59	9.2	2101	2	S57245	insulin receptor (	214	57	8.9	1557	2	G86419	probable reverse t
142	59	9.2	2135	2	T14602	variant-specific s	215	57	8.9	1790	1	MMFFB1	laminin beta-1 cha
143	58.5	9.1	115	2	T16069	hypothetical prote	216	57	8.9	2610	2	T20968	hypothetical prote
144	58.5	9.1	162	2	B72465	hypothetical prote	217	56.5	8.8	81	2	D95014	competence-induced
145	58.5	9.1	416	2	T02194	probable pectinase	218	56.5	8.8	106	2	E75371	hypothetical prote
146	58.5	9.1	738	2	I60486	gene trg protein -	219	56.5	8.8	139	2	B70049	flagellar protein
147	58.5	9.1	776	2	T20738	hypothetical prote	220	56.5	8.8	164	2	T00891	hypothetical prote
148	58.5	9.1	1019	2	A38738	coagulation factor	221	56.5	8.8	208	2	S28722	hypothetical prote
149	58.5	9.1	1083	2	C88854	protein FilA10.3 [	222	56.5	8.8	220	2	S29195	antisikasin - Hydra
150	58.5	9.1	1238	2	T40120	C2H2 type zinc fin	223	56.5	8.8	249	2	T37920	hypothetical prote
151	58.5	9.1	1737	2	T00209	MEGF8 protein - hu	224	56.5	8.8	263	2	T25665	hypothetical prote
152	58.5	9.1	3051	2	S42373	hypothetical prote	225	56.5	8.8	304	2	T02125	chlorophyll a/b-bi
153	58	9.0	114	2	S75565	hypothetical prote	226	56.5	8.8	330	2	D71600	rifin PFB1035w - m
154	58	9.0	136	2	T48713	hypothetical prote	227	56.5	8.8	349	2	T36055	probable secreted
155	58	9.0	243	2	A72602	hypothetical prote	228	56.5	8.8	350	2	S63248	hypothetical prote
156	58	9.0	248	2	B84682	probable carbonic	229	56.5	8.8	356	2	B86934	benzoate X recepto
157	58	9.0	346	2	T11023	NADH2 dehydrogenas	230	56.5	8.8	388	2	JC7510	hypothetical prote
158	58	9.0	346	2	T12380	NADH2 dehydrogenas	231	56.5	8.8	408	2	B84743	cell wall-binding
159	58	9.0	346	2	T12381	NADH2 dehydrogenas	232	56.5	8.8	424	2	AD2017	hypothetical prote
160	58	9.0	346	2	B90612	NADH dehydrogenase	233	56.5	8.8	429	2	T26152	retrovirus-related
161	58	9.0	346	2	T12410	NADH2 dehydrogenas	234	56.5	8.8	445	2	C47757	hypothetical prote
162	58	9.0	346	2	T12383	NADH2 dehydrogenas	235	56.5	8.8	513	2	G84770	transcription fact
163	58	9.0	413	2	D71112	hypothetical prote	236	56.5	8.8	532	2	S22662	hypothetical prote
164	58	9.0	443	2	T48708	hypothetical prote	237	56.5	8.8	620	2	S56790	probable membrane
165	58	9.0	464	2	A28569	alpha-methylidopa-h	238	56.5	8.8	627	2	T04562	hypothetical prote
166	58	9.0	470	2	T22785	hypothetical prote	239	56.5	8.8	774	2	T07265	neprilysin (SC 3.4
167	58	9.0	572	2	C42679	protein-tyrosine-p	240	56.5	8.8	905	2	A54654	centromere protein
168	58	9.0	603	2	B84744	hypothetical prote	241	56.5	8.8	994	2	S19595	chloride channel p
169	58	9.0	605	2	JC5673	receptor tyrosine	242	56.5	8.8	1246	2	JQ0406	hypothetical prote
170	58	9.0	610	2	I48612	developmental kina	243	56.5	8.8	1347	2	T45632	helicase homolog F
171	58	9.0	626	2	I48614	developmental kina	244	56.5	8.8	1513	2	T23681	hypothetical prote
172	58	9.0	685	1	Q3ECS7	hypothetical 77K p	245	56.5	8.8	1551	2	T18941	hypothetical prote
173	58	9.0	694	2	T10565	hypothetical prote	246	56.5	8.8	1876	2	T28627	vitellogenin - Rip
174	58	9.0	707	2	S50144	Gonyaulax-luciferi	247	56.5	8.8	2823	2	F87908	protein T22A3.8 [l
175	58	9.0	811	2	S36109	osteoblast-specifi	248	56.5	8.8	2823	2	T23064	hypothetical prote

249	56.5	8.8	3102	2	T43291	laminin alpha chain	322	55	8.5	436	2	T36104	conserved hypotet
250	56	8.7	118	2	T49372	hypothetical prote	323	55	8.5	458	2	D70410	cytosolic axial fi
251	56	8.7	135	2	B38253	kappa-enhancer-bin	324	55	8.5	462	2	I38404	neu diff differentia
252	56	8.7	135	2	E75078	hypothetical prote	325	55	8.5	533	1	A38228	dimethylaniline mo
253	56	8.7	135	2	P80328	polyprotein - hepa	326	55	8.5	531	2	B32891	finger protein 2,
254	56	8.7	135	2	P80327	polyprotein - hepa	327	55	8.5	715	4	TVMSMY	transforming prote
255	56	8.7	138	2	S67968	transition protein	328	55	8.5	862	2	B36786	hypothetical prote
256	56	8.7	145	2	A99583	50S ribosomal prot	329	55	8.5	879	2	T22033	hypothetical prote
257	56	8.7	289	2	A48913	KRAB zinc finger p	330	55	8.5	891	2	G84693	probable proline-r
258	56	8.7	411	2	F97760	hypothetical prote	331	55	8.5	943	2	T16768	hypothetical prote
259	56	8.7	492	2	P80326	polyprotein - hepa	332	55	8.5	1139	2	T08421	resistance protein
260	56	8.7	516	2	G70149	hypothetical prote	333	55	8.5	1560	2	T42727	proliferation pote
261	56	8.7	597	2	D98186	adenine deaminase	334	55	8.5	4196	2	T43274	dynain heavy chain
262	56	8.7	597	2	AF3100	adenine deaminase	335	54.5	8.5	1102	2	G33334	probable head-tail
263	56	8.7	605	2	T05243	hypothetical prote	336	54.5	8.5	116	2	S85691	probable head-tail
264	56	8.7	653	2	C97768	hypothetical prote	337	54.5	8.5	116	2	A90876	probable head-tail
265	56	8.7	678	2	G98037	glycine-tRNA ligas	338	54.5	8.5	116	2	E90853	probable head-tail
266	56	8.7	716	2	JQ1366	polyprotein - hepa	339	54.5	8.5	116	2	F90909	probable head-tail
267	56	8.7	721	2	D83110	exodeoxyribonuclea	340	54.5	8.5	144	2	AF2695	conserved hypotet
268	56	8.7	735	2	T13646	hypothetical prote	341	54.5	8.5	144	2	F97477	hypothetical prote
269	56	8.7	794	2	T10519	pre-pro-legumin -	342	54.5	8.5	180	1	RKPM55	ribulose-bisphosph
270	56	8.7	857	2	T05352	hypothetical prote	343	54.5	8.5	182	2	S32748	evel protein - zeb
271	56	8.7	944	2	S01909	hairy wing supplre	344	54.5	8.5	223	2	S45355	vascular endothell
272	56	8.7	1020	2	T51925	Ca2+-transporting	345	54.5	8.5	232	2	A41551	hypothetical prote
273	56	8.7	1217	1	EGSM5G	epidermal growth f	346	54.5	8.5	255	2	T52352	merozoite antigen
274	56	8.7	1246	2	S56752	helicase SKI2W - h	347	54.5	8.5	255	2	A60637	hypothetical prote
275	56	8.7	1801	1	MMRTS	laminin beta-2 cha	348	54.5	8.5	284	2	S74256	homeotic protein s
276	56	8.7	2391	2	G89779	hypothetical prote	349	54.5	8.5	285	2	T27458	hypothetical prote
277	56	8.7	2416	2	T13825	adenomatous polypo	350	54.5	8.5	288	2	E86717	hypothetical prote
278	56	8.7	3011	1	GNWVC3	genome polyprotein	351	54.5	8.5	323	2	E72327	astb/chuk-related
279	56	8.7	3433	1	GNWVKY	genome polyprotein	352	54.5	8.5	340	2	T02120	hypothetical prote
280	55.5	8.6	131	2	T52597	squamosa promoter	353	54.5	8.5	344	2	F62627	.T6J4.6 protein - A
281	55.5	8.6	224	2	G70851	probable gid prote	354	54.5	8.5	367	2	H71440	hypothetical prote
282	55.5	8.6	244	2	A75408	triasephosphate is	355	54.5	8.5	377	2	B82370	phosphoribosylamin
283	55.5	8.6	252	2	B86422	FIN18.10 protein -	356	54.5	8.5	386	2	S68016	ATPase/RNA helicas
284	55.5	8.6	257	2	G82119	probable esterase/	357	54.5	8.5	414	2	T15947	hypothetical prote
285	55.5	8.6	302	2	T45890	splicing factor-1i	358	54.5	8.5	422	2	T24865	hypothetical prote
286	55.5	8.6	305	2	C39240	finger protein mfg	359	54.5	8.5	515	2	H8618	protein W06F12.2 (
287	55.5	8.6	319	2	T51280	hypothetical prote	360	54.5	8.5	543	2	H84724	probable ARI-like
288	55.5	8.6	365	2	T22584	hypothetical prote	361	54.5	8.5	547	2	C96828	unknown protein F1
289	55.5	8.6	368	1	I39598	N-Acylamino acid r	362	54.5	8.5	562	2	T28242	hypothetical prote
290	55.5	8.6	376	2	AD2697	hypothetical prote	363	54.5	8.5	568	2	T26243	hypothetical prote
291	55.5	8.6	386	2	S41497	thyroid hormone re	364	54.5	8.5	571	2	S00566	convicilin precurs
292	55.5	8.6	494	2	T19550	hypothetical prote	365	54.5	8.5	598	2	A57040	T-cell nuclear rec
293	55.5	8.6	510	1	FOLJTM	gag polyprotein -	366	54.5	8.5	598	2	A46225	nuclear orphan rec
294	55.5	8.6	542	2	A45661	zinc finger protei	367	54.5	8.5	598	2	I84692	hypothetical prote
295	55.5	8.6	562	2	G88408	protein nhr-6 [imp	368	54.5	8.5	625	2	T48465	hypothetical prote
296	55.5	8.6	619	1	T43348	nuclear steroid ho	369	54.5	8.5	625	2	D87793	protein C27A12.2 l
297	55.5	8.6	700	2	B69667	ribonucleoside-dip	370	54.5	8.5	692	2	C81653	probable thiol-dis
298	55.5	8.6	707	2	S68958	finger protein - m	371	54.5	8.5	707	1	A64047	ribonucleoside-tri
299	55.5	8.6	728	2	H64346	hypothetical prote	372	54.5	8.5	729	2	T23972	hypothetical prote
300	55.5	8.6	749	2	A45294	Balbani ring 2.1	373	54.5	8.5	900	2	B87957	protein Y106G6D.7
301	55.5	8.6	1028	2	AF3286	Arp-dependent DNA	374	54.5	8.5	948	2	T26417	hypothetical prote
302	55.5	8.6	1371	2	T29019	hypothetical prote	375	54.5	8.5	1006	2	S20126	exoribonuclease RA
303	55.5	8.6	1808	2	T15099	hypothetical prote	376	54.5	8.5	1047	1	OYRTBR	atrial natriuretic
304	55.5	8.6	2195	2	T34264	hypothetical prote	377	54.5	8.5	1102	2	S55100	hypothetical prote
305	55.5	8.6	2337	2	T45115	N-type calcium cha	378	54.5	8.5	1678	2	D86481	189.6K hypotetica
306	55.5	8.6	2355	1	JQ1532	genome polyprotein	379	54.5	8.5	1700	2	S08167	Balbani ring 3 pr
307	55.5	8.6	2339	2	A42566	omega-conotoxin-se	380	54.5	8.5	3010	1	GNWVTW	genome polyprotein
308	55	8.5	56	2	T30739	hypothetical prote	381	54.5	8.5	3011	1	S40770	genome polyprotein
309	55	8.5	144	2	H75636	transposase-relate	382	54.5	8.5	4485	2	T08044	dynain gamma heavy
310	55	8.5	153	2	S75561	hypothetical prote	383	54.5	8.5	5149	2	F83345	probable non-ribos
311	55	8.5	155	2	A86765	mutator protein Wu	384	54	8.4	51	2	S00016	probable membrane
312	55	8.5	177	2	E64910	probable lysozyme	385	54	8.4	98	2	E64720	protamine 2 - rat
313	55	8.5	181	2	AF3291	5-formyltetrahydro	386	54	8.4	104	2	S57666	ribosomal protein
314	55	8.5	186	2	AF0248	conserved hypotet	387	54	8.4	105	2	B71672	probable squamosa-
315	55	8.5	214	2	S00832	finger protein (cl	388	54	8.4	129	2	H84749	4-hydroxybenzoyl-C
316	55	8.5	246	2	T34067	hypothetical prote	389	54	8.4	167	2	E83743	squamosa promoter
317	55	8.5	271	2	T48994	pirin-like protein	390	54	8.4	167	2	T52599	squamosa promoter
318	55	8.5	325	2	T31474	hypothetical prote	391	54	8.4	174	2	T52600	conserved hypotet
319	55	8.5	359	2	S28831	microtubule-associ	392	54	8.4	184	2	AB0635	uref protein - Pro
320	55	8.5	388	2	T27645	hypothetical prote	393	54	8.4	205	2	F43719	lipoprotein [impor
321	55	8.5	393	2	S62335	171-7 protein - fr	394	54	8.4	209	2	D90593	

395	54	8.4	218	2	A40513	hypothetical prote	468	53.5	8.3	571	2	T20359	hypothetical prote
396	54	8.4	232	2	S42392	G-box-binding prot	469	53.5	8.3	602	2	T42401	ubiquitin thiolest
397	54	8.4	251	2	B39685	GRESAG protein 2.1	470	53.5	8.3	614	2	T19963	hypothetical prote
398	54	8.4	256	2	S57747	SURF-2 protein - h	471	53.5	8.3	619	1	OYBO70	guanylate cyclase
399	54	8.4	257	2	T49701	hypothetical prote	472	53.5	8.3	619	1	OYTB1	guanylate cyclase
400	54	8.4	275	2	C87634	conserved hypotet	473	53.5	8.3	619	2	S23097	guanylate cyclase
401	54	8.4	298	1	HLMS1	MHC class I histoc	474	53.5	8.3	619	2	A45625	phosphoenolpyruvat
402	54	8.4	332	2	S11714	transcription init	475	53.5	8.3	700	2	I77463	luteinizing hormon
403	54	8.4	346	2	B90614	NADH dehydrogenase	476	53.5	8.3	700	2	A49744	luteolin-choriogon
404	54	8.4	354	2	T46014	squamosa promoter-	477	53.5	8.3	712	2	T30960	hypothetical prote
405	54	8.4	359	2	A49973	prostanoid EP rece	478	53.5	8.3	729	2	T10692	polynucleotide ade
406	54	8.4	362	2	A53058	prostaglandin F2-a	479	53.5	8.3	731	2	B31383	hrpM protein - Pae
407	54	8.4	371	2	D52266	cell division prot	480	53.5	8.3	798	2	A40526	integrin beta-7 ch
408	54	8.4	405	2	T29639	hypothetical prote	481	53.5	8.3	811	2	AF0680	probable dimethyl
409	54	8.4	443	2	C88427	protein R07E5.6 [i	482	53.5	8.3	815	2	AC0394	probable acyl-CoA
410	54	8.4	478	2	S44249	bet protein - huma	483	53.5	8.3	885	2	JC4732	beta-N-acetylthios
411	54	8.4	493	2	T48219	hypothetical prote	484	53.5	8.3	986	2	T52176	aldehyde oxidase (
412	54	8.4	495	2	T36043	probable integrase	485	53.5	8.3	1046	2	AD2959	aldehyde oxidase (
413	54	8.4	529	2	AH3554	sugar transport AT	486	53.5	8.3	1046	2	B98324	probable rnd efflu
414	54	8.4	539	2	S50626	CKI3 protein - yea	487	53.5	8.3	1165	2	S27809	GTPase-activating
415	54	8.4	555	2	A22208	hypothetical prote	488	53.5	8.3	1168	2	I56985	kalinin B1 - mouse
416	54	8.4	568	2	T17308	hypothetical prote	489	53.5	8.3	1268	2	B36502	insulin receptor-r
417	54	8.4	580	2	A37107	spermatogenesis pr	490	53.5	8.3	1332	2	D84669	aldehyde oxidase [
418	54	8.4	585	2	F33913	hypothetical prote	491	53.5	8.3	1721	1	I38902	retinoblastoma bin
419	54	8.4	588	1	FWCNAB	alpha-globulin B p	492	53.5	8.3	2531	2	A46019	nosch-1 protein -
420	54	8.4	590	2	H71977	hypothetical prote	493	53.5	8.3	2706	2	T28155	variant-specific s
421	54	8.4	592	2	S43597	coiled-coil protei	494	53.5	8.3	3011	1	GNMVCH	genome polyprotein
422	54	8.4	620	2	T16166	hypothetical prote	495	53	8.2	57	2	H64023	hypothetical prote
423	54	8.4	632	2	J50631	alpha-amylase (EC	496	53	8.2	71	2	G72519	hypothetical prote
424	54	8.4	632	2	T2454	hypothetical prote	497	53	8.2	129	2	G72519	hypothetical prote
425	54	8.4	651	2	T32875	hypothetical prote	498	53	8.2	139	2	B39644	actin polymerizati
426	54	8.4	695	2	I54325	hypothetical prote	499	53	8.2	144	2	S23659	superoxide dismuta
427	54	8.4	779	2	S36111	gene XE7 protein -	500	53	8.2	152	2	S07505	endooxyribonucle
428	54	8.4	836	2	S36110	osteoblast-specifi	501	53	8.2	156	2	NRH01	pancreatic ribonuc
429	54	8.4	1191	2	S35305	osteoblast-specifi	502	53	8.2	159	2	T15298	hypothetical prote
430	54	8.4	1258	2	T14855	reverse transcript	503	53	8.2	174	2	B27482	hypothetical prote
431	54	8.4	1516	2	T01055	hypothetical prote	504	53	8.2	174	2	D83692	hypothetical prote
432	54	8.4	1584	2	T00026	brain-specific ang	505	53	8.2	184	2	AG0300	conserved hypotet
433	54	8.4	1963	1	MMKW	myosin heavy chain	506	53	8.2	196	2	PS0412	hypothetical prote
434	54	8.4	4976	1	T14165	peptide synthetase	507	53	8.2	203	2	T32346	conserved hypotet
435	53.5	8.3	115	2	S22588	V1 protein - tomat	508	53	8.2	216	2	AC0715	hemopoietic cell s
436	53.5	8.3	135	2	T15610	hypothetical prote	509	53	8.2	219	1	A37243	H+-transporting tw
437	53.5	8.3	136	2	T22959	hypothetical prote	510	53	8.2	225	2	T11279	bovine corneal pro
438	53.5	8.3	145	2	I54504	NGK5 secreted spli	511	53	8.2	239	2	T01406	hypothetical prote
439	53.5	8.3	174	2	A81080	single-strand bind	512	53	8.2	254	2	T20882	hypothetical prote
440	53.5	8.3	184	2	F75481	hypothetical prote	513	53	8.2	274	2	C84226	oligopeptide ABC t
441	53.5	8.3	225	1	MNNZP2	nonstructural prot	514	53	8.2	306	2	F97345	probable hydrolase
442	53.5	8.3	225	1	MNNZVT	nonstructural prot	515	53	8.2	324	2	B87196	flagellar M-ring p
443	53.5	8.3	232	2	B83732	hypothetical prote	516	53	8.2	341	2	B86598	flagellar m-ring p
444	53.5	8.3	251	2	I57668	luteinizing hormon	517	53	8.2	341	2	D72025	cysteine proteinas
445	53.5	8.3	252	2	T44299	hypothetical prote	518	53	8.2	343	2	D86198	thrombosmodulin - b
446	53.5	8.3	291	2	A98322	alanine catabolic	519	53	8.2	356	2	A25918	hypothetical prote
447	53.5	8.3	291	2	A83231	conserved hypotet	520	53	8.2	359	2	T06604	hypothetical prote
448	53.5	8.3	298	2	B97186	probable glycosylt	521	53	8.2	382	2	T25538	transforming growt
449	53.5	8.3	324	2	S44956	lmb1 protein - Str	522	53	8.2	410	2	A41397	transforming growt
450	53.5	8.3	342	2	I77461	luteinizing hormon	523	53	8.2	410	2	A55706	transforming growt
451	53.5	8.3	345	2	S59236	SAE2 protein - yea	524	53	8.2	412	2	A36169	transforming growt
452	53.5	8.3	355	2	C83850	gamma-D-glutamyl-L	525	53	8.2	412	2	G83472	hypothetical prote
453	53.5	8.3	360	2	B36470	Wnt-2 protein - mo	526	53	8.2	424	1	T21181	acid phosphatase (
454	53.5	8.3	381	2	T29300	hypothetical prote	527	53	8.2	455	2	S65157	hypothetical prote
455	53.5	8.3	389	2	I49640	transcription fact	528	53	8.2	458	2	H75278	probable Na+/H+ an
456	53.5	8.3	390	2	S44285	EAR2 protein - mou	529	53	8.2	480	2	AH1481	beta-glucosidase h
457	53.5	8.3	395	2	T08350	hypothetical prote	530	53	8.2	490	2	S67581	STP4 protein - yea
458	53.5	8.3	399	2	S47071	finger protein HZF	531	53	8.2	497	2	S43745	phosphatidylinosit
459	53.5	8.3	403	2	S02709	ear-2 protein - hu	532	53	8.2	498	2	H85040	hypothetical prote
460	53.5	8.3	467	2	AC2015	hypothetical prote	533	53	8.2	531	2	T51922	hypothetical prote
461	53.5	8.3	477	2	T47753	hypothetical prote	534	53	8.2	554	1	TVVBBF	large T antigen -
462	53.5	8.3	492	2	T02458	hypothetical prote	535	53	8.2	577	2	T12536	hypothetical prote
463	53.5	8.3	530	2	T20360	hypothetical prote	536	53	8.2	583	2	A32861	type II site-speci
464	53.5	8.3	555	1	SVHQMA	malate synthase (E	537	53	8.2	612	2	T10727	protein kinase Xa2
465	53.5	8.3	558	2	G83049	DNA repair protein	538	53	8.2	622	2	A34711	kinase-related pro
466	53.5	8.3	563	1	VCNMV7	env polyprotein -	539	53	8.2	629	2	T07426	probable polygalac
467	53.5	8.3	564	2	S92466	urocanate hydratase	540	53	8.2	670	2	T02019	callus-associated

541	53	8.2	710	2	I48668	zinc finger protei	614	52	8.1	67	2	T14467	pollen coat protei
542	53	8.2	782	2	S04047	finger protein zfy	615	52	8.1	113	2	J66936	probable membrane
543	53	8.2	783	2	A31491	sex-determining re	616	52	8.1	114	2	SC5238	galactosylceramide
544	53	8.2	827	2	JT0968	1,4-alpha-glucan b	617	52	8.1	141	2	A64536	hypothetical prote
545	53	8.2	884	2	TJ25205	hypothetical prote	618	52	8.1	156	2	JC5160	eosinophil-associa
546	53	8.2	952	2	T02751	DNA-directed RNA p	619	52	8.1	159	2	S37766	hypothetical prote
547	53	8.2	996	2	T10725	protein kinase Xa2	620	52	8.1	166	2	H75500	hypothetical prote
548	53	8.2	1002	2	T43236	carboxypeptidase C	621	52	8.1	196	2	I38022	hypothetical prote
549	53	8.2	1019	2	A80677	protein R52.2 (lmp	622	52	8.1	233	2	T26781	hypothetical prote
550	53	8.2	1025	1	A57676	protein kinase Xa2	623	52	8.1	241	2	T25886	hypothetical prote
551	53	8.2	1186	2	T33754	O/E-1-associated z	624	52	8.1	262	2	T02724	gag protein homolo
552	53	8.2	1365	2	S14871	suppressor two of	625	52	8.1	263	2	E97774	hypothetical prote
553	53	8.2	1538	2	H70846	hypothetical glyci	626	52	8.1	273	2	G84130	ABC transporter (p
554	53	8.2	1617	2	T28153	complement C4 - ch	627	52	8.1	275	2	A36415	32K protein - vacc
555	53	8.2	1732	2	E71442	hypothetical prote	628	52	8.1	276	2	S64103	hypothetical prote
556	53	8.2	1980	2	S54307	myosin heavy chain	629	52	8.1	279	2	T70612	hypothetical prote
557	53	8.2	2120	2	T30243	alpha tectorin - c	630	52	8.1	309	2	AH0946	probable lipase ST
558	53	8.2	2240	2	T37057	probable multi-dom	631	52	8.1	311	2	A82361	integrase/recombin
559	53	8.2	2703	1	A24420	notch protein - fr	632	52	8.1	320	2	T36823	probable integral
560	53	8.2	2895	2	T08437	hyperplastic discs	633	52	8.1	323	2	T47574	embryonic abundant
561	53	8.2	2910	2	T42214	otogelin - mouse	634	52	8.1	348	2	T08327	hypothetical prote
562	53	8.2	3430	1	GNWTWV	genome polyprotein	635	52	8.1	353	2	E81680	conserved hypotet
563	53	8.2	3795	2	T00831	hypothetical prote	636	52	8.1	354	2	S27013	GTP-binding regula
564	52.5	8.2	91	2	A83527	probable acylphosp	637	52	8.1	358	2	T17619	hypothetical prote
565	52.5	8.2	122	2	AD1092	hypothetical prote	638	52	8.1	377	2	T37403	35K myristylprotei
566	52.5	8.2	147	2	G86884	50S ribosomal prot	639	52	8.1	377	2	F72165	A17L protein - var
567	52.5	8.2	173	2	D83486	cobinamide kinase	640	52	8.1	377	2	T28558	hypothetical prote
568	52.5	8.2	183	2	C85439	probable cytoskele	641	52	8.1	378	2	I42518	A16L protein - vac
569	52.5	8.2	207	2	G83538	probable oxidoredu	642	52	8.1	408	2	S58791	bone morphogenetic
570	52.5	8.2	211	2	S56602	Yjfv protein - Esc	643	52	8.1	436	2	A38145	invariant surface
571	52.5	8.2	225	1	JQ2040	nonstructural prote	644	52	8.1	440	2	T24232	hypothetical prote
572	52.5	8.2	250	2	C86429	hypothetical prote	645	52	8.1	445	2	T49556	epithelial zinc-fi
573	52.5	8.2	252	2	E69034	hypothetical prote	646	52	8.1	448	2	A41725	integrase - Saccha
574	52.5	8.2	277	2	G87775	protein C24A11.9 l	647	52	8.1	452	2	S47633	RXR protein - Afri
575	52.5	8.2	309	2	C65217	alloase kinase (EC	648	52	8.1	468	2	JN0016	peripherin interme
576	52.5	8.2	348	2	A56197	nuclear hormone re	649	52	8.1	496	2	T33496	hypothetical prote
577	52.5	8.2	353	2	AI0036	conserved hypotet	650	52	8.1	503	2	E83490	probable MFS trans
578	52.5	8.2	361	2	S57182	probable polygalac	651	52	8.1	507	2	S52348	hypothetical prote
579	52.5	8.2	361	2	T01998	hypothetical prote	652	52	8.1	517	2	B40583	heat shock transcr
580	52.5	8.2	364	2	AF2459	hypothetical prote	653	52	8.1	521	2	S12152	gag polyprotein -
581	52.5	8.2	365	2	A53277	MHC class I histoc	654	52	8.1	551	2	A30342	interleukin-2 rece
582	52.5	8.2	367	2	AH0675	hydrogenase (EC 1.	655	52	8.1	559	2	T26141	hypothetical prote
583	52.5	8.2	369	2	S13721	Wnt-1 protein prec	656	52	8.1	560	2	S27874	steroid hormone re
584	52.5	8.2	417	2	T49847	hypothetical prote	657	52	8.1	568	2	G02753	testis specific ba
585	52.5	8.2	453	2	B88040	protein lin-42 (lin	658	52	8.1	578	2	T51888	asparagine synthas
586	52.5	8.2	455	2	S05573	deoxyribodipyrimid	659	52	8.1	589	2	E97376	sulfite reductase
587	52.5	8.2	478	2	T34338	hypothetical prote	660	52	8.1	589	2	AD2594	hypothetical prote
588	52.5	8.2	578	2	T51230	telomere repeat-bi	661	52	8.1	591	2	C69899	Fanconi anemia gro
589	52.5	8.2	599	2	I51405	protein-tyrosine-p	662	52	8.1	600	2	I49656	conserved hypotet
590	52.5	8.2	666	2	D82386	methyl-accepting c	663	52	8.1	627	2	D84494	probable Tail-like
591	52.5	8.2	676	1	A39379	hatching-suppress	664	52	8.1	657	1	W1WL18	E1 protein - human
592	52.5	8.2	715	2	B71418	hypothetical prote	665	52	8.1	662	2	A45155	mucin FIM-C.1 - Af
593	52.5	8.2	762	2	C96653	hypothetical prote	666	52	8.1	664	2	S60062	hevin precursor -
594	52.5	8.2	769	2	A41029	integrin beta-8 ch	667	52	8.1	665	2	S70706	probable protein k
595	52.5	8.2	788	2	AB1991	hypothetical prote	668	52	8.1	682	2	T10319	envelope protein E
596	52.5	8.2	806	2	G95362	probable [imported	669	52	8.1	701	1	S33709	DHR39-short protei
597	52.5	8.2	927	2	T47827	squamosa promoter	670	52	8.1	709	2	AE3468	diguanylate cyclas
598	52.5	8.2	1008	2	T32986	hypothetical prote	671	52	8.1	738	2	S40992	hypothetical prote
599	52.5	8.2	1023	2	T13068	CLOCK protein - fr	672	52	8.1	808	1	S33708	nuclear steroid/th
600	52.5	8.2	1045	2	S23570	pol polyprotein ho	673	52	8.1	886	2	T16536	hypothetical prote
601	52.5	8.2	1133	2	S54496	probable membrane	674	52	8.1	903	2	T20804	hypothetical prote
602	52.5	8.2	1323	2	B88257	protein let-23 (im	675	52	8.1	905	2	T23510	hypothetical prote
603	52.5	8.2	1374	2	S70712	protein-tyrosine k	676	52	8.1	910	2	S40930	hypothetical prote
604	52.5	8.2	1616	2	G70668	polyketide synthas	677	52	8.1	910	2	AI0796	NADH2 dehydrogenas
605	52.5	8.2	1898	1	A45973	trichohyalin - hum	678	52	8.1	971	2	T24866	hypothetical prote
606	52.5	8.2	1951	2	B43963	RNA viral polymera	679	52	8.1	993	2	D96812	protein F3F9.12 [1
607	52.5	8.2	2150	2	S13553	hypothetical prote	680	52	8.1	1045	2	T16275	hypothetical prote
608	52.5	8.2	2427	2	T16613	hypothetical prote	681	52	8.1	1091	1	PL0009	complement C3d/Eps
609	52.5	8.2	2531	2	S18188	notch protein homo	682	52	8.1	1113	2	S30301	exclusion repair pr
610	52.5	8.2	3033	1	GNWJ08	genome polyprotein	683	52	8.1	1135	2	T42368	DNA-directed RNA p
611	52.5	8.2	3396	2	T22613	hypothetical prote	684	52	8.1	1464	2	S58984	development protei
612	52.5	8.2	3796	2	T18514	lysosomal traffick	685	52	8.1	1847	2	T18308	probable vitellog
613	52.5	8.2	3856	2	T51174	ataxia-telangiecta	686	52	8.1	2207	2	T24629	glutamate synthase

687	52	8.1	3075	2	S14458	laminin alpha-1 ch	760	51.5	8.0	772	2	H86016	hypothetical prote
688	52	8.1	3163	2	AB0233	yersiniabactin bio	761	51.5	8.0	793	2	S73662	probable lipoprote
689	52	8.1	3163	2	T17440	probable polyketid	762	51.5	8.0	808	2	C85764	probable oxidoredu
690	52	8.1	3635	2	T10053	laminin alpha 5 ch	763	51.5	8.0	810	1	S45907	myb-related protei
691	51.5	8.0	103	2	S33337	protamine P2 - pig	764	51.5	8.0	836	2	AF3233	conserved hypothet
692	51.5	8.0	108	2	H81098	hypothetical prote	765	51.5	8.0	848	2	E85087	hypothetical prote
693	51.5	8.0	117	2	S54126	hypothetical 14.3K	766	51.5	8.0	884	2	T18649	hypothetical prote
694	51.5	8.0	122	2	S53234	globulin-10 - maiz	767	51.5	8.0	909	1	QXLL2	LDL receptor 2 pre
695	51.5	8.0	134	2	AG3208	hypothetical prote	768	51.5	8.0	1019	2	C96519	probable disease r
696	51.5	8.0	144	2	F90217	LSU ribosomal prot	769	51.5	8.0	1039	2	T22982	hypothetical prote
697	51.5	8.0	151	2	S43296	bone morphogenetic	770	51.5	8.0	1133	1	EGRT	epidermal growth f
698	51.5	8.0	161	2	I37034	eosinophil-derived	771	51.5	8.0	1184	2	A39800	calcium-activated
699	51.5	8.0	161	2	I61897	eosinophil-derived	772	51.5	8.0	1187	2	C84568	hypothetical prote
700	51.5	8.0	161	2	A33922	eosinophil-derived	773	51.5	8.0	1192	2	H88293	protein F59B40.1 [
701	51.5	8.0	169	1	Q8ECA1	cell division inhi	774	51.5	8.0	1244	2	T49632	hypothetical prote
702	51.5	8.0	169	2	H85622	hypothetical prote	775	51.5	8.0	1259	2	T16038	hypothetical prote
703	51.5	8.0	169	2	B90759	suppressor of lon	776	51.5	8.0	1416	2	B88550	protein ZC84.1 [im
704	51.5	8.0	170	2	T15991	hypothetical prote	777	51.5	8.0	1436	2	B81704	conserved hypothet
705	51.5	8.0	174	2	T08702	hypothetical prote	778	51.5	8.0	1454	2	S53398	hypothetical prote
706	51.5	8.0	177	2	E90971	probable endolysin	779	51.5	8.0	1476	2	A45773	kelch protein, lon
707	51.5	8.0	177	2	E85744	probable lysozyme	780	51.5	8.0	1560	2	T00080	hypothetical prote
708	51.5	8.0	188	2	T21208	hypothetical prote	781	51.5	8.0	1657	2	T19536	hypothetical prote
709	51.5	8.0	203	2	T49324	hypothetical prote	782	51.5	8.0	1693	2	T30867	Rho-guanine nucleo
710	51.5	8.0	208	2	T34626	probable polypeptid	783	51.5	8.0	1706	2	I84499	zinc finger protei
711	51.5	8.0	210	2	T05541	heat shock protein	784	51.5	8.0	1712	2	A38261	masking protein pr
712	51.5	8.0	217	2	S01358	salivary glue prot	785	51.5	8.0	2019	1	JQ1322	tenascin precursor
713	51.5	8.0	247	2	H86145	F22I4.7 protein -	786	51.5	8.0	2124	2	H83357	probable non-ribos
714	51.5	8.0	263	1	HLMSBK	H-2 class II histo	787	51.5	8.0	2844	2	S28291	hypothetical prote
715	51.5	8.0	280	2	A10190	probable hydrolase	788	51.5	8.0	3033	1	JQ1303	genome polyprotein
716	51.5	8.0	314	2	I37383	FAS soluble protei	789	51.5	8.0	3672	2	T23433	hypothetical prote
717	51.5	8.0	317	2	T24468	hypothetical prote	790	51.5	8.0	3704	2	T37316	probable laminin a
718	51.5	8.0	326	2	C95937	hypothetical expor	791	51.5	8.0	3712	2	S18253	laminin alpha-1 ch
719	51.5	8.0	335	2	A40036	apoptosis-mediati	792	51.5	8.0	4845	2	T31067	BIR repeat contain
720	51.5	8.0	335	2	A53434	cell surface glyco	793	51	7.9	62	2	B58213	protamine I - Amer
721	51.5	8.0	338	2	C75607	conserved hypothet	794	51	7.9	73	2	AG1852	hypothetical prote
722	51.5	8.0	347	2	F90904	hypothetical prote	795	51	7.9	99	2	F90262	hypothetical prote
723	51.5	8.0	347	2	G85712	unknown protein en	796	51	7.9	106	2	D31201	hypothetical prote
724	51.5	8.0	360	2	JC6322	methyltransferase	797	51	7.9	115	2	S64490	hypothetical prote
725	51.5	8.0	361	1	F65012	hypothetical prote	798	51	7.9	128	1	TGHU	beta-thromboglobul
726	51.5	8.0	361	2	A91037	probable peptidase	799	51	7.9	134	2	B46178	probable transcrip
727	51.5	8.0	361	2	C85881	probable peptidase	800	51	7.9	139	2	S06550	finger protein (cl
728	51.5	8.0	367	2	F95159	prephenate dehydro	801	51	7.9	141	2	F71070	hypothetical prote
729	51.5	8.0	367	2	F98025	prephenate dehydro	802	51	7.9	142	2	JT0573	retinoic acid-indu
730	51.5	8.0	373	2	A55718	interleukin-2 rece	803	51	7.9	149	1	NRMS	pancreatic ribonuc
731	51.5	8.0	377	2	T32798	hypothetical prote	804	51	7.9	177	2	E75026	hypothetical prote
732	51.5	8.0	382	2	AG0188	histidinol-phospha	805	51	7.9	184	2	E87506	hypothetical prote
733	51.5	8.0	387	2	A86302	hypothetical prote	806	51	7.9	193	2	S26597	protein F3M18.20 [
734	51.5	8.0	391	2	T25211	hypothetical prote	807	51	7.9	204	2	B86410	hypothetical prote
735	51.5	8.0	395	2	C88955	protein K04F1.10 [	808	51	7.9	210	2	T36893	hydroxyacylglutath
736	51.5	8.0	400	2	T46383	hypothetical prote	809	51	7.9	218	2	A83314	hypothetical prote
737	51.5	8.0	404	2	T50335	mating pheromone r	810	51	7.9	224	2	B81783	hypothetical prote
738	51.5	8.0	413	2	S59650	hypothetical prote	811	51	7.9	230	2	T30153	hypothetical prote
739	51.5	8.0	434	2	T11967	nodule-specific hy	812	51	7.9	236	2	T36446	hypothetical prote
740	51.5	8.0	443	2	T21499	hypothetical prote	813	51	7.9	241	2	F69165	ribosomal protein
741	51.5	8.0	454	2	T02593	hypothetical prote	814	51	7.9	247	1	JG6540	placenta specific-
742	51.5	8.0	471	2	G81156	transporter, Nadc	815	51	7.9	257	2	AH1072	conserved hypothet
743	51.5	8.0	471	2	A81948	probable transmemb	816	51	7.9	282	2	H89815	hypothetical prote
744	51.5	8.0	476	2	E97631	probable membrane	817	51	7.9	303	2	S41156	wingless protein -
745	51.5	8.0	476	2	S68965	legumin precursor	818	51	7.9	317	2	C38178	Te1B protein - pla
746	51.5	8.0	479	2	T40683	cell cycle protein	819	51	7.9	339	2	B34895	transcription fact
747	51.5	8.0	507	2	S56143	cell cycle protein	820	51	7.9	346	2	T11076	NADH2 dehydrogenas
748	51.5	8.0	519	1	F0WJG4	gag polyprotein -	821	51	7.9	377	2	H36849	Al61 protein - var
749	51.5	8.0	538	2	E96492	hypothetical prote	822	51	7.9	378	2	H01134	protein C10G8.1 [i
750	51.5	8.0	556	1	S24395	protein-tyrosine-p	823	51	7.9	385	2	H89046	serum response ele
751	51.5	8.0	605	2	S06398	alpha-globulin typ	824	51	7.9	410	2	A44391	probable transport
752	51.5	8.0	605	2	S74882	hypothetical prote	825	51	7.9	417	2	F90916	membrane protein y
753	51.5	8.0	610	2	G86407	hypothetical prote	826	51	7.9	417	2	F64915	probable transport
754	51.5	8.0	613	2	G82338	conserved hypothet	827	51	7.9	417	2	C85765	failed axon connec
755	51.5	8.0	620	2	T23522	hypothetical prote	828	51	7.9	418	2	S58776	bZIP DNA-binding p
756	51.5	8.0	641	2	T17278	hypothetical prote	829	51	7.9	420	2	T14911	female-specific do
757	51.5	8.0	684	2	T40319	hypothetical prote	830	51	7.9	427	2	A32372	sensory transducti
758	51.5	8.0	696	2	AB1566	hypothetical prote	831	51	7.9	434	2	F69081	hypothetical prote
759	51.5	8.0	749	2	H91170	hypothetical membr	832	51	7.9	439	2	T31734	

833	7.9	51	442	2	AF2539	manganese transpor	906	50.5	7.8	227	2	T11172	H+-transporting tw
834	7.9	51	446	2	B69899	L-amino acid oxida	907	50.5	7.8	227	2	PH1215	ig epsilon chain C
835	7.9	51	455	2	A36471	transcription fact	908	50.5	7.8	239	2	B65825	hypothetical prote
836	7.9	51	456	2	C82785	hypothetical prote	909	50.5	7.8	240	2	A39842	insulin-like growt
837	7.9	51	459	2	G71431	hypothetical prote	910	50.5	7.8	242	1	F75433	probable phosphoe
838	7.9	51	462	2	T14020	probable acid phos	911	50.5	7.8	243	2	G82163	leucyl/phenylalan
839	7.9	51	465	2	S23502	hepatocyte nuclear	912	50.5	7.8	246	2	D82078	conserved hypotet
840	7.9	51	489	2	F82085	glutamate synthase	913	50.5	7.8	250	1	A49053	CD27 antigen precu
841	7.9	51	497	2	F82985	conserved hypotet	914	50.5	7.8	256	2	JC4627	fibroblast growth
842	7.9	51	500	2	G01646	fusca protein homo	915	50.5	7.8	260	2	E71975	hypothetical prote
843	7.9	51	506	1	FOLJG3	gag polyprotein -	916	50.5	7.8	269	2	F71323	conserved hypotet
844	7.9	51	507	2	T11559	gag protein - simi	917	50.5	7.8	272	2	D83154	probable permease
845	7.9	51	507	2	S04237	gag polyprotein -	918	50.5	7.8	287	1	A28168	arylamine N-acetyl
846	7.9	51	521	1	FOLJCA	gag polyprotein -	919	50.5	7.8	324	2	S07735	probable malate de
847	7.9	51	521	1	S53091	gag polyprotein -	920	50.5	7.8	326	2	S09773	hypothetical prote
848	7.9	51	522	1	FOLJGG	gag polyprotein -	921	50.5	7.8	327	2	B84781	hypothetical prote
849	7.9	51	524	2	S38539	disintegrin-like m	922	50.5	7.8	339	2	S37920	MAK1 protein precu
850	7.9	51	532	2	S51130	dimethylalaniline m	923	50.5	7.8	352	2	JCS388	replication initia
851	7.9	51	549	2	B32372	male-specific doub	924	50.5	7.8	355	2	T50479	G protein alpha ch
852	7.9	51	560	2	A83155	probable medium-ch	925	50.5	7.8	360	2	A53611	interleukin-8 rece
853	7.9	51	561	2	T23722	hypothetical prote	926	50.5	7.8	368	1	W2WL6	E2 protein - human
854	7.9	51	573	1	HMM860	chaperonin groEL p	927	50.5	7.8	372	2	T47344	hypothetical prote
855	7.9	51	573	1	HHR760	chaperonin groEL p	928	50.5	7.8	373	2	S41452	glutamate-ammonia
856	7.9	51	573	2	A34173	mitochondrial prot	929	50.5	7.8	376	2	S49801	OGG1 protein - yea
857	7.9	51	582	2	I48673	matrix metalloprot	930	50.5	7.8	376	2	A48060	erythroid Kruppel-
858	7.9	51	587	2	F83336	inner membrane cop	931	50.5	7.8	389	2	B49905	protein secretion
859	7.9	51	592	2	T13742	hypothetical prote	932	50.5	7.8	390	2	S73459	heat shock protein
860	7.9	51	616	2	T11850	DNA primase (EC 2.	933	50.5	7.8	409	2	D83326	probable acyl-CoA
861	7.9	51	647	2	S36575	E1 protein - human	934	50.5	7.8	423	2	T20857	hypothetical prote
862	7.9	51	670	2	I65967	disintegrin-like m	935	50.5	7.8	427	2	AC0203	chemotaxis MotB pr
863	7.9	51	696	2	T02829	long chain fatty a	936	50.5	7.8	434	2	S51644	secreted/adhesive
864	7.9	51	749	2	T10232	hypothetical prote	937	50.5	7.8	438	2	C86244	DnaJ homolog, 4706
865	7.9	51	768	2	T37601	probable transcript	938	50.5	7.8	444	2	T11155	linoleoyl-CoA deaa
866	7.9	51	775	2	I49237	Azo protein - mous	939	50.5	7.8	467	2	A57627	p55 erythrocyte me
867	7.9	51	778	2	AG0906	aerobic respiratio	940	50.5	7.8	474	2	T20108	hypothetical prote
868	7.9	51	778	2	T43223	hypothetical prote	941	50.5	7.8	477	2	S33403	hypothetical prote
869	7.9	51	788	2	T45221	DNA damage checkp	942	50.5	7.8	480	2	S52306	zinc finger protei
870	7.9	51	788	1	S28302	ribonucleoside-dip	943	50.5	7.8	488	2	B75551	glutamate synthase
871	7.9	51	813	2	T04313	protein kinase Xa2	944	50.5	7.8	522	1	I37037	involucrin - commo
872	7.9	51	825	2	I46078	endothelin convert	945	50.5	7.8	531	2	B54096	flavin-containing
873	7.9	51	841	2	C87331	ISCC2, transposase	946	50.5	7.8	538	2	T50606	hypothetical prote
874	7.9	51	844	2	T52396	formin-binding pro	947	50.5	7.8	565	2	F70192	hypothetical prote
875	7.9	51	870	2	B82732	glycerol-3-phospha	948	50.5	7.8	565	2	D64058	outer membrane pro
876	7.9	51	884	1	IJMSCE	E-cadherin precurs	949	50.5	7.8	583	2	G84829	probable PTR2 fami
877	7.9	51	884	2	S34438	uvomorulin - mous	950	50.5	7.8	596	2	JC4299	orphan nuclear rec
878	7.9	51	899	2	B48586	suppressor of hair	951	50.5	7.8	596	2	I80177	TR4 orphan recepto
879	7.9	51	953	2	F96498	hypothetical prote	952	50.5	7.8	596	2	A57031	nuclear receptor f
880	7.9	51	961	2	H84787	probable receptor-	953	50.5	7.8	607	2	A47757	retrovirus-related
881	7.9	51	991	2	T25412	hypothetical prote	954	50.5	7.8	615	2	I59309	TR4 orphan recepto
882	7.9	51	998	1	QOBBB1	B1 protein - black	955	50.5	7.8	627	2	G86156	T14P4.5 protein -
883	7.9	51	998	2	S41397	protein A - flock	956	50.5	7.8	629	2	I54075	gene mTR2R1 protei
884	7.9	51	1106	2	T44598	hypothetical prote	957	50.5	7.8	629	2	S36551	E1 protein - human
885	7.9	51	1106	2	T13938	gene shuttle craft	958	50.5	7.8	639	2	T15795	hypothetical prote
886	7.9	51	1355	2	T00075	hypothetical prote	959	50.5	7.8	686	2	T15795	myeloperoxidase (E
887	7.9	51	1557	2	T13160	protein CNK - frui	960	50.5	7.8	718	2	S06068	hypothetical prote
888	7.9	51	1584	2	T22674	hypothetical prote	961	50.5	7.8	726	2	S74514	hypothetical prote
889	7.9	51	1588	2	T38660	probable transcrip	962	50.5	7.8	746	2	T28004	hypothetical prote
890	7.9	51	1722	2	E89753	protein FliC7.4 [1	963	50.5	7.8	770	2	T01527	hypothetical prote
891	7.9	51	2157	1	GNVY13	genome polyprotein	964	50.5	7.8	779	2	D84866	glycogen phosphory
892	7.9	51	2224	1	KFHU5	coagulation factor	965	50.5	7.8	800	2	D86712	dimethylsulfoxide
893	7.9	51	2321	2	S78549	notch3 protein - h	966	50.5	7.8	808	2	E64914	probable oxidoredu
894	7.9	51	2452	1	RNZO2L	DNA-directed RNA p	967	50.5	7.8	808	2	B85764	probable oxidoredu
895	7.9	51	3014	1	JCS620	genome polyprotein	968	50.5	7.8	813	2	JCS785	ATP-dependent RNA
896	50.5	7.8	82	2	T10329	hypothetical prote	969	50.5	7.8	849	1	T09349	S-receptor kinase
897	50.5	7.8	113	2	B39437	exopolysaccharide	970	50.5	7.8	853	2	H70939	probable nirB prot
898	50.5	7.8	147	2	T30616	hypothetical prote	971	50.5	7.8	864	2	S61148	SBE2 protein - yea
899	50.5	7.8	160	2	I84444	eosinophil-derived	972	50.5	7.8	876	2	PC2219	polypeptide - hepa
900	50.5	7.8	174	2	A49181	alpha B-crystallin	973	50.5	7.8	880	2	T02245	hypothetical prote
901	50.5	7.8	184	2	A61196	genome polyprotein	974	50.5	7.8	893	2	T15183	hypothetical prote
902	50.5	7.8	194	2	A54317	probable nonstruct	975	50.5	7.8	909	1	QRXLL1	SCPL receptor 1 pre
903	50.5	7.8	226	2	C25973	pertussis toxin ch	976	50.5	7.8	946	2	S28061	SCPL protein - rat
904	50.5	7.8	226	2	B95975	galactosyltransfer	977	50.5	7.8	955	2	E84845	probable villin 2
905	50.5	7.8	227	2	F90616	ATP synthase FO ch	978	50.5	7.8	956	2	A89153	protein C24B5.3 [1

979	50.5	7.8	963	2	T19140	hypothetical prote	1052	50	7.8	342	2	I47175	Ig alpha chain C r
980	50.5	7.8	976	2	T50669	villin 2 (imported	1053	50	7.8	354	2	JC7662	G protein alpha su
981	50.5	7.8	987	2	AI2011	peptide synthetase	1054	50	7.8	361	2	JC5798	conserved hypothet
982	50.5	7.8	991	2	T01372	hypothetical prote	1055	50	7.8	363	2	JC5536	C-Fringe protein 1
983	50.5	7.8	993	2	S49461	synaptonemal compl	1056	50	7.8	363	2	A48338	hypothetical prote
984	50.5	7.8	1015	2	T13062	CLOCK protein - fr	1057	50	7.8	367	2	H83202	poly(beta-d-mannur
985	50.5	7.8	1027	2	T13071	CLOCK protein - fr	1058	50	7.8	368	2	JN0777	poly(beta-D-mannur
986	50.5	7.8	1047	1	OYHUBR	natruietic peptid	1059	50	7.8	371	2	S46335	env polyprotein -
987	50.5	7.8	1047	2	I45882	guanylate cyclase	1060	50	7.8	376	2	AD1621	heat shock protein
988	50.5	7.8	1077	2	T41146	probable cysteine-	1061	50	7.8	377	2	T43739	heat shock protein
989	50.5	7.8	1164	2	AC2136	multifunctional pe	1062	50	7.8	377	2	AH1258	heat shock protein
990	50.5	7.8	1167	2	T34020	zinc finger protei	1063	50	7.8	390	2	T48524	lysophospholipase-
991	50.5	7.8	1178	2	S78475	mannosylphosphoryl	1064	50	7.8	403	2	B88633	protein F56B3.9 [i
992	50.5	7.8	1182	2	G71607	probable integral	1065	50	7.8	411	2	A55610	corticotropin-rele
993	50.5	7.8	1236	1	VHWWE	structural polypro	1066	50	7.8	415	2	T35773	translation elonga
994	50.5	7.8	1292	2	T09229	galactose binding	1067	50	7.8	421	2	T35205	citrate synthase-1
995	50.5	7.8	1404	2	T13420	probable carboxype	1068	50	7.8	433	2	T31639	hypothetical prote
996	50.5	7.8	1406	2	T13421	probable carboxype	1069	50	7.8	440	2	JC4530	peroxisome prolif
997	50.5	7.8	1465	2	T23056	chromodomain helic	1070	50	7.8	451	2	A70539	hypothetical prote
998	50.5	7.8	1735	2	S54784	sex-limited protei	1071	50	7.8	454	2	T27249	hypothetical prote
999	50.5	7.8	1736	2	A29176	sex-limited protei	1072	50	7.8	463	2	C47301	virB6 homolog - Bo
1000	50.5	7.8	2180	2	T29764	hypothetical prote	1073	50	7.8	465	2	H86352	protein F2E2.2 [im
1001	50.5	7.8	2248	2	A35938	profilaggrin - hum	1074	50	7.8	474	2	T13575	hypothetical prote
1002	50.5	7.8	2453	2	S60254	nuclear receptor c	1075	50	7.8	480	2	T46925	hypothetical prote
1003	50.5	7.8	2870	2	H98974	cyclic beta 1-2 gl	1076	50	7.8	481	2	JC5378	protein disulfide-
1004	50.5	7.8	3010	1	A45573	genome polyprotein	1077	50	7.8	491	2	T01856	hypothetical prote
1005	50.5	7.8	3010	1	GNWVCJ	genome polyprotein	1078	50	7.8	500	2	A82127	two-component sens
1006	50.5	7.8	3010	1	GNWVCJ	genome polyprotein	1079	50	7.8	517	2	D84512	hypothetical prote
1007	50.5	7.8	3106	1	S53868	laminin alpha-2 ch	1080	50	7.8	521	1	FOLJST	gag polyprotein -
1008	50.5	7.8	4543	1	A53102	alpha-2-macroglobu	1081	50	7.8	521	2	S08435	gag polyprotein -
1009	50	7.8	56	2	I37964	zinc finger protei	1082	50	7.8	522	1	FOLJG2	gag polyprotein -
1010	50	7.8	103	2	PH1045	Ig light chain v r	1083	50	7.8	524	2	G84595	hypothetical prote
1011	50	7.8	105	2	T19159	hypothetical prote	1084	50	7.8	526	2	T20086	hypothetical prote
1012	50	7.8	116	2	H80822	probable head-tail	1085	50	7.8	561	2	T27318	chaperonin GroEL p
1013	50	7.8	116	2	H85843	unknown protein en	1086	50	7.8	573	1	A32800	transcription fact
1014	50	7.8	120	2	A97655	hypothetical prote	1087	50	7.8	578	2	T40984	env polyprotein -
1015	50	7.8	120	2	AG2878	conserved hypothet	1088	50	7.8	586	1	VCLJMP	env polyprotein -
1016	50	7.8	154	2	JQ2228	trans-activating p	1089	50	7.8	592	2	G89159	sensory transducti
1017	50	7.8	160	2	I37033	eosinophil cationi	1090	50	7.8	616	2	QJ1441	hypothetical 67K p
1018	50	7.8	169	2	T34520	hypothetical prote	1091	50	7.8	626	2	T27319	hypothetical prote
1019	50	7.8	185	2	JN0766	adrenomedullin pre	1092	50	7.8	630	2	H89056	protein K09H11.4 [
1020	50	7.8	186	2	T32656	hypothetical prote	1093	50	7.8	643	2	S36499	E1 protein - human
1021	50	7.8	189	2	E69743	hypothetical prote	1094	50	7.8	680	2	T25832	hypothetical prote
1022	50	7.8	190	2	AD2232	hypothetical prote	1095	50	7.8	680	2	T27078	hypothetical prote
1023	50	7.8	192	2	F70359	hypothetical prote	1096	50	7.8	682	2	S71476	homeotic protein H
1024	50	7.8	200	2	I51551	platelet-derived g	1097	50	7.8	686	2	AB2362	ribonuclease II [i
1025	50	7.8	215	2	S09220	platelet-derived g	1098	50	7.8	697	2	T03722	EXO70 protein - mo
1026	50	7.8	226	2	I51550	platelet-derived g	1099	50	7.8	705	2	S76729	disintegrin [EC 3.
1027	50	7.8	232	2	A60083	neural induction h	1100	50	7.8	748	2	S66129	complement factor
1028	50	7.8	241	2	C97305	D-alanyl-D-alanine	1101	50	7.8	764	1	BBHU	hypothetical prote
1029	50	7.8	251	2	T25820	hypothetical prote	1102	50	7.8	769	2	E56613	transcription elon
1030	50	7.8	254	2	AB0763	thiosulfate reduct	1103	50	7.8	772	2	JC4636	hypothetical prote
1031	50	7.8	254	2	C57143	thiosulfate-dithio	1104	50	7.8	807	2	T32463	hypothetical prote
1032	50	7.8	255	2	G64320	hypothetical prote	1105	50	7.8	816	2	C88196	protein ZK1127.7 [
1033	50	7.8	256	2	T24711	hypothetical prote	1106	50	7.8	820	2	G82168	trimethylamine-N-o
1034	50	7.8	264	2	T22054	hypothetical prote	1107	50	7.8	827	2	H83217	probable transcrip
1035	50	7.8	266	2	H83008	N-formylglutamate	1108	50	7.8	828	2	E81651	conserved hypothet
1036	50	7.8	271	2	F83081	hypothetical prote	1109	50	7.8	860	2	T27084	hypothetical prote
1037	50	7.8	278	2	D84492	hypothetical prote	1110	50	7.8	975	2	I48974	receptor-protein t
1038	50	7.8	282	2	T18608	hypothetical prote	1111	50	7.8	977	2	S49004	tyrosine kinase Mp
1039	50	7.8	286	2	T42610	probable immediate	1112	50	7.8	1020	2	H96793	unknown protein F1
1040	50	7.8	292	2	T28817	hypothetical prote	1113	50	7.8	1058	2	T30580	p-type ATPase - sl
1041	50	7.8	293	2	B26637	neurogenic repetit	1114	50	7.8	1110	2	T19673	hypothetical prote
1042	50	7.8	297	2	B84788	hypothetical prote	1115	50	7.8	1146	2	B35962	protein-tyrosine k
1043	50	7.8	308	2	S22930	ubiquinol-cytochro	1116	50	7.8	1182	2	A35962	protein-tyrosine k
1044	50	7.8	314	1	A35268	nudulation protein	1117	50	7.8	1254	2	I48161	p-185 precursor -
1045	50	7.8	316	2	E81321	probable cation tr	1118	50	7.8	1284	2	T40879	probable helicase
1046	50	7.8	316	2	G96513	hypothetical prote	1119	50	7.8	1378	2	T47605	RING finger-like p
1047	50	7.8	318	2	AG0099	general secretion	1120	50	7.8	1462	2	S75142	sensory transducti
1048	50	7.8	325	2	E96620	protein T30E16.27	1121	50	7.8	1549	1	A40691	trichosyalin - she
1049	50	7.8	326	2	AB3100	hypothetical prote	1122	50	7.8	1615	2	JC6510	ras-responsive ele
1050	50	7.8	326	2	H98186	probable mikimopin	1123	50	7.8	1648	2	F84833	probable SNF2/SNF2
1051	50	7.8	341	2	B87011	conserved hypothet	1124	50	7.8	1813	2	T30564	resistance protein



1125	7.8	50	2139	2	A35672	crumbs protein - f	1198	49.5	7.7	407	2	T14909	bZIP DNA-binding p
1126	7.8	50	2182	2	T14320	calcineurin inhibi	1199	49.5	7.7	408	2	JC4938	hepatocyte nuclear
1127	7.8	50	2629	2	T32735	telomerase- associa	1200	49.5	7.7	409	2	S24460	probable membrane
1128	7.8	50	2871	2	A55567	fibrillin 1 - bovi	1201	49.5	7.7	410	2	S77844	alanine-tRNA ligas
1129	7.8	50	2907	2	A57278	fibrillin-2 precu	1202	49.5	7.7	419	2	D82067	UDP-N-acetylglucos
1130	7.8	50	3002	2	A47221	fibrillin-1 precu	1203	49.5	7.7	420	2	S71199	dnaj protein homol
1131	49.5	7.7	50	2	T07556	hypothetical prote	1204	49.5	7.7	420	2	T49127	Delta6 fatty acid
1132	49.5	7.7	108	2	A83406	hypothetical prote	1205	49.5	7.7	444	2	JG0180	hepatocyte nuclear
1133	49.5	7.7	117	1	B59316	ghrelin precursor	1206	49.5	7.7	445	2	C86447	F5D14.3 protein -
1134	49.5	7.7	131	2	P64154	hypothetical prote	1207	49.5	7.7	465	2	JC4937	hepatocyte nuclear
1135	49.5	7.7	140	2	D72680	hypothetical prote	1208	49.5	7.7	465	2	S52074	EGR alpha transcrr
1136	49.5	7.7	148	2	S09979	ferredoxin [2Fe-2S	1209	49.5	7.7	469	2	A57531	F22D16.15 protein
1137	49.5	7.7	150	2	A84488	hypothetical prote	1210	49.5	7.7	497	2	G86158	Hepatic transposo
1138	49.5	7.7	156	2	T02166	cysteine proteinas	1211	49.5	7.7	504	2	JC6096	Hepatic transposo
1139	49.5	7.7	161	1	S76604	hypothetical prote	1212	49.5	7.7	510	2	A53802	hypothetical prote
1140	49.5	7.7	162	2	A10884	hydrogenase-2 comp	1213	49.5	7.7	511	2	D70507	hypothetical prote
1141	49.5	7.7	163	2	D87293	Fur family protein	1214	49.5	7.7	512	2	AC3203	IS3 family transpo
1142	49.5	7.7	169	2	C29016	cell division inhi	1215	49.5	7.7	512	2	AD2835	IS3 family transpo
1143	49.5	7.7	171	2	S78525	alpha-amylase inhi	1216	49.5	7.7	512	2	AD3049	probable transposo
1144	49.5	7.7	171	2	A99190	hypothetical prote	1217	49.5	7.7	512	2	G97612	probable transposo
1145	49.5	7.7	171	2	AH3096	conserved hypotet	1218	49.5	7.7	512	2	G98236	probable copper-bi
1146	49.5	7.7	173	2	A95864	hypothetical prote	1219	49.5	7.7	516	2	C64735	DNA repair protein
1147	49.5	7.7	174	2	S58758	alpha-crystallin c	1220	49.5	7.7	534	2	G82272	hypothetical prote
1148	49.5	7.7	174	2	S47069	finger protein HZF	1221	49.5	7.7	555	2	H96762	ENL (translocation
1149	49.5	7.7	187	1	Y0ECKS	KS71A fibrial pro	1222	49.5	7.7	559	2	B44265	outer membrane pro
1150	49.5	7.7	187	2	C43597	pilin type F7-1 pr	1223	49.5	7.7	565	2	B57148	netrin-2 precursor
1151	49.5	7.7	191	2	AE2559	hypothetical prote	1224	49.5	7.7	581	2	B54665	hypothetical prote
1152	49.5	7.7	193	2	AF1823	hypothetical prote	1225	49.5	7.7	583	2	T17326	protein F40E10.4 l
1153	49.5	7.7	207	1	A64915	ycdy protein homol	1226	49.5	7.7	601	2	D89711	hypothetical prote
1154	49.5	7.7	207	2	F85764	probable oxidoredu	1227	49.5	7.7	612	2	T22025	hypothetical prote
1155	49.5	7.7	207	2	A90916	probable oxidoredu	1228	49.5	7.7	616	2	A95012	hypothetical prote
1156	49.5	7.7	207	2	T50206	hypothetical zinc	1229	49.5	7.7	616	2	D97883	hypothetical prote
1157	49.5	7.7	209	2	B42687	neurotrophin-4 pre	1230	49.5	7.7	665	2	A12733	NADH ubiquinone ox
1158	49.5	7.7	212	2	A82128	thymidylate kinase	1231	49.5	7.7	665	2	C97515	NADH-ubiquinone ox
1159	49.5	7.7	219	1	A39574	leukocyte antigen	1232	49.5	7.7	673	2	T40817	zinc finger protei
1160	49.5	7.7	221	2	S65476	ras-homolog GTPase	1233	49.5	7.7	681	2	S36534	B1 protein - human
1161	49.5	7.7	233	2	B84237	hypothetical prote	1234	49.5	7.7	694	2	T01134	probable protein k
1162	49.5	7.7	236	2	F84586	hypothetical prote	1235	49.5	7.7	730	2	T05345	hypothetical prote
1163	49.5	7.7	241	1	HLNSTR	class I-related se	1236	49.5	7.7	732	2	A35505	primosomal replica
1164	49.5	7.7	244	1	LNRTWC	mannose-binding le	1237	49.5	7.7	744	2	T13429	hypothetical prote
1165	49.5	7.7	246	2	T28166	hypothetical prote	1238	49.5	7.7	749	2	T34090	hypothetical prote
1166	49.5	7.7	257	2	F75084	hypothetical prote	1239	49.5	7.7	758	2	B84933	5-methyltetrahydro
1167	49.5	7.7	266	2	T15066	hypothetical prote	1240	49.5	7.7	765	2	T15447	hypothetical prote
1168	49.5	7.7	268	2	T10304	inhibitor of apopt	1241	49.5	7.7	773	2	A83888	hypothetical prote
1169	49.5	7.7	268	2	A53989	apoptosis-inhibiti	1242	49.5	7.7	777	2	S48100	ADAM 5 protein pre
1170	49.5	7.7	269	2	T64151	hypothetical prote	1243	49.5	7.7	796	2	S57844	lethal(3)malignant
1171	49.5	7.7	280	2	T19363	hypothetical prote	1244	49.5	7.7	805	2	T34212	hypothetical prote
1172	49.5	7.7	287	2	A11072	conserved hypotet	1245	49.5	7.7	812	2	B97401	uridylyltransferas
1173	49.5	7.7	294	2	G90032	hypothetical prote	1246	49.5	7.7	827	2	A69793	conserved hypotet
1174	49.5	7.7	299	2	T15240	hypothetical prote	1247	49.5	7.7	862	2	E84567	probable trehalose
1175	49.5	7.7	304	2	D83104	hypothetical prote	1248	49.5	7.7	864	2	T49574	probable carnitine
1176	49.5	7.7	306	2	E83197	transcription regu	1249	49.5	7.7	880	2	AE0179	probable ATPase ch
1177	49.5	7.7	317	2	T33935	hypothetical prote	1250	49.5	7.7	882	2	AE0119	Clp ATPase [import
1178	49.5	7.7	321	1	F87102	probable phosphoes	1251	49.5	7.7	942	2	AB2619	metabotropic gluta
1179	49.5	7.7	322	2	A21125	MHC class I histoc	1252	49.5	7.7	952	2	T18837	hypothetical prote
1180	49.5	7.7	325	2	S20045	MHC class I histoc	1253	49.5	7.7	964	2	T49038	hypothetical prote
1181	49.5	7.7	326	2	T33343	hypothetical prote	1254	49.5	7.7	968	2	T52186	phosphoenolpyruvat
1182	49.5	7.7	332	2	T01475	env polyprotein -	1255	49.5	7.7	991	2	T49540	procollagen C-endo
1183	49.5	7.7	335	2	A46345	B2 protein - human	1256	49.5	7.7	1028	2	B24785	hypothetical prote
1184	49.5	7.7	336	2	S36530	hypothetical prote	1257	49.5	7.7	1141	2	T29104	Tbc1 protein - mou
1185	49.5	7.7	337	2	T30730	hypothetical prote	1258	49.5	7.7	1221	2	E83327	conserved hypotet
1186	49.5	7.7	338	2	T21946	transcription fact	1259	49.5	7.7	1271	2	S37958	myosin heavy chain
1187	49.5	7.7	347	2	A46403	benzoate transport	1260	49.5	7.7	1311	2	C84528	hypothetical prote
1188	49.5	7.7	387	2	D82134	phage-related inte	1261	49.5	7.7	1334	2	E86451	probable copia-typ
1189	49.5	7.7	387	2	D65177	probable membrane	1262	49.5	7.7	1372	2	T25933	hypothetical prote
1190	49.5	7.7	394	2	B67162	replication protei	1263	49.5	7.7	1427	2	T39219	atp-binding casset
1191	49.5	7.7	397	2	AC3521	hypothetical prote	1264	49.5	7.7	1472	2	A26122	alpha-2-macroglobu
1192	49.5	7.7	398	2	T26284	conserved hypotet	1265	49.5	7.7	1490	2	F88311	hypothetical prote
1193	49.5	7.7	399	2	AD2917	hypothetical prote	1266	49.5	7.7	1490	2	T24502	protein T0608.10 l
1194	49.5	7.7	399	2	G97691	MFS permease [drug	1267	49.5	7.7	1545	2	T14288	DNA (cytosine-5-) -
1195	49.5	7.7	400	2	AG2866	probable efflux pr	1268	49.5	7.7	1545	2	T14288	P-glycoprotein E -
1196	49.5	7.7	400	2	D97643		1269	49.5	7.7	1677	2	T18344	
1197	49.5	7.7	406	2	F86454	CDS protein F9L1.1	1270	49.5	7.7				

1271	49.5	7.7	2150	2	S71629	sensory transducti	1344	49	7.6	410	2	H97597	hypothetical prote
1272	49.5	7.7	2210	1	RRXPLC	genome polyprotein	1345	49	7.6	430	2	S66671	neuron-derived rec
1273	49.5	7.7	2257	2	T18492	hypothetical prote	1346	49	7.6	431	2	I49149	CRF receptor - mou
1274	49.5	7.7	2895	2	H85362	hypothetical prote	1347	49	7.6	431	2	C86178	hypothetical prote
1275	49.5	7.7	3133	2	S52093	hemocytin - silkw	1348	49	7.6	433	2	T31511	hypothetical prote
1276	49.5	7.7	4544	1	S02392	alpha-2-macroglob	1349	49	7.6	434	2	A43252	probable transcrip
1277	49	7.6	69	2	S17518	opa protein - frui	1350	49	7.6	434	2	T01390	hypothetical prote
1278	49	7.6	87	2	S00180	spermatid protein	1351	49	7.6	437	1	A48051	translation releas
1279	49	7.6	94	2	S32939	AUA1 protein - yea	1352	49	7.6	437	1	S50853	probable transport
1280	49	7.6	95	2	S72980	hypothetical prote	1353	49	7.6	438	2	A83544	glutamate CoA-tr
1281	49	7.6	96	2	AE1822	transcription regu	1354	49	7.6	447	2	F69399	probable CoA-tr
1282	49	7.6	101	2	D56272	probable pheromone	1355	49	7.6	459	2	A22842	(2'-5')oligo(A) sy
1283	49	7.6	102	2	A72507	hypothetical prote	1356	49	7.6	470	2	S33639	finger protein esc
1284	49	7.6	105	1	JN0483	ribosomal protein	1357	49	7.6	472	2	JC7626	amino acid transpo
1285	49	7.6	105	2	G97825	30S ribosomal prot	1358	49	7.6	473	2	AG3537	6-oxohexanoate deh
1286	49	7.6	105	2	T08720	ribosomal protein	1359	49	7.6	476	2	T42692	hypothetical prote
1287	49	7.6	106	2	T36973	hypothetical prote	1360	49	7.6	483	2	T17346	hypothetical prote
1288	49	7.6	121	2	T28046	hypothetical prote	1361	49	7.6	495	1	I37062	involucrin S - gor
1289	49	7.6	128	2	A72678	hypothetical prote	1362	49	7.6	501	2	JC7877	toxins-60A - Okinaw
1290	49	7.6	130	1	RWMS58	T-cell receptor al	1363	49	7.6	513	2	A38193	phosphoprotein pho
1291	49	7.6	137	1	BGP62	spermatid transiti	1364	49	7.6	526	2	A86097	hypothetical prote
1292	49	7.6	137	2	AF0362	probable exported	1365	49	7.6	526	2	E91256	hypothetical prote
1293	49	7.6	147	2	A36790	hypothetical prote	1366	49	7.6	529	2	S46116	probable regulator
1294	49	7.6	152	2	A53274	complement factor	1367	49	7.6	530	2	F71445	hypothetical prote
1295	49	7.6	152	2	AE1812	hypothetical prote	1368	49	7.6	535	2	S44827	F54F2.2 protein -
1296	49	7.6	182	2	D82925	hypothetical prote	1369	49	7.6	538	1	S12570	homeotic protein b
1297	49	7.6	183	1	FRHUH	ferritin heavy cha	1370	49	7.6	538	2	G83653	oligopeptide ABC t
1298	49	7.6	188	2	F95322	hypothetical prote	1371	49	7.6	546	2	T24679	hypothetical prote
1299	49	7.6	203	2	T33864	hypothetical prote	1372	49	7.6	547	2	G83116	pyochelin biosynth
1300	49	7.6	211	2	F86488	hypothetical prote	1373	49	7.6	559	2	T12680	peroxisomal target
1301	49	7.6	217	2	T40730	protein T32E20.33	1374	49	7.6	578	2	D95400	probable oxidoredu
1302	49	7.6	222	2	T47742	probable rna-bindi	1375	49	7.6	578	2	T50812	asparagine synthas
1303	49	7.6	224	2	C31201	hypothetical prote	1376	49	7.6	593	1	F70349	NADH2 dehydrogenas
1304	49	7.6	226	2	A70754	GLI-related finger	1377	49	7.6	595	2	F85438	NADH2 dehydrogenas
1305	49	7.6	228	2	B72655	hypothetical prote	1378	49	7.6	605	1	I37061	involucrin M - gor
1306	49	7.6	228	2	T47425	probable transcrip	1379	49	7.6	612	2	S35471	gag-like protein -
1307	49	7.6	234	2	C83097	NAC domain-like pr	1380	49	7.6	613	2	T00077	DNA topoisomerase
1308	49	7.6	239	2	H84886	InaA protein PA37	1381	49	7.6	619	2	A82638	neuron-derived rec
1309	49	7.6	241	2	T34379	probable VAMP-asso	1382	49	7.6	625	2	S71930	neuron derived orp
1310	49	7.6	247	2	S57136	hypothetical prote	1383	49	7.6	628	2	JC2493	probable polygalac
1311	49	7.6	261	2	S29360	probable ribosomal	1384	49	7.6	632	2	T07587	involucrin L - gor
1312	49	7.6	261	2	D90819	Fc gamma (IgG) rec	1385	49	7.6	635	1	I37060	involucrin L - gor
1313	49	7.6	273	2	B85627	probable antitermi	1386	49	7.6	640	1	UZADP7	terminal protein p
1314	49	7.6	277	2	S4324	probable antitermi	1387	49	7.6	643	1	S15616	E1 protein - human
1315	49	7.6	277	2	D84596	platelet glycoprot	1388	49	7.6	643	2	A41120	prostaglandin tran
1316	49	7.6	298	2	G75140	hypothetical prote	1389	49	7.6	644	1	W1WL58	E1 protein - human
1317	49	7.6	305	2	T25117	hypothetical prote	1390	49	7.6	658	2	T16040	hypothetical prote
1318	49	7.6	306	2	A75316	hypothetical prote	1391	49	7.6	669	2	T08827	hypothetical prote
1319	49	7.6	311	2	T12500	hypothetical prote	1392	49	7.6	681	2	I38755	transcription fact
1320	49	7.6	315	1	B69812	ferrichrome ABC tr	1393	49	7.6	682	2	G86300	F19K19.13 protein
1321	49	7.6	346	2	S10188	NADH2 dehydrogenas	1394	49	7.6	694	2	S32958	probable membrane
1322	49	7.6	346	2	T11194	NADH2 dehydrogenas	1395	49	7.6	732	2	AF0938	primosomal protein
1323	49	7.6	346	2	B90624	NADH dehydrogenas	1396	49	7.6	740	2	S61568	probable membrane
1324	49	7.6	348	2	T13817	NADH2 dehydrogenas	1397	49	7.6	744	2	S70619	finger protein bow
1325	49	7.6	354	1	WNECPW	glycine betaine/L-	1398	49	7.6	749	2	G86186	hypothetical prote
1326	49	7.6	354	2	AB0842	glycine betaine/L-	1399	49	7.6	755	2	S42452	structural polypro
1327	49	7.6	354	2	E91071	hypothetical prote	1400	49	7.6	788	2	A37057	integrin beta-6 ch
1328	49	7.6	354	2	H85915	hypothetical prote	1401	49	7.6	789	2	A39564	transcription repr
1329	49	7.6	364	2	S28771	polygalacturonase	1402	49	7.6	790	2	A35797	probable DNA-bindi
1330	49	7.6	366	2	I53488	prostaglandin F2 a	1403	49	7.6	793	2	S68238	trp-1 protein - hu
1331	49	7.6	366	2	S51281	F2-alpha receptor	1404	49	7.6	810	2	I38361	TRPC1 protein - hu
1332	49	7.6	367	2	AC1135	B. subtilis floN p	1405	49	7.6	833	1	T24682	hypothetical prote
1333	49	7.6	374	2	AD1493	conserved hypothet	1406	49	7.6	835	1	I57441	involucrin - orang
1334	49	7.6	374	2	T35581	probable O-sialogl	1407	49	7.6	838	2	T20125	hypothetical prote
1335	49	7.6	379	2	S58457	ubiquinol-cytochro	1408	49	7.6	859	1	JQ2267	lipoxigenase (EC 1
1336	49	7.6	381	2	F87197	probable anion tra	1409	49	7.6	860	1	QRHULD	LDL receptor precu
1337	49	7.6	396	2	T23767	hypothetical prote	1410	49	7.6	865	2	H71447	trehalose-6-phosph
1338	49	7.6	398	2	B86298	protein F309.11 li	1411	49	7.6	877	2	C46356	env polyprotein -
1339	49	7.6	401	2	T51493	stearoyl-acyl carr	1412	49	7.6	886	2	S07132	hypothetical prote
1340	49	7.6	401	2	D87368	imidazolonepropion	1413	49	7.6	904	1	VCLJBT	env polyprotein pr
1341	49	7.6	408	1	BMHU4	bone morphogenetic	1414	49	7.6	905	2	T23229	hypothetical prote
1342	49	7.6	409	2	S70704	carbon catabolite	1415	49	7.6	935	2	A64608	excinuclease ABC c
1343	49	7.6	410	2	AH2819	cyclopropane-fatty	1416	49	7.6	941	2	H71906	excinuclease ABC c





RESULT 9  
T49804  
hypothetical protein B11B22.60 [imported] - *Neurospora crassa*  
C:Species: *Neurospora crassa*  
C:Date: 02-Jun-2000 #sequence revision 02-Jun-2000 #text change 09-Jul-2004

Cell 60, 211-224, 1990

A:Reference number: A32693; MUID:90124631; PMID:2105166

A:Accession: B32693

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-746 <WLO>

A:Cross-references: UNIPROT:P16376; UNIPARC:UPI0000124PA1; GB:M28863; GB:M28864

C:Genetics:

A:Gene: FlyBase:svp

A:Cross-references: FlyBase:FBgn0003651

C:Keywords: alternative splicing; DNA binding; steroid hormone receptor; transcription

F:198-453/Domain: erba transforming protein homology <ERBA>

F:200-220/Region: zinc finger

F:236-260/Region: zinc finger

Query Match 10.9%; Score 70; DB 2; Length 746;

Best Local Similarity 26.7%; Pred. No. 21;

Matches 27; Conservative 12; Mismatches 28; Indels 34; Gaps 5;

QY 21 SSSLNPG-----VARGHRDRGQASRRWLQEGGQCECKDWFRLAPRRKFTWTVSG 69

DB 183 SOSNSGSGQIDSKQNIQVCGDKSGHYGQFTCEG-----CKSFPRKSVRRN-LTYSC 236

QY 70 LPKQPCPDHFHFGNVKKTTHQRRHKPNKHSRACQQLKQC 110

DB 237 RGRNCPID-----QHRRNQCYCR-----LKKC 260

RESULT 12

T24061

hypothetical protein R09A8.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T24061

R:Wilkinson, J.

submitted to the EMBL Data Library, November 1995

A:Reference number: Z19836

A:Accession: T24061

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1095 <WLI>

A:Cross-references: UNIPROT:Q21852; UNIPARC:UPI000007CD18; EMBL:Z68009; PIDN:CAA92003.1;

A:Experimental source: clone R09A8

C:Genetics:

A:Gene: CESP:R09A8.1

A:Map position: X

A:Introns: 48/2; 189/1; 285/3; 347/3; 402/3; 482/3; 543/3; 619/1; 693/1; 771/1; 835/1; 1

Query Match 10.9%; Score 70; DB 2; Length 1095;

Best Local Similarity 31.6%; Pred. No. 30;

Matches 24; Conservative 10; Mismatches 32; Indels 10; Gaps 3;

QY 20 VSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFRLAPRRKFTWTVSGLPKQCPDH 79

DB 305 VOSSLVNGNRSTDTRVNA-QRFASGTGFVEKECRWDQLVEKKQ-----KKEVNSDH 355

QY 80 FKGNVKKTTHQRRHKR 95

DB 356 KKAN-RITSHLEHNSR 370

RESULT 13

T27283

hypothetical protein Y64GI0A.f - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T27283

R:Ainscough, R.

submitted to the EMBL Data Library, September 1999

A:Reference number: Z20336

A:Accession: T27283

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1620 <WLI>

A:Cross-references: UNIPARC:UPI000017BCB4; EMBL:AL110498; NID:e1542303; PIDN:CAB54471.1;

A:Experimental source: clone Y64GI0A

C:Genetics:

A:Gene: CESP:Y64GI0A.f

A:Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1; 71

Query Match 10.9%; Score 70; DB 2; Length 1620;

Best Local Similarity 30.0%; Pred. No. 42;

Matches 21; Conservative 10; Mismatches 35; Indels 4; Gaps 3;

QY 46 GGOQCECKDWF-LRAPRRKFTWTVSGLPKQPCDHFHFGNVKKTTH--QRHHRKPNKHSRA 102

DB 261 GRAQCQYPGFHLSDYDRSCVDIDECAKN--GCEHFCENVAGTYRCKREGQLGRDGR 319

QY 103 COQFLKQCL 112

DB 320 CEMLGGCQV 329

RESULT 14

C34768

ORF2 protein - Orf virus (strain N22)

C:Species: Orf virus

C:Date: 23-Aug-1991 #sequence\_revision 23-Aug-1991 #text\_change 09-Jul-2004

C:Accession: C34768

R:Fraser, K.W.; Hill, D.F.; Mercer, A.A.; Robinson, A.J.

Virology 176, 379-389, 1990

A:Title: Sequence analysis of the inverted terminal repetition in the genome of the para

A:Reference number: A34768; MUID:90266454; PMID:2129563

A:Accession: C34768

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-221 <FRA>

A:Cross-references: UNIPROT:Q85299; UNIPARC:UPI00000F1366; GB:M30023; EMBL:M37623; NID:g

Query Match 10.8%; Score 69.5; DB 2; Length 221;

Best Local Similarity 29.2%; Pred. No. 8.3;

Matches 33; Conservative 8; Mismatches 37; Indels 35; Gaps 6;

QY 26 PGVARGHRDRGQASRRWLQEGGQCECKDWFRLAPRRKFTWTVSGLPKK-----QCP 76

DB 83 PAAARGARRCCARRARGGGGWP---RRWRPRAARRG---SGPPARAPAAALAPDQAP 135

QY 77 CDHFKGNVKKTR-----HQR--HHRKPNKHSRACQQLKQCLRS 114

DB 136 ----RSKYKQDLAVETLPPQPTPTLPPARRQHRSSQACTPRRRCGCSARS 184

RESULT 15

THHUB

thrombomodulin precursor [validated] - human

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1998 #sequence\_revision 12-May-1995 #text\_change 09-Jul-2004

C:Accession: A41442; A28307; A29680; A27073; JX0264; S38954

R:Shirai, T.; Shiojiri, S.; Ito, H.; Yamamoto, S.; Kusumoto, H.; Deyashiki, Y.; Maruyama,

J. Biochem. 103, 281-285, 1988

A:Title: Gene structure of human thrombomodulin, a cofactor for thrombin-catalyzed activa

A:Reference number: A41442; MUID:88227901; PMID:2836377

A:Accession: A41442

A:Molecule type: DNA

A:Residues: 1-575 <SHI>

A:Cross-references: UNIPROT:P07204; UNIPARC:UPI00000498FB; DBJ:D00210; NID:g220126; PIDN

R:Jackman, R.W.; Beeler, D.L.; Fritze, L.; Soff, G.; Rosenberg, R.D.

Proc. Natl. Acad. Sci. U.S.A. 84, 6425-6429, 1987

A:Title: Human thrombomodulin gene is intron depleted: nucleic acid sequences of the cDN

A:Reference number: A28307; MUID:87317665; PMID:2819876

A:Accession: A28307

A:Molecule type: DNA; mRNA

A:Residues: 1-472,'A',474-575 <JAC>

A:Cross-references: UNIPARC:UPI000000002BD; GB:J02973; NID:g338658; PIDN:AAAG1175.1; PID:g

R:Suzuki, K.; Kusumoto, H.; Deyashiki, Y.; Nishioka, J.; Maruyama, I.; Kawahara

EMBO J. 6, 1891-1897, 1987

A:Title: Structure and expression of human thrombomodulin, a thrombin receptor on endothe

A;Reference number: A29680; MUID:88004395; PMID:2820710  
A;Accession: A29680  
A;Molecule type: mRNA  
A;Residues: 1-575 <SUZ>  
A;Cross-references: UNIPARC:UPI00000498FB; GB:X05495; NID:g37123; PIDN:CAA29045.1; PID:9  
A;Experimental source: lung endothelium  
A;Note: Part of this sequence, including the amino end of the mature protein, were deter  
R;Wen, D.; Dittman, W.A.; Ye, R.D.; Deaven, L.L.; Majerus, P.W.; Sadler, J.E.  
Biochemistry 26, 4350-4357, 1987  
A;Title: Human thrombomodulin: complete cDNA sequence and chromosome localization of the  
A;Reference number: A27073; MUID:88024950; PMID:2822087  
A;Accession: A27073  
A;Molecule type: mRNA  
A;Residues: 1-472, 'A', 474-575 <WEN>  
A;Cross-references: UNIPARC:UPI00000002BD; GB:M16552; NID:g339656; PIDN:AAB59508.1; PID:  
A;Experimental source: placenta  
A;Note: Parts of this sequence were determined by protein sequencing  
R;Yamamoto, S.; Mizoguchi, T.; Tamaki, T.; Ohkuchi, M.; Kimura, S.; Aoki, N.  
J. Biochem. 113, 433-440, 1993.  
A;Title: Urinary thrombomodulin, its isolation and characterization.  
A;Reference number: JX0264; MUID:93293792; PMID:8390446  
A;Accession: JX0264  
A;Molecule type: protein; mRNA  
A;Residues: 19-472, 'A', 474-486 <YAM>  
A;Cross-references: UNIPARC:UPI0000173341  
A;Experimental source: urine  
A;Note: the urinary form appears to be identical with that circulating in plasma  
R;Gerlitz, B.; Hassell, T.; Vlahos, C.J.; Parkinson, J.F.; Bang, N.U.; Grinnell, B.W.  
Biochem. J. 295, 131-140, 1993  
A;Title: Identification of the predominant glycosaminoglycan-attachment site in soluble  
serine.  
A;Reference number: S38954; MUID:94029900; PMID:8216207  
A;Accession: S38954  
A;Molecule type: protein  
A;Residues: 475-491, 'X', 493-494 <GER>  
A;Cross-references: UNIPARC:UPI0000173342  
A;Note: the residue designated 'X' was determined to be a Ser with covalently bound chon  
R;Meininger, D.P.; Komives, E.A.  
submitted to the Brookhaven Protein Data Bank, September 1995  
A;Reference number: A67369; PDB:1ZAQ  
A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue  
R;Tullinsky, A.; Mathews, I.I.  
submitted to the Brookhaven Protein Data Bank, August 1994  
A;Reference number: A52804; PDB:1HLT  
A;Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 426-442  
R;Hrabal, R.; Komives, E.A.; Ni, F.  
submitted to the Brookhaven Protein Data Bank, November 1995  
A;Reference number: A65583; PDB:1FGD  
A;Contents: annotation; conformation by (1)H-NMR, residues 427-444  
R;Hrabal, R.; Komives, E.A.; Ni, F.  
Protein Sci. 5, 195-203, 1996  
A;Title: Structural resiliency of an EGF-like subdomain bound to its target protein, thr  
A;Reference number: A58595; MUID:96276211; PMID:8745396  
A;Contents: annotation; conformation by (1)H-NMR  
C;Genetics:  
A;Gene: GDB:THBD  
A;Cross-references: GDB:119613; OMIM:188040  
A;Map position: 20p11.2-20p11.2  
A;Introns: #status absent  
C;Complex: homodimer, urinary form  
C;Function:  
A;Description: inhibits thrombin activation of fibrinogen; cofactor for thrombin activat  
A;Pathway: blood coagulation moderation  
A;Note: the membrane-bound form is located on the endothelium luminal surface of arterie  
A;Note: thrombin complexed with the membrane-bound form is subject to endocytosis  
C;Superfamily: thrombomodulin; C-type lectin homology; EGF homology  
C;Keywords: anticoagulant; beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coag  
e protein  
F;1-18/Domain: signal sequence #status predicted <SIG>  
F;19-575/Product: thrombomodulin, membrane-bound form #status predicted <MAT>  
F;19-513/Domain: extracellular #status predicted <EXT>  
F;19-486/Product: thrombomodulin, urinary form #status experimental <MAU>  
F;24-167/Domain: C-type lectin homology <LCH>

F;177-199/Region: PEST sequence  
F;201-233/Region: PEST sequence  
F;245-280/Domain: EGF homology <EG1>  
F;288-323/Domain: EGF homology <EG2>  
F;329-362/Domain: EGF homology <EG3>  
F;369-404/Domain: EGF homology <EG4>  
F;408-439/Domain: EGF homology <EG5>  
F;445-480/Domain: EGF homology <EG6>  
F;485-513/Region: PEST sequence  
F;517-539/Domain: transmembrane #status predicted <TMN>  
F;540-575/Domain: intracellular #status predicted <INT>  
F;47,115,116,382,409/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;174,225,411,504/Binding site: carbohydrate (Thr) (covalent) #status predicted  
F;245-256,252-265,267-280,288-296,292-308,310-323,329-340,336-349,351-362,369-378,374-388  
F;334,498/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F;342/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental  
F;490,492/Binding site: chondroitin sulfate (Ser) (covalent) (partial) #status experiment  
Query Match 10.8%; Score 69.5; DB 1; Length 575;  
Best Local Similarity 23.5%; Pred. No. 19;  
Matches 24; Conservative 11; Mismatches 26; Indels 41; Gaps 5;  
QY 5 ISSLLLLLPMLMSVSSSLNPGVARGHRDRGQASRRW---LQGGQCECKDWFLRAPR 61  
DB 209 VGSSAAVFLGLQLMCTAP--FGAVQGHWR-EAPGAWDCSVENGCCERACN----- 257  
QY 62 RKFMVTYSGLPKKQCP-----CDHF 80  
DB 258 ----AIPGAPQCPCAGALQADGRCTASATQSCNDLCEHF 295

Search completed: August 3, 2006, 09:57:13  
Job time : 48 secs

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OM protein - protein search, using sw model

Run on: August 3, 2006, 09:56:38 ; Search time 299 Seconds

(without alignments)

368.150 Million cell updates/sec

Title: US-10-015-967-2

Perfect score: 644

Sequence: 1 MKVLISLLLLPLMLMSV.....SRACQFLKQCQLRSFALPL 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

UniProt 7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	644	100.0	119	2	Q6UXB2 HUMAN
2	456	70.8	119	2	Q5UW37 MOUSE
3	322	50.0	128	2	Q8R3U6 MOUSE
4	81	12.6	170	2	Q52VK8_CIOIN
5	81	12.6	170	2	Q52VK8_CIOIN
6	81	12.6	397	2	Q52VK2_CIOIN
7	81	12.6	487	2	Q3CNY9 ALTAT
8	80.5	12.5	188	2	Q32PK5 BRARE
9	80.5	12.5	188	2	Q5RHD0 BRARE
10	80.5	12.5	613	2	Q5RHD1 BRARE
11	80	12.4	844	2	Q4BU62 BURV1
12	79.5	12.3	662	2	Q61TA9 CAEBR
13	77.5	12.0	170	2	Q52VJ5_CIOIN
14	77.5	12.0	192	2	Q6NDV5 RHOPA
15	77.5	12.0	337	2	Q62022 CAEBL
16	77.5	12.0	398	2	Q52VK3_CIOIN
17	77.5	12.0	449	2	Q810M4 CAEBL
18	77	12.0	335	2	Q74EB4 GEOSL
19	77	12.0	2269	1	L SV41
20	76.5	11.9	411	2	Q9W745 XENLA
21	76.5	11.9	825	2	Q4SAD2_TETNG
22	76	11.8	376	2	Q5AH87 CANAL
23	75.5	11.7	323	2	Q6BJ36 DEBHA
24	75	11.6	373	2	Q5SHK7 THET8
25	75	11.6	373	2	Q72HX1 THET2
26	75	11.6	413	2	Q4FZU0 RAT
27	75	11.6	1817	2	Q7XW82 ORYSA
28	75	11.6	1835	2	Q3WGB8 SACTO
29	74.5	11.6	373	2	Q5A2C5 CANAL
30	74.5	11.6	448	1	VDR COTJA
31	74.5	11.6	451	1	VDR_CHICK

32	74	11.5	145	2	Q4RDG3_TETNG	Q4rdg3 tetraodon n
33	74	11.5	169	2	Q89B64 BRAJA	Q89b64 bradyrhizob
34	74	11.5	311	2	Q2JRM6_9CVAN	Q2jrm6 cyanobacter
35	74	11.5	356	2	Q4IQ10_GIBZE	Q4iq10 gibberella
36	74	11.5	662	2	Q3JVR4_BURP1	Q3jvr4 burholderi
37	74	11.5	1501	2	Q2M1B4_DROPS	Q2m1b4 drosophila
38	73	11.3	209	2	Q2WBP5_HYDMA	Q2wbp5 hydra magni
39	73	11.3	217	2	Q5Z4A7_ORYSA	Q5z4a7 oryza sativ
40	73	11.3	564	2	Q7SCU8_NEUCR	Q7scu8 nematospora
41	73	11.3	797	2	Q2OTM6_ORYSA	Q2otm6 oryza sativ
42	72.5	11.3	246	2	Q2UT28_ASPOR	Q2ut28 aspergillus
43	72.5	11.3	289	2	Q5FUS3_GLUOX	Q5fus3 gluconobact
44	72.5	11.3	783	2	Q60T21_CAEBR	Q60t21 caenorhabdi
45	72.5	11.3	3313	1	CELR3 RAT	Q887g7 rat
46	72	11.2	278	2	Q89VG7 BRAJA	Q89vg7 bradyrhizob
47	72	11.2	1575	2	Q6TXJ1_RAT	Q6txj1 rattus norv
48	71.5	11.1	108	2	Q82328_ARATH	Q82328 arabidopsis
49	71.5	11.1	483	2	Q5SNF1_CRYNE	Q5snf1 cryptococcu
50	71.5	11.1	483	2	Q8KBT7_CRYNE	Q8kbt7 cryptococcu
51	71	11.0	188	2	Q8TEV2_HUMAN	Q8tev2 homo sapien
52	71	11.0	410	2	Q6PHF2_BRARE	Q6phf2 brachydanio
53	71	11.0	411	1	NR2F1 BRARE	Q06725 brachydanio
54	71	11.0	601	2	Q5ZMB1_CHICK	Q5zmb1 gallus gall
55	71	11.0	1798	1	LAMB2_HUMAN	P55268 homo sapien
56	71	11.0	2262	1	L PI2HT	P26676 h large str
57	71	11.0	2263	2	Q4R4G3_PI2H	Q4r4g3 human parai
58	71	11.0	3190	2	Q01368_DROME	Q01368 drosophila
59	71	11.0	3276	2	Q9W321_DROME	Q9w321 drosophila
60	70.5	10.9	160	2	Q9SQH1_ARAHY	Q9sqh1 arachis hyp
61	70.5	10.9	383	2	Q6AN18_DESPS	Q6an18 desulfotale
62	70.5	10.9	747	2	Q53LB6_ORYSA	Q53lb6 oryza sativ
63	70.5	10.9	1104	2	Q443W5_SOLUS	Q443w5 solibacter
64	70.5	10.9	1290	2	Q96UA3_NEUCR	Q96ua3 nematospora
65	70	10.9	117	2	Q6RUI8_HUMAN	Q6ru18 homo sapien
66	70	10.9	131	2	Q4S580_TETNG	Q4s580 tetraodon n
67	70	10.9	331	2	Q6DG16_BRARE	Q6dgl6 brachydanio
68	70	10.9	543	1	7UP1_DROME	P16375 drosophila
69	70	10.9	743	2	Q97120_SCHMA	Q97120 schistosoma
70	70	10.9	746	1	7UP2_DROME	P16376 drosophila
71	70	10.9	1095	2	Q21852_CAEBL	Q21852 caenorhabdi
72	70	10.9	1851	2	Q9TVQ2_CAEBL	Q9tvq2 caenorhabdi
73	69.5	10.8	221	2	Q85299_9POKV	Q85299 orf virus
74	69.5	10.8	310	2	Q62436_ORYSA	Q62436 oryza sativ
75	69.5	10.8	324	2	Q4S635_TETNG	Q4s635 tetraodon n
76	69.5	10.8	575	1	TREM_HUMAN	P07204 homo sapien
77	69.5	10.8	575	1	TREM_SAISC	P07107 saimiri sci
78	69.5	10.8	575	2	Q8IV29_HUMAN	Q8iv29 homo sapien
79	69.5	10.8	595	2	Q88ZE7_LACPL	Q88ze7 lactobacill
80	69.5	10.8	617	2	Q5BBX3_EMENI	Q5bbx3 aspergillus
81	69.5	10.8	653	2	Q8JTG6_9PAPI	Q8jtg6 human papil
82	69.5	10.8	706	2	Q2T9G7_HUMAN	Q2t9g7 homo sapien
83	69.5	10.8	1116	2	Q381X0_9TRYP	Q381x0 trypanosoma
84	69.5	10.8	1325	1	UBF42_HUMAN	Q9hfj4 homo sapien
85	69.5	10.8	1387	2	Q4RKM6_TETNG	Q4rkm6 tetraodon n
86	69	10.7	111	2	Q9FWV9_ORYSA	Q9fwv9 oryza sativ
87	69	10.7	125	2	Q5BJC5_BRARE	Q5bjc5 brachydanio
88	69	10.7	174	1	Y4473_PSEAR	Q9hvu8 pseudomonas
89	69	10.7	191	2	Q872V1_NEUCR	Q872v1 nematospora
90	69	10.7	210	2	Q5K943_CRYNE	Q5k943 cryptococcu
91	69	10.7	314	1	SIX3_CHICK	Q42406 gallus gall
92	69	10.7	378	1	GLR1_ASPAC	Q74213 aspergillus
93	69	10.7	400	2	Q8LEL2_ARATH	Q8lel2 arabidopsis
94	69	10.7	413	2	Q9C8W2_ARATH	Q9c8w2 arabidopsis
95	69	10.7	454	2	Q90ZE8_ONCMA	Q90ze8 oncorhynch
96	69	10.7	527	2	Q9SKW4_ARATH	Q9skw4 arabidopsis
97	69	10.7	599	2	Q5NI25_FRATT	Q5ni25 francisella
98	69	10.7	1077	2	Q8N279_HUMAN	Q8n279 homo sapien
99	69	10.7	1081	2	Q9BE73_MACFA	Q9be73 macaca fasc
100	68.5	10.6	154	2	Q6VWH1_ANOGA	Q6vwh1 anopheles g
101	68.5	10.6	198	2	Q5JKU3_ORYSA	Q5jku3 oryza sativ
102	68.5	10.6	336	2	Q3HYJ9_STRPU	Q3hyj9 strongyloce
103	68.5	10.6	356	2	Q581I4_HORSE	Q581i4 equus cabal
104	68.5	10.6	381	2	Q26641_STRPU	Q26641 strongyloce

105	68.5	10.6	381	2	QSR8V3_PONPY	Q5r8v3 pongo pygma	178	66.5	10.3	1772	2	Q4Q8V1_LEIMA	Q4Q8V1 leishmania
106	68.5	10.6	405	2	Q7ZXI7_XENLA	Q7zx17 xenopus lae	179	66.5	10.3	2571	1	STAB1_MOUSE	Q8r4y4 mus musculus
107	68.5	10.6	405	2	Q9PS79_9PIPI	Q9ps79 xenopus xc	180	66.5	10.3	3301	1	CELK3_MOUSE	Q91z10 mus musculus
108	68.5	10.6	422	1	VDR_MOUSE	P48281 mus musculus	181	66	10.2	181	2	Q6IKZ4_DROME	Q61kz4 drosophila
109	68.5	10.6	422	1	VDR_XENLA	Q13124 xenopus lae	182	66	10.2	255	2	Q84B45_9BACT	Q84b45 uncultured
110	68.5	10.6	422	2	Q3UJ07_MOUSE	Q3u0j7 mus musculus	183	66	10.2	256	2	Q7OHL6_ANOGA	Q7ohl6 anopheles g
111	68.5	10.6	422	2	Q4FJVB_MOUSE	Q4fjv8 mus musculus	184	66	10.2	301	2	Q82XU4_NITEU	Q82xu4 nitrosomona
112	68.5	10.6	422	2	Q922X0_MOUSE	Q922x0 m vitamin d	185	66	10.2	339	2	Q9ZBX7_STRCO	Q9zbx7 streptomyce
113	68.5	10.6	423	1	VDR_RAT	P13053 rattus norv	186	66	10.2	375	2	Q5Z6Q1_ORYSA	Q5z6q1 oryza sativ
114	68.5	10.6	424	1	VDR_BOVIN	Q28037 bos taurus	187	66	10.2	432	2	Q5BC72_EMENI	Q5bc72 aspergillus
115	68.5	10.6	427	1	VDR_HUMAN	P11473 homo sapien	188	66	10.2	452	2	Q8UMM5_ONCMA	Q8umw5 oncorhynch
116	68.5	10.6	427	1	VDR_SAGOE	Q95mh5 saguinus oe	189	66	10.2	454	2	Q98SW7_ONCMY	Q98sw7 oncorhynch
117	68.5	10.6	471	2	Q5U626_HUMAN	Q5u626 homo sapien	190	66	10.2	551	2	Q5VP90_ORYSA	Q5vp90 oryza sativ
118	68.5	10.6	643	1	VEI_HPV40	P36727 human papil	191	66	10.2	558	2	Q3ZSR8_BRARE	Q3zsk8 brachydanio
119	68.5	10.6	1006	2	P73012_SNY3	P73012 synechocyst	192	66	10.2	577	2	Q7T0V3_XENLA	Q7t0v3 xenopus lae
120	68.5	10.6	1168	2	Q60XC0_CAEBR	Q60xc0 caenorhabdi	193	66	10.2	736	2	Q3TYB3_MOUSE	Q3tyb3 mus musculus
121	68.5	10.6	1186	2	Q553F8_DICDI	Q553f8 dictyosteli	194	66	10.2	799	2	Q95P95_CRAGI	Q95p95 crassostrea
122	68	10.6	189	2	Q93IU7_922Z	Q93iu7 uncultured	195	66	10.2	1034	2	Q4P583_USTMA	Q4p583 ustilago ma
123	68	10.6	209	2	Q683L7_HYDMA	Q683l7 hydra magni	196	66	10.2	116	2	Q7SP44_ALV	Q7sp44 avian leuko
124	68	10.6	283	2	Q43508_LYCES	Q43508 lycopersico	197	66	10.2	182	2	Q4D179_TRYCR	Q4d179 trypanosoma
125	68	10.6	291	2	Q9IAK3_XENLA	Q9iak3 xenopus lae	198	66	10.2	1539	1	JAD1D_HUMAN	Q47gp0 dechloromon
126	68	10.6	482	2	Q49BF8_SCHMD	Q49bf8 schmidtea m	199	66	10.2	3135	2	Q813B5_PLAF7	Q813b5 plasmodium
127	68	10.6	539	2	Q9XHV3_ORYSA	Q9xhv3 oryza sativ	200	65.5	10.2	116	2	Q9D2T8_MOUSE	Q9d2t8 mus musculus
128	68	10.6	559	2	Q475V9_AZOVI	Q475v9 azotobacter	201	65.5	10.2	156	2	Q7SP44_ALV	Q7sp44 avian leuko
129	68	10.6	518	2	Q60K76_CAEBR	Q60k76 caenorhabdi	202	65.5	10.2	182	2	Q4D179_TRYCR	Q4d179 trypanosoma
130	68	10.6	773	2	Q6CILL_ERWCT	Q6cyl1 erwinia car	203	65.5	10.2	279	2	Q47GP0_DECAR	Q47gp0 dechloromon
131	68	10.6	914	2	Q400V8_KINRA	Q40uv8 kinococcus	204	65.5	10.2	326	2	Q8BN88_MOUSE	Q8bn88 mus musculus
132	68	10.6	1343	2	Q65W9X_ORYSA	Q65w9x oryza sativ	205	65.5	10.2	353	2	Q2PCF0_CUPSA	Q2pcf0 cupienius
133	67.5	10.5	158	2	Q52VK1_CIOIN	Q52vk1 ciona intes	206	65.5	10.2	397	2	Q91720_XENLA	Q91720 xenopus lae
134	67.5	10.5	199	2	Q6TJG3_DROME	Q6tjg3 drosophila	207	65.5	10.2	413	2	Q9KTP1_VIBCH	Q9ktp1 vibrio chol
135	67.5	10.5	211	2	Q4472S_SOLUS	Q4472s solibacter	208	65.5	10.2	425	2	Q91B74_PAROL	Q91b74 paralichthy
136	67.5	10.5	262	2	Q60U59_CAEBR	Q60u59 caenorhabdi	209	65.5	10.2	638	2	Q3MZ24_9DELT	Q3mz24 syntrophoba
137	67.5	10.5	374	2	Q5DVI8_CYPCA	Q5dvi8 cyprinus ca	210	65.5	10.2	646	1	VEI_HPV07	Q05133 human papil
138	67.5	10.5	433	2	Q671M5_9PHYC	Q671m5 chlorella v	211	65.5	10.2	679	2	Q60UD9_CAEBR	Q60ud9 caenorhabdi
139	67.5	10.5	443	2	Q86GV5_BRAFL	Q86gv5 brachioosto	212	65.5	10.2	706	1	FZD6_HUMAN	Q60353 homo sapien
140	67.5	10.5	453	2	Q9PTN2_BRARE	Q9ptn2 brachydanio	213	65.5	10.2	706	2	Q6NOA5_HUMAN	Q6noa5 homo sapien
141	67.5	10.5	454	2	Q52V4S_CIOIN	Q52v4s ciona intes	214	65.5	10.2	707	2	Q8MXB9_HUMAN	Q8mx89 homo sapien
142	67.5	10.5	473	2	Q75CK9_ASHGO	Q75ck9 ashbya goss	215	65.5	10.2	711	2	Q5RCM4_PONPY	Q5rcn4 pongo pygma
143	67.5	10.5	567	2	Q7ZXRO_XENLA	Q7zxr0 xenopus lae	216	65.5	10.2	712	1	Q338K3_ORYSA	Q338k3 oryza sativ
144	67.5	10.5	572	2	Q4FYC7_LEIMA	Q4fyc7 leishmania	217	65.5	10.2	712	1	FZD6_CANPA	Q8wmu5 canis famli
145	67.5	10.5	1069	2	Q9BPS2_BOMMO	Q9bps2 bombyx mori	218	65.5	10.2	768	2	Q629D7_CAEBR	Q629d7 caenorhabdi
146	67	10.4	331	2	Q4KRX6_CRAVI	Q4kxr6 crassostrea	219	65.5	10.2	1218	2	Q5H8C5_COPCI	Q5h8c5 coprinus ci
147	67	10.4	376	1	CR2_AEATH	Q91xw3 arabidopsis	220	65.5	10.2	1428	2	Q6L634_COPCI	Q6l634 coprinus ci
148	67	10.4	452	2	Q3UMM8_MOUSE	Q3umm8 mus musculus	221	65.5	10.2	1497	2	Q86BF5_DROME	Q86bf5 drosophila
149	67	10.4	454	2	Q8QGE2_SALSA	Q8qge2 salmo salar	222	65.5	10.2	2087	2	Q86BF6_DROME	Q86bf6 drosophila
150	67	10.4	475	1	HUTM_BACSU	P42087 bacillus su	223	65.5	10.2	2111	1	GLT1_SCHPO	Q9c102 schizosacch
151	67	10.4	529	1	ZN490_HUMAN	Q9ulm2 homo sapien	224	65	10.1	142	2	Q43F42_9CHLB	Q43f42 chlorobium
152	67	10.4	537	2	Q55KG5_CRYNE	Q55kg5 cryptococcu	225	65	10.1	150	2	Q2XSW8_SESIN	Q2xsw8 sesamum ind
153	67	10.4	743	2	Q83111_ADEMI	Q83111 murine aden	226	65	10.1	152	2	Q9H807_HUMAN	Q9h8q7 homo sapien
154	67	10.4	1062	1	INVS_MOUSE	Q83111 mus musculus	227	65	10.1	155	2	Q9JKG2_MUSCR	Q9jkg2 mus caroli
155	66.5	10.3	103	2	Q9YCZ2_AERPE	Q9ycz2 aeropyrum p	228	65	10.1	251	2	Q5Z6R3_ORYSA	Q5z6r3 oryza sativ
156	66.5	10.3	155	2	Q4WIY8_ASPFU	Q4wiy8 aspergillus	229	65	10.1	345	2	P79353_HORSE	P79353 equus cabal
157	66.5	10.3	297	2	Q5N8V8_ORYSA	Q5n8v8 oryza sativ	230	65	10.1	363	1	PGLR1_COLLN	PGLR1 collen
158	66.5	10.3	304	2	Q5NKR5_AZOSE	Q5nkr5 azocarcus sp	231	65	10.1	441	1	COAT_SOCMV	COAT socmv
159	66.5	10.3	368	2	Q2XIAL_PSEPU	Q2xial pseudomonas	232	65	10.1	450	2	Q8R250_MOUSE	Q8r2s0 mus musculus
160	66.5	10.3	398	2	Q74LP3_LACJO	Q74lp3 lactobacilli	233	65	10.1	563	2	Q2QTR1_ORYSA	Q2qtr1 oryza sativ
161	66.5	10.3	407	2	Q54TF7_DICDI	Q54tf7 dictyosteli	234	65	10.1	564	2	Q3UJY9_MOUSE	Q3ujy9 mus musculus
162	66.5	10.3	419	2	Q62681_RAT	Q62681 rattus norv	235	65	10.1	574	2	Q3UKZ9_MOUSE	Q3ukz9 m blatiocys
163	66.5	10.3	420	2	Q32NY6_MOUSE	Q32ny6 mus musculus	236	65	10.1	594	2	Q5R8L9_PONPY	Q5r8l9 pongo pygma
164	66.5	10.3	422	1	COT1_MOUSE	Q60632 mus musculus	237	65	10.1	623	1	ASH2L_MOUSE	Q91x20 mus musculus
165	66.5	10.3	422	2	COT1_MOUSE	Q60632 mus musculus	238	65	10.1	623	2	Q3UIF9_MOUSE	Q3uif9 mus musculus
166	66.5	10.3	423	1	COT1_HUMAN	Q91430 brachydanio	239	65	10.1	628	1	ASH2L_HUMAN	Q9u1f3 homo sapien
167	66.5	10.3	424	1	COT1_BOVIN	Q9trt8 bos taurus	240	65	10.1	678	2	Q9VLG5_DROME	Q9vlg5 drosophila
168	66.5	10.3	444	2	Q2TCL1_CHICK	Q2tcl1 gallus gall	241	65	10.1	715	2	Q4DLG2_TRYCR	Q4dlg2 trypanosoma
169	66.5	10.3	552	2	Q4DZ60_TRYCR	Q4dz60 trypanosoma	242	65	10.1	878	2	Q7NXY3_CHRVO	Q7nxy3 chromobacte
170	66.5	10.3	571	2	Q2LZ77_DROPS	Q2lz77 drosophila	243	65	10.1	1064	1	JMW2A_PONPY	Q5td88 pongo pygma
171	66.5	10.3	579	2	Q6NZC6_MOUSE	Q6nzc6 mus musculus	244	65	10.1	1096	1	PHF2_MOUSE	Q9wtu0 mus musculus
172	66.5	10.3	606	2	Q3RVF4_RALME	Q3rvf4 ralstonia m	245	65	10.1	1096	2	Q4VXB9_HUMAN	Q4vxb9 homo sapien
173	66.5	10.3	731	2	Q7Z4S7_HUMAN	Q7z4s7 homo sapien	246	65	10.1	1101	1	PHF2_HUMAN	Q75151 homo sapien
174	66.5	10.3	746	2	Q4REU2_TETNG	Q4reu2 tetraodon n	247	65	10.1	30	2	Q9S871_MOMCH	Q9s871 momordica c
175	66.5	10.3	777	2	Q8BV42_MOUSE	Q8bv42 mus musculus	248	64.5	10.0	46	2	Q42535_BRARE	Q42535 brachydanio
176	66.5	10.3	1020	2	Q2CMX9_ORYSA	Q2cmx9 oryza sativ	249	64.5	10.0	81	1	LCR41_ARATH	P82756 arabidopsis
177	66.5	10.3	1043	2	Q4IKM0_GIBZE	Q4ikm0 gibberella	250	64.5	10.0				

251	64.5	10.0	121	2	Q4TFN0_TETNG	Q4tfn0 tetraodon n	324	63.5	9.9	456	2	Q4H2T9_CIOIN	Q4h2t9 ciona intes
252	64.5	10.0	140	2	Q8L694_BOMCH	Q8l694 momordica c	325	63.5	9.9	464	2	Q5VT39_HUMAN	Q5vt39 homo sapien
253	64.5	10.0	161	2	Q878D3_BOMMO	Q878d3 bombyx mori	326	63.5	9.9	464	2	Q96BR6_HUMAN	Q96br6 homo sapien
254	64.5	10.0	227	1	CPSP5_BOVIN	CPSP5 bos taurus	327	63.5	9.9	464	2	Q9H9Q6_HUMAN	Q9h9q6 homo sapien
255	64.5	10.0	227	1	CPSP5_HUMAN	Q43809 h cleavage	328	63.5	9.9	570	2	Q9DLK5_ALV	Q9dlk5 avian leuko
256	64.5	10.0	227	1	CPSP5_MOUSE	Q9cqi3 mus musculus	329	63.5	9.9	625	2	Q4F6E6_USTMA	Q4f6e6 ustilago ma
257	64.5	10.0	227	1	CPSP5_PONPY	Q5rai8 pongo pygma	330	63.5	9.9	762	2	Q4R497_MACFA	Q4r497 macaca fasc
258	64.5	10.0	227	1	CPSP5_RAT	Q4k6m5 rattus norv	331	63.5	9.9	912	2	Q4E2Q6_TRYCR	Q4e2q6 trypanosoma
259	64.5	10.0	230	2	Q5LZT2_LEICH	Q31zt2 leishmania	332	63.5	9.9	927	2	Q6Z635_ORYSA	Q6z635 oryza sativ
260	64.5	10.0	251	2	Q30J67_BRARE	Q70vz9 ciona intes	333	63.5	9.9	1040	2	Q699V1_SIVCZ	Q699v1 chimpanzee
261	64.5	10.0	277	2	Q93863_MYCCE	Q50j67 brachydanio	334	63.5	9.9	1100	2	Q3JU50_BURP1	Q3ju50 burkholderi
262	64.5	10.0	359	2	Q23772_CHITE	Q93863 mycobacteri	335	63.5	9.9	1100	2	Q63VH9_BURPS	Q63vh9 burkholderi
263	64.5	10.0	369	2	Q3BJL2_MACMU	Q23772 chironomus	336	63.5	9.9	1136	2	Q604F4_9TELE	Q604f4 sternopygus
264	64.5	10.0	386	2	Q5FNW1_GLUOX	Q38jl2 macaca mula	337	63.5	9.9	2405	2	Q5T1R5_HUMAN	Q5t1r5 homo sapien
265	64.5	10.0	389	2	Q70VZ9_CIOIN	Q70vz9 gluconobact	338	63.5	9.9	2406	2	Q5T1R4_HUMAN	Q5t1r4 homo sapien
266	64.5	10.0	397	2	Q5DTZ6_MOUSE	Q70vz9 ciona intes	339	63.5	9.9	2406	2	Q9BZS0_HUMAN	Q9bzso homo sapien
267	64.5	10.0	419	2	Q7QXL3_GIALA	Q5dtz6 mus musculus	340	63.5	9.9	2414	2	Q9HCL7_HUMAN	Q9hcl7 homo sapien
268	64.5	10.0	421	2	Q969A9_BOMMO	Q7qxl3 giardia lam	341	63	9.8	146	2	Q58L11_9CAUD	Q58l11 cyanophage
269	64.5	10.0	431	2	Q8U5W7_AGR75	Q969a9 bombyx mori	342	63	9.8	160	1	ECF_PANTR	P47780 pan troglod
270	64.5	10.0	499	2	Q4RTT7_TETNG	Q8u5w7 agrobacteri	343	63	9.8	174	2	Q95LE0_CANFA	Q95le0 canis famli
271	64.5	10.0	530	2	Q5D5L4_ALV	Q4rtt7 tetraodon n	344	63	9.8	244	2	Q8AVH6_XENLA	Q8avh6 xenopus lae
272	64.5	10.0	534	1	ZN397_HUMAN	Q5d5l4 avian leuko	345	63	9.8	244	2	Q9PMD9_XENLA	Q9pmd9 xenopus lae
273	64.5	10.0	615	2	Q7XG33_ORYSA	Q8nf99 homo sapien	346	63	9.8	245	2	Q5TYZ2_BRARE	Q5tyz2 brachydanio
274	64.5	10.0	622	1	MAK_MOUSE	Q7xg33 oryza sativ	347	63	9.8	245	2	Q7T3G8_BRARE	Q7t3g8 brachydanio
275	64.5	10.0	741	2	Q6K9F7_ORYSA	Q94117 oryza sativ	348	63	9.8	246	1	SIX6_HUMAN	Q95475 homo sapien
276	64.5	10.0	796	2	Q4TBV7_TETNG	Q6k9f7 oryza sativ	349	63	9.8	246	1	SIX6_MOUSE	Q9qz28 mus musculus
277	64.5	10.0	1081	2	Q6AHT3_PNECA	Q4tbv7 tetraodon n	350	63	9.8	246	2	Q6NT42_HUMAN	Q6nt42 homo sapien
278	64.5	10.0	1500	2	Q5UTU2_ANOGA	Q6aht3 pneumocysti	351	63	9.8	266	2	Q4SYA8_TETNG	Q4syas8 tetraodon n
279	64.5	10.0	1530	2	Q7PRV6_ANOGA	Q5ut2 anopheles g	352	63	9.8	273	2	Q5WIZ7_BACSK	Q5wiz7 bacillus cl
280	64.5	10.0	179	2	Q2KM69_STRIN	Q7prv6 anopheles g	353	63	9.8	292	2	Q4OOR2_DESAC	Q4oor2 desulfuromo
281	64	9.9	201	2	Q5HXK1_GLUOX	Q2km69 streptococc	354	63	9.8	298	2	Q5M8S8_HUMAN	Q5m8s8 homo sapien
282	64	9.9	246	1	SIX6_CHICK	Q5hsk1 gluconobact	355	63	9.8	305	2	Q6P051_HUMAN	Q6p051 homo sapien
283	64	9.9	260	2	Q2SNZ4_9GAMM	Q93307 gallus gall	356	63	9.8	332	1	SIX3_HUMAN	Q53343 homo sapien
284	64	9.9	282	2	Q61D23_CABER	Q2snz4 habella che	357	63	9.8	332	2	Q53T42_HUMAN	Q53t42 homo sapien
285	64	9.9	317	2	Q31QV7_SYNP7	Q61d23 caenorhabdi	358	63	9.8	333	1	SIX3_MOUSE	Q62333 mus musculus
286	64	9.9	317	2	Q5N3D9_SYNP6	Q31qv7 synchococc	359	63	9.8	333	2	Q4QQQ3_MOUSE	Q4qqq3 mus musculus
287	64	9.9	334	2	Q68119_RHOCA	Q5n3d9 synchococc	360	63	9.8	337	2	Q9ET75_RAT	Q9et75 rattus norv
288	64	9.9	345	2	Q32R13_EPTBU	Q68119 rhodobacter	361	63	9.8	342	2	Q7Z2T4_BUFMA	Q7z2t4 bufo marinu
289	64	9.9	357	2	Q3XSB3_9PROT	Q32r13 eptatretus	362	63	9.8	346	2	Q955U6_TRATE	Q955u6 tragopan te
290	64	9.9	417	2	Q681B0_ARATH	Q3xsb3 magnetococc	363	63	9.8	347	2	Q52KB8_MOUSE	Q52kb8 mus musculus
291	64	9.9	418	2	Q67ZU1_ARATH	Q681b0 arabidopsis	364	63	9.8	348	2	Q343V0_RHOPA	Q343v0 rhodopeudo
292	64	9.9	431	2	Q6LUA2_PHOPR	Q67zu1 arabidopsis	365	63	9.8	371	1	RAD14_YEAST	P28519 saccharomyc
293	64	9.9	454	2	Q6SES0_SALSA	Q6lua2 photobacter	366	63	9.8	376	2	Q8LAC2_ARATH	Q8lac2 arabidopsis
294	64	9.9	472	2	Q5WNE1_CABER	Q6ses0 salmo salar	367	63	9.8	377	2	Q3UQ14_MOUSE	Q3uq14 mus musculus
295	64	9.9	540	2	Q8XH9G_CLOPE	Q5wne1 caenorhabdi	368	63	9.8	395	2	Q98DM3_RHTLO	Q98dm3 rhizobium l
296	64	9.9	552	2	Q5KBF3_ORYNE	Q8xh9g clostridium	369	63	9.8	413	2	Q2PQ08_GLOMR	Q2pq08 glossina mo
297	64	9.9	1290	2	Q4DIT1_TRYCR	Q5kbf3 cryptococcu	370	63	9.8	447	2	Q8NZL6_HUMAN	Q8nzl6 homo sapien
298	64	9.9	2040	2	Q4NSI1_TETNG	Q4dit1 trypanosoma	371	63	9.8	453	2	Q304A5_ARATH	Q304a5 arabidopsis
299	64	9.9	811	2	Q8S7P4_ORYSA	Q4nsi1 tetraodon n	372	63	9.8	462	2	Q49674_ARATH	Q49674 arabidopsis
300	64	9.9	856	2	Q3POM6_NITHA	Q8s7p4 oryza sativ	373	63	9.8	464	2	Q7FAG5_ORYSA	Q7fag5 oryza sativ
301	64	9.9	915	2	Q75G97_ORYSA	Q3pom6 nitrobacter	374	63	9.8	464	2	Q91JQ3_MOUSE	Q91jq3 mus musculus
302	64	9.9	952	2	Q5KBF3_ORYNE	Q75g97 oryza sativ	375	63	9.8	473	2	Q60S28_CABBR	Q60s28 caenorhabdi
303	64	9.9	1290	2	Q4DIT1_TRYCR	Q5kbf3 cryptococcu	376	63	9.8	475	2	Q4SCV3_TETNG	Q4scv3 tetraodon n
304	63.5	9.9	215	2	Q8N930_HUMAN	Q4dit1 trypanosoma	377	63	9.8	488	2	Q8VS81_PARVE	Q8vs81 paracoccus
305	63.5	9.9	218	2	Q69CH9_9VIRU	Q8n930 homo sapien	378	63	9.8	490	2	Q9XEV7_ORYSA	Q9xev7 oryza sativ
306	63.5	9.9	218	2	Q69CH9_9VIRU	Q69ch9 infectious	379	63	9.8	493	2	Q9BMU6_AEDAE	Q9bmu6 aedes aegyp
307	63.5	9.9	223	2	Q3EBD5_ARATH	Q69ch9 infectious	380	63	9.8	509	2	Q7OCB4_ANOGA	Q7ocb4 anopheles g
308	63.5	9.9	233	2	Q42672_CARPA	Q3ebd5 arabidopsis	381	63	9.8	536	2	Q5SBA8_DICDI	Q5sba8 dictyosteli
309	63.5	9.9	262	1	UTP11_CABEL	Q42672 carica papa	382	63	9.8	556	2	Q36EAB_9GAMM	Q36eab shewanella
310	63.5	9.9	303	2	Q2UBY6_ASPOR	Q09462 caenorhabdi	383	63	9.8	603	1	FBX46_MOUSE	Q8b980 mus musculus
311	63.5	9.9	315	2	Q8UW70_XENLA	Q2uby6 aspergillus	384	63	9.8	603	2	Q4KLY2_RAT	Q4kly2 rattus norv
312	63.5	9.9	326	1	ZN673_HUMAN	Q8uw70 xenopus lae	385	63	9.8	646	1	FBX46_HUMAN	Q6p167 homo sapien
313	63.5	9.9	334	2	Q6NTM2_XENLA	Q4380 homo sapien	386	63	9.8	689	2	Q583T7_9TRYP	Q583t7 trypanosoma
314	63.5	9.9	335	2	Q4V7Y2_XENOPUS	Q6ncm2 xenopus lae	387	63	9.8	721	2	Q4SQB3_TETNG	Q4sqb3 tetraodon n
315	63.5	9.9	342	2	Q61580_DROSIL	Q4v7y2 xenopus lae	388	63	9.8	954	2	Q7RZU4_NEUCR	Q7rzu4 neurtospor
316	63.5	9.9	343	2	Q5GVW7_XANOR	Q61580 drosophila	389	63	9.8	972	1	PARG_RAT	Q9qym2 rattus norv
317	63.5	9.9	350	2	Q3KPP9_XENLA	Q5gvw7 xanthomonas	390	63	9.8	1068	2	Q69ZG6_MOUSE	Q69zg6 mus musculus
318	63.5	9.9	361	2	Q8FFD6_ECUL6	Q3kpp9 xenopus lae	391	63	9.8	1120	2	Q7XNT5_ORYSA	Q7xnt5 oryza sativ
319	63.5	9.9	378	2	Q5VT38_HUMAN	Q8ffd6 escherichia	392	63	9.8	1175	2	Q4HER3_TETNG	Q4her3 tetraodon n
320	63.5	9.9	391	2	Q3GRG2_9GAMM	Q5vt38 homo sapien	393	63	9.8	1650	2	Q4B809_TRYCR	Q4b809 trypanosoma
321	63.5	9.9	397	2	Q4PSE7_ARATH	Q3grg2 psychrobact	394	63	9.8	2096	2	Q2R0G5_ORYSA	Q2r0g5 oryza sativ
322	63.5	9.9	404	2	Q6P115_BRARE	Q4pse7 arabidopsis	395	62.5	9.7	116	2	Q9C336_MOUSE	Q9c336 mus musculus
323	63.5	9.9	454	2	Q6Q247_CHICK	Q6p115 brachydanio	396	62.5	9.7	119	2	Q9DAL9_MOUSE	Q9dal9 mus musculus
						Q6q247 gallus gall							

397	62.5	9.7	148	2	Q6H5T8_ORYSA	Q6H5T8_oryza sativ	470	62	9.6	297	2	Q5B1S4_EMENI	Q5B1S4_aspergillus
398	62.5	9.7	156	1	RNAS7_HUMAN	Q9H1E1_homo sapien	471	62	9.6	310	2	Q3H4L3_9ACTO	Q3H4L3_nocardioidei
399	62.5	9.7	156	2	Q546N3_HUMAN	Q89EN3_homo sapien	472	62	9.6	316	2	Q39D11_BURS3	Q39D11_burkholderi
400	62.5	9.7	191	2	Q89HK5_BRAJA	Q89HK5_bradyrhizob	473	62	9.6	323	2	Q5F3E3_CHICK	Q5F3E3_gallus gall
401	62.5	9.7	192	2	Q8VJR4_MYCTU	Q5BVR4_mycobacteri	474	62	9.6	332	2	Q8HHF1_9TYRA	Q8HHF1_pachyrhampu
402	62.5	9.7	202	2	Q5BYW7_SCHJA	Q5BYW7_schistosoma	475	62	9.6	332	2	Q8HHF2_9TYRA	Q8HHF2_tityra caya
403	62.5	9.7	218	2	Q621H9_BURMA	Q621H9_burkholderi	476	62	9.6	346	2	Q392Y2_BURS3	Q392Y2_burkholderi
404	62.5	9.7	221	2	Q4SSA9_TETNG	Q4SSA9_tetradodon n	477	62	9.6	346	2	Q958E3_TINMA	Q958E3_tinamus maj
405	62.5	9.7	223	2	Q5D9Q3_SCHJA	Q5D9Q3_schistosoma	478	62	9.6	371	1	RN02_YEAST	P12687_saccharomyC
406	62.5	9.7	227	1	CPSP5_XENLA	Q6JDE4_xenopus lae	479	62	9.6	390	2	Q6LGC9_POPR	Q6LGC9_photobacter
407	62.5	9.7	228	1	CPSP5_BRARE	Q7CTC6_brachydanio	480	62	9.6	464	2	Q5WN10_CABBR	Q5WN10_caenorhabdi
408	62.5	9.7	229	2	Q4SIH0_TETNG	Q4SIH0_tetradodon n	481	62	9.6	488	2	Q7R740_PLAYO	Q7R740_plasmodium
409	62.5	9.7	259	2	Q8KW83_9RHOB	Q8KW83_ruesgeria sp	482	62	9.6	519	2	Q4R6H6_NACFA	Q4R6H6_macaca fasc
410	62.5	9.7	292	2	Q82PK3_STRAW	Q82FK1_striptomyce	483	62	9.6	559	2	Q3UP18_MOUSE	Q3UP18_mus musculu
411	62.5	9.7	298	2	Q84NF7_9CONI	Q84NF7_calitropi	484	62	9.6	559	2	Q31WM0_MOUSE	Q31WM0_mus musculu
412	62.5	9.7	326	2	Q4QRA0_RAT	Q4QRA0 rattus norv	485	62	9.6	564	2	Q3P2U9_9GAMM	Q3P2U9_shewanella
413	62.5	9.7	326	2	Q8C882_MOUSE	Q8C882_mus musculu	486	62	9.6	567	2	Q2UUMA_ASPOR	Q2UUMA_aspergillus
414	62.5	9.7	326	2	Q9JJK5_MOUSE	Q9JDK1_m adult mal	487	62	9.6	577	1	NR4A2_XENLA	Q4913_xenopus lae
415	62.5	9.7	326	2	Q9JJK5_MOUSE	Q9JJK5_mus musculu	488	62	9.6	577	1	Q61NV4_XENLA	Q61NV4_xenopus lae
416	62.5	9.7	326	2	Q922K5_RAT	Q922K5 rattus norv	489	62	9.6	587	2	Q5KNM4_CRYNE	Q5KNM4_cryptococu
417	62.5	9.7	328	2	Q59V90_CANAL	Q59V90 candida alb	490	62	9.6	587	2	Q322X6_MOUSE	Q322X6_mus musculu
418	62.5	9.7	339	2	Q7YRQ3_BOVIN	Q7YRQ3 bos taurus	491	62	9.6	655	2	Q2R0U5_ORYSA	Q2R0U5_oryza sativ
419	62.5	9.7	340	2	Q3WEG6_9ACTO	Q3WEG6 frankia sp.	492	62	9.6	728	2	Q06054_MOUSE	Q06054_mus musculu
420	62.5	9.7	355	2	Q9CVN0_MOUSE	Q9CVN0_mus musculu	493	62	9.6	782	2	Q4CQL3_TRYCR	Q4CQL3_trypanosoma
421	62.5	9.7	366	2	Q8WT79_9NEOP	Q8WT79 chimarra ro	494	62	9.6	803	2	Q4CNG7_TRYCR	Q4CNG7_trypanosoma
422	62.5	9.7	367	2	Q8BWF5_MOUSE	Q8BWF5_mus musculu	495	62	9.6	803	2	Q4CUS4_TRYCR	Q4CUS4_trypanosoma
423	62.5	9.7	388	2	Q6PDE6_BRARE	Q6PDE6_brachydanio	496	62	9.6	817	2	Q5DZB6_VIBF1	Q5DZB6_vibrio fusc
424	62.5	9.7	389	2	Q6PH18_BRARE	Q6PH18_brachydanio	497	62	9.6	954	2	Q6AMQ1_DROME	Q6AMQ1_drosophila
425	62.5	9.7	404	2	Q6DCH6_XENLA	Q6DCH6 xenopus lae	498	62	9.6	954	2	Q9VU43_DROME	Q9VU43_drosophila
426	62.5	9.7	410	1	COT2_CHICK	Q90733_gallus gall	499	62	9.6	1161	2	Q7EYN1_ORYSA	Q7EYN1_oryza sativ
427	62.5	9.7	414	1	COT2_BOVIN	Q9TTR7_bos taurus	500	62	9.6	1183	2	Q9VB40_DROME	Q9VB40_drosophila
428	62.5	9.7	414	1	COT2_HUMAN	P24468_homo sapien	501	62	9.6	1453	2	Q5CF69_ARATH	Q5CF69_arabidopsis
429	62.5	9.7	414	1	COT2_MOUSE	Q90918_rattus norv	502	62	9.6	1670	1	CO4A3_HUMAN	Q01955_homo sapien
430	62.5	9.7	414	1	COT2_RAT	Q90918 rattus norv	503	62	9.6	2098	2	Q3QG46_9GAMM	Q3QG46_shewanella
431	62.5	9.7	414	1	Q3UST6_MOUSE	Q3UST6_mus musculu	504	62	9.6	2135	2	Q4SZ58_TETNG	Q4SZ58_tetradodon n
432	62.5	9.7	419	2	Q6KRY3_VIBCH	Q6KRY3 vibrio chol	505	62	9.6	3026	2	Q26030_PLAFA	Q26030_plasmodium
433	62.5	9.7	420	2	Q6H817_SALSA	Q6H817 salmo salar	506	62	9.6	4796	2	Q4Q363_LEIMA	Q4Q363_leishmania
434	62.5	9.7	420	2	Q91B71_PAROL	Q91B71 paralichthy	507	61.5	9.5	107	2	Q37U65_SPHAR	Q37U65_novosphingo
435	62.5	9.7	444	2	Q46W12_RALEJ	Q46W12 raietonia e	508	61.5	9.5	115	2	Q2XSV6_SGEMI	Q2XSV6_tomato yell
436	62.5	9.7	450	2	Q8BW19_MOUSE	Q8BW19_mus musculu	509	61.5	9.5	122	2	Q3QJMS_9GAMM	Q3QJMS_shewanella
437	62.5	9.7	450	2	Q8C178_MOUSE	Q8C178_mus musculu	510	61.5	9.5	127	2	Q7XZ60_GRIJA	Q7XZ60_griffithsia
438	62.5	9.7	472	2	Q3WE50_9ACTO	Q3WE50 frankia sp.	511	61.5	9.5	138	2	Q3ENG5_BACTI	Q3ENG5_bacillus th
439	62.5	9.7	550	2	Q4D876_TRYCR	Q4D876 trypanosoma	512	61.5	9.5	167	2	Q6Q2J3_XENLA	Q6Q2J3_xenopus lae
440	62.5	9.7	550	2	Q8CDL5_MOUSE	Q8CDL5_mus musculu	513	61.5	9.5	169	2	Q89G37_BRAJA	Q89G37_bradyrhizob
441	62.5	9.7	563	2	Q64SA4_BACFR	Q64SA4 bacteroides	514	61.5	9.5	201	2	Q4P089_USTMA	Q4P089_ustilago ma
442	62.5	9.7	565	2	Q3KQV3_HUMAN	Q3KQV3_homo sapien	515	61.5	9.5	209	2	Q6RG09_9VIRU	Q6RG09_hypoosoter d
443	62.5	9.7	720	2	Q9N003_MACFA	Q9N003 macaca fasc	516	61.5	9.5	219	2	Q5VYT7_HUMAN	Q5VYT7_homo sapien
444	62.5	9.7	752	2	Q61V72_HUMAN	Q61V72_homo sapien	517	61.5	9.5	239	2	Q53K64_ORYSA	Q53K64_oryza sativ
445	62.5	9.7	766	2	Q6P0Z1_BRARE	Q6P0Z1 brachydanio	518	61.5	9.5	243	2	Q5L4A0_9FLAV	Q5L4A0_cy1014 viru
446	62.5	9.7	766	2	Q6TELS_BRARE	Q6TELS brachydanio	519	61.5	9.5	253	2	Q5U3Z5_RAT	Q5U3Z5_rattus norv
447	62.5	9.7	840	2	Q19777_CAEEL	Q19777 caenorhabdi	520	61.5	9.5	300	2	Q7MBY5_BORPA	Q7MBY5_bordetella
448	62.5	9.7	982	2	Q4D985_TRYCR	Q4D985 trypanosoma	521	61.5	9.5	300	2	Q7WPI1_BORBR	Q7WPI1_brachydanio
449	62.5	9.7	1026	2	Q6PFI5_BRARE	Q6PFI5 brachydanio	522	61.5	9.5	300	2	Q7T3B4_BRARE	Q7T3B4_babesia bov
450	62.5	9.7	1060	2	Q3SPX7_9BRAD	Q3SPX7 bradyrhizob	523	61.5	9.5	306	2	Q2TV48_BABBO	Q2TV48_babesia bov
451	62.5	9.7	1232	2	Q41ZHO_AZOVI	Q41ZHO azotobacter	524	61.5	9.5	326	2	Q803V5_BRARE	Q803V5_brachydanio
452	62.5	9.7	1612	2	Q416D6_GIBZE	Q416D6 gibberella	525	61.5	9.5	347	2	Q58BR6_BRARE	Q58BR6_brachydanio
453	62.5	9.7	1614	2	Q3ZTP0_MICMU	Q3ZTP0 microcebus	526	61.5	9.5	352	2	Q58DN5_BOVIN	Q58DN5_bos taurus
454	62.5	9.7	2038	2	Q4E222_TRYCR	Q4E222 trypanosoma	527	61.5	9.5	361	1	Q8UYW1_SGEMI	Q8UYW1_squash leaf
455	62.5	9.7	2282	2	Q6SNP9_MOUSE	Q6SNP9_mus musculu	528	61.5	9.5	369	1	IL2RG_HUMAN	P31751_homo sapien
456	62	9.6	48	2	Q53RW8_HUMAN	Q53RW8_homo sapien	529	61.5	9.5	382	2	Q4I0P5_GIBZE	Q4I0P5_gibberella
457	62	9.6	88	2	Q9TFJ0_ARATH	Q9TFJ0 arabidopsis	530	61.5	9.5	398	2	Q5MGH5_LONON	Q5MGH5_lonomia obl
458	62	9.6	93	2	Q61IG3_DROME	Q61IG3 drosophila	531	61.5	9.5	398	2	Q8A3G3_BACTN	Q8A3G3_bacteroides
459	62	9.6	135	2	Q6FFY4_ACTAD	Q6FFY4 acinetobact	532	61.5	9.5	401	1	NR2F5_BRARE	Q05QJ0_entamoeba h
460	62	9.6	147	2	Q5UI18_HORVD	Q5UI18 hordeum vul	533	61.5	9.5	403	1	NR2F5_BRARE	Q05QJ0_entamoeba h
461	62	9.6	157	2	Q61TX2_CAEBR	Q61TX2 caenorhabdi	534	61.5	9.5	431	2	Q49155_NAIZE	Q49155_zea mays (m
462	62	9.6	192	2	Q7PL04_ANOGA	Q7PL04 anopheles g	535	61.5	9.5	432	2	Q49154_NAIZE	Q49154_zea mays (m
463	62	9.6	210	2	Q61I77_DROME	Q61I77 drosophila	536	61.5	9.5	441	2	Q5MQC6_9CORA	Q5MQC6_human coron
464	62	9.6	211	2	Q6V277_9BACT	Q6V277 symbiont ba	537	61.5	9.5	464	2	Q8GR22_ORYSA	Q8GR22_oryza sativ
465	62	9.6	217	1	GP111_CANGA	Q6FED1 candida gla	538	61.5	9.5	537	2	Q4J5M5_AZOVI	Q4J5M5_azotobacter
466	62	9.6	226	2	Q5BXH7_SCHJA	Q5BXH7 schistosoma	539	61.5	9.5	545	1	ZNF77_HUMAN	Q415M5_zygospore
467	62	9.6	235	2	Q22621_CAEEL	Q22621 caenorhabdi	540	61.5	9.5	581	2	Q5V7Y6_HALMA	Q5V7Y6_haloarcula
468	62	9.6	284	2	Q2ULB0_ASPOR	Q2ULB0 aspergillus	541	61.5	9.5	605	2	Q4HW21_GIBZE	Q4HW21_gibberella
469	62	9.6	293	2	Q73709_BRARE	Q73709 brachydanio	542	61.5	9.5	623	1	VEIN_DROME	Q94918_drosophila

543	61.5	9.5	623	2	Q59E20_DROME	Q59e20 drosophila	616	61	9.5	392	2	Q4PB11_USTMA	Q4pb11 ustilago ma
544	61.5	9.5	690	2	Q3WSA6_9RHIZ	Q3wsa6 mesorhizobi	617	61	9.5	398	2	Q7AB12_ECO57	Q7ab12 escherichia
545	61.5	9.5	696	2	Q3UVG7_MOUSE	Q3uv7 mus musculus	618	61	9.5	402	2	Q5QZP3_IDILO	Q5qzp3 idiomarina
546	61.5	9.5	774	2	Q3PEE8_PARDE	Q3pee8 paracoccus	619	61	9.5	416	2	Q4IQV6_GIBZE	Q4iqv6 gibberella
547	61.5	9.5	789	2	Q3NNC3_ZYMO	Q3nnc3 zymononas m	620	61	9.5	429	2	Q14401_SCLSC	Q14401 sclerotinia
548	61.5	9.5	808	2	Q3JHW2_BURP1	Q3jhw2 burkholderia	621	61	9.5	432	2	Q4S157_MAZE	Q4s157 zea mays m
549	61.5	9.5	809	2	Q8C8A8_MOUSE	Q8c8a8 mus musculus	622	61	9.5	457	2	Q2JHAB_9CYAN	Q2jhab cyanobacter
550	61.5	9.5	864	1	ADA15_MOUSE	Q88839 mus musculus	623	61	9.5	458	1	ZN275_HUMAN	Q9fr44 arabidopsis
551	61.5	9.5	864	2	Q3UE21_MOUSE	Q3ue21 m bone marr	624	61	9.5	491	1	PEAM1_ARATH	Q73np5 treponema d
552	61.5	9.5	864	2	Q3UE21_MOUSE	Q3ue21 mus musculus	625	61	9.5	495	2	Q73NP5_TREDE	Q4QX2 leishmania
553	61.5	9.5	866	2	Q6F352_ORYSA	Q6f352 oryza sativ	626	61	9.5	520	2	Q4QX2_LEIMA	Q4qxc6 caenorhabdi
554	61.5	9.5	874	2	Q6DC11_XENLA	Q6dc11 xenopus lae	627	61	9.5	536	2	Q9XTC6_CAEEL	Q3nms shewanella
555	61.5	9.5	900	2	Q4IXJ0_AZOBACT	Q4ixj0 azotobacter	628	61	9.5	542	2	Q3NNU8_SHEFR	Q8ekj5 shewanella
556	61.5	9.5	983	1	NBRI_RAT	Q501r9 rattus norv	629	61	9.5	556	1	HUTU_SHEON	Q361w0 shewanella
557	61.5	9.5	1118	2	Q7Y006_ORYSA	Q7y006 oryza sativ	630	61	9.5	556	2	Q4QJVS_TETNG	Q4rjv5 tetraodon n
558	61.5	9.5	2035	2	Q4DZFL_TRYCR	Q4dzfl trypanosoma	631	61	9.5	577	2	Q2ZAI8_9GAMM	Q2za18 shewanella
559	61	9.5	95	2	Q6YZ56_ORYSA	Q6yz56 oryza sativ	632	61	9.5	584	2	Q2ZAI8_9GAMM	Q2za18 shewanella
560	61	9.5	119	2	Q3Q442_9GAMM	Q3q442 shewanella	633	61	9.5	593	2	Q8INE2_DROME	Q8ine2 drosophila
561	61	9.5	134	2	Q4WYK2_ASFPF	Q4wyk2 aspergillus	634	61	9.5	621	2	Q5JQV7_ORYSA	Q5jqv7 oryza sativ
562	61	9.5	137	2	Q6YT91_ORYSA	Q6yt91 oryza sativ	635	61	9.5	629	2	Q8IN39_DROME	Q8in39 drosophila
563	61	9.5	153	2	Q9LI15_ARATH	Q9li15 arabidopsis	636	61	9.5	684	2	Q8S2Z8_DROME	Q8s2z8 drosophila
564	61	9.5	158	2	Q3B7G7_BRARE	Q3b7g7 brachydanio	637	61	9.5	746	2	Q8TGI7_TALEM	Q8tgi7 talaromyces
565	61	9.5	171	2	Q8ERN0_SHEON	Q8ern0 shewanella	638	61	9.5	776	2	Q33AE0_ORYSA	Q33ae0 oryza sativ
566	61	9.5	172	2	Q4IYB4_AZOV1	Q4iyb4 azotobacter	639	61	9.5	784	2	Q7SFE3_NEUCR	Q7sfe3 neutrospora
567	61	9.5	181	1	SPL5_ARATH	Q9s758 arabidopsis	640	61	9.5	795	1	DEGY_CAEEL	Q01635 caenorhabdi
568	61	9.5	183	1	GSPH_ABRHY	P31735 aeromonas h	641	61	9.5	820	2	Q4QDA1_LEIMA	Q4qda1 leishmania
569	61	9.5	184	2	Q9VK16_DROME	Q9vk16 drosophila	642	61	9.5	846	2	Q95US1_LOCM1	Q95us1 locusta mig
570	61	9.5	222	2	Q8H4Q5_ORYSA	Q8h4q5 oryza sativ	643	61	9.5	893	2	Q8GCM9_CHRVO	Q8gcm9 chromobacte
571	61	9.5	227	2	Q6YWZ7_ORYSA	Q6ywz7 oryza sativ	644	61	9.5	901	2	Q6NZS3_BRARE	Q6nzs3 brachydanio
572	61	9.5	245	2	Q54125_DICDI	Q54125 dictyosteli	645	61	9.5	901	2	Q7ZVY7_BRARE	Q7zv7 brachydanio
573	61	9.5	255	2	Q9N6L7_DROSI	Q9n6l7 drosophila	646	61	9.5	912	2	Q4SL99_TETNG	Q4sl99 tetraodon n
574	61	9.5	255	2	Q9N6N5_DROSI	Q9n6n5 drosophila	647	61	9.5	961	1	MEI9_DROME	Q24087 drosophila
575	61	9.5	255	2	Q9NGS5_DROSI	Q9ngs5 drosophila	648	61	9.5	1000	2	Q96V19_PNECA	Q96v19 pneumocysti
576	61	9.5	257	2	Q2LL45_BORAV	Q2ll45 bordetella	649	61	9.5	1014	2	Q74673_PNEJI	Q74673 pneumocysti
577	61	9.5	268	2	Q59HE1_HUMAN	Q59hei homo sapien	650	61	9.5	1028	2	Q7Y1N2_ORYSA	Q7yin2 oryza sativ
578	61	9.5	286	2	Q5JNG1_ORYSA	Q5jng1 oryza sativ	651	61	9.5	1064	1	JMU24_HUMAN	Q75164 homo sapien
579	61	9.5	301	2	Q7W1H8_BORPA	Q7w1h8 bordetella	652	61	9.5	1068	2	Q5JTG3_DROME	Q5jtg3 drosophila
580	61	9.5	302	2	Q7WP88_BORBR	Q7wp88 bordetella	653	61	9.5	1092	2	Q4WEI8_ASFPF	Q4wei8 aspergillus
581	61	9.5	308	2	Q5C3G7_SCHJA	Q5c3g7 schistosoma	654	61	9.5	1095	2	Q7RSJ8_PLAVO	Q7rsj8 plasmodium
582	61	9.5	309	2	P79352_HORSE	P79352 equus caball	655	61	9.5	1246	2	Q4RKK1_TETNG	Q4rkk1 tetraodon n
583	61	9.5	325	2	Q98NW3_RHILO	Q98nw3 rhizobium l	656	61	9.5	1259	2	Q5RAJ0_PONPY	Q5ra10 pongo pygma
584	61	9.5	327	1	FKBP6_MOUSE	Q91xw8 mus musculus	657	61	9.5	1264	2	Q3U2X9_MOUSE	Q3u2x9 mus musculus
585	61	9.5	327	2	Q81C1Y_MOUSE	Q81c1y mus musculus	658	61	9.5	1340	2	Q9WQO1_DROME	Q9wqo1 drosophila
586	61	9.5	327	2	Q91VB7_MOUSE	Q91vb7 mus musculus	659	61	9.5	1375	2	Q3USI2_MOUSE	Q3usi2 mus musculus
587	61	9.5	332	2	Q6K1D2_9GALL	Q6k1d2 crax globul	660	61	9.5	1545	2	Q30DN6_CANFA	Q30dn6 canis fami
588	61	9.5	332	2	Q8SEE4_CRABL	Q8see4 crax blumen	661	61	9.5	1556	2	Q38JA7_CANFA	Q38ja7 canis fami
589	61	9.5	333	2	Q2PTB0_PSEAE	Q2ptb0 pseudomonas	662	61	9.5	1557	2	Q5JUJ3_HUMAN	Q5juj3 homo sapien
590	61	9.5	333	2	Q8GL60_9BACT	Q8gl60 uncultured	663	61	9.5	1560	1	JADIC_HUMAN	Q41229 homo sapien
591	61	9.5	340	2	Q8M809_9COLU	Q8m809 streptopeli	664	61	9.5	1560	2	Q5JUX5_HUMAN	Q5jux5 homo sapien
592	61	9.5	346	2	Q79393_RHEAM	Q79393 rhea ameri	665	61	9.5	1619	2	Q9UJ97_ANOGA	Q9uj97 anopheles g
593	61	9.5	346	2	Q3B9P1_9EMBE	Q3b9p1 myioborus m	666	61	9.5	1623	2	Q9UJ97_ANOGA	Q9uj97 anopheles g
594	61	9.5	346	2	Q4VD77_NECMO	Q4vd77 necrosytes	667	61	9.5	1799	2	Q8ROY0_MOUSE	Q8roy0 mus musculus
595	61	9.5	346	2	Q7IN06_9EMBE	Q7in06 parula supe	668	61	9.5	2068	2	Q67WF0_ORYSA	Q67wf0 oryza sativ
596	61	9.5	346	2	Q85UK3_COTCH	Q85uk3 coturnix ch	669	61	9.5	3063	2	Q81284_PLAP7	Q81284 plasmodium
597	61	9.5	346	2	Q8M458_9EMBE	Q8m458 microligea	670	60.5	9.4	98	2	Q3GNL0_9GAMM	Q3gnl0 psychobact
598	61	9.5	346	2	Q9GM1 SPIZA AMERI	Q9gm1 spiza ameri	671	60.5	9.4	106	1	GASA4_ARATH	Q46630 arabidopsis
599	61	9.5	346	2	Q9MAV8_PARGU	Q9mv8 parula gutt	672	60.5	9.4	118	2	Q3NU02_SHEFR	Q3nu02 shewanella
600	61	9.5	346	2	Q9TCR8_9ICTE	Q9tc8 icterus mes	673	60.5	9.4	133	2	Q4SXT9_TETNG	Q4sxt9 tetraodon n
601	61	9.5	346	2	Q9TCM7_9ICTE	Q9tc7 icterus mes	674	60.5	9.4	162	1	HSPB6_RAT	Q97541 rattus norv
602	61	9.5	346	2	Q9TCW8_RHEAM	Q9tcw8 icterus mes	675	60.5	9.4	210	2	Q40919_HHV8	Q40919 human herpe
603	61	9.5	346	2	Q9TCW3_RHEAM	Q9tcw3 rhea ameri	676	60.5	9.4	210	2	P90486_HHV8	P90486 human herpe
604	61	9.5	346	2	Q5J683_9EMBE	Q5j683 basileuteru	677	60.5	9.4	217	2	Q9HA66_HUMAN	Q9ha66 homo sapien
605	61	9.5	346	2	Q6V8L5_9PASE	Q6v8l5 prunella at	678	60.5	9.4	220	2	Q4TGF7_TETNG	Q4tgf7 tetraodon n
606	61	9.5	346	2	Q6WR71_9AVES	Q6wr71 crotophaga	679	60.5	9.4	244	2	Q6DFT8_XENLA	Q6dff8 xenopus lae
607	61	9.5	346	2	Q8M459_9EMBE	Q8m459 hemispingus	680	60.5	9.4	256	2	Q9HY17_PSEAE	Q9hy17 pseudomonas
608	61	9.5	346	2	Q8SIP8_9CORV	Q8sip8 eurocephalu	681	60.5	9.4	272	1	SIX3_ORYLA	Q73916 oryza lat
609	61	9.5	346	2	Q9MDH2_PARGU	Q9mdh2 parula gutt	682	60.5	9.4	290	2	Q3EB42_ARATH	Q3eb42 arabidopsis
610	61	9.5	348	2	Q4VD74_9FALC	Q4vd74 gyps fulvus	683	60.5	9.4	316	2	Q9N1Y1_PIG	Q9n1y1 sus scrofa
611	61	9.5	362	2	Q8C2F8_MOUSE	Q8c2f8 mus musculus	684	60.5	9.4	322	2	Q9HNV6_HALSA	Q9hmv6 halobacteri
612	61	9.5	364	1	YBOX2_HUMAN	Q9y2t7 homo sapien	685	60.5	9.4	326	2	Q5M800_HUMAN	Q5m800 homo sapien
613	61	9.5	364	2	Q3GW96_9ACTO	Q3gw96 nocardioid	686	60.5	9.4	326	2	Q9BVC4_HUMAN	Q9bvc4 homo sapien
614	61	9.5	383	2	Q2JVZ0_9CYAN	Q2jvz0 cyanobacter	687	60.5	9.4	326	2	Q4SG3_TETNG	Q4sg3 tetraodon n
615	61	9.5	383	2	Q4SEK7_TETNG	Q4sek7 tetraodon n	688	60.5	9.4	327	2	Q8WU15_HUMAN	Q8wu15 homo sapien

689	60.5	9.4	328	2	Q2UJF2	ASPOR	Q2UJF2	aspergillus	762	60	9.3	294	2	073708	BRARE	073708	brachydanio
690	60.5	9.4	343	2	Q7PZ69	ANOCA	Q7PZ69	anopheles g	763	60	9.3	294	2	06PCA5	BRARE	06PCA5	brachydanio
691	60.5	9.4	344	2	Q8VC87	MOUSE	Q8VC87	mus musculus	764	60	9.3	307	2	Q9NXH7	HUMAN	Q9NXH7	homo sapien
692	60.5	9.4	348	1	NR1I3	CALUR	P62044	callothinus	765	60	9.3	308	2	05DHU6	SCHJA	05DHU6	schistosoma
693	60.5	9.4	348	2	Q2T9C7	BURTH	Q2T9C7	burkholderi	766	60	9.3	319	2	093529	XENLA	093529	xenopus lae
694	60.5	9.4	353	2	Q66KP5	XENLA	Q66KP5	xenopus lae	767	60	9.3	326	2	Q510B4	XENTR	Q510B4	xenopus tro
695	60.5	9.4	362	1	CPPL	ARATH	Q91L77	arabidopsis	768	60	9.3	326	2	Q6PA72	XENLA	Q6PA72	xenopus lae
696	60.5	9.4	365	2	Q8KS88	ECOLI	Q8KS88	escherichia	769	60	9.3	327	2	Q983K7	RHILO	Q983K7	rhizobium 1
697	60.5	9.4	377	2	Q6LEVS	PLAF7	Q6LEVS	plasmodium	770	60	9.3	333	2	Q57YK9	9TRYP	Q57YK9	trypanosoma
698	60.5	9.4	382	2	Q3GH98	CHLVI	Q3GH98	prothecoch	771	60	9.3	337	2	Q7NR98	CHRVO	Q7NR98	chromobace
699	60.5	9.4	388	2	Q7XHC8	ORYSA	Q7XHC8	oryza sativ	772	60	9.3	346	2	Q8HJD2	9PASE	Q8HJD2	nectarinia
700	60.5	9.4	388	2	Q857Z9	ORYSA	Q857Z9	oryza sativ	773	60	9.3	346	2	Q8M807	9COLU	Q8M807	streptopeli
701	60.5	9.4	395	2	Q7SHK2	NEUCR	Q7SHK2	neurospora	774	60	9.3	346	2	Q9B6T3	EUDL	Q9B6T3	eudromia el
702	60.5	9.4	396	2	Q9XW00	CABEL	Q9XW00	caenorhabdi	775	60	9.3	346	2	Q8B6T3	EUDL	Q8B6T3	eudromia el
703	60.5	9.4	405	2	Q9VXS3	DROME	Q9VXS3	drosophila	776	60	9.3	346	2	Q8B6T3	EUDL	Q8B6T3	eudromia el
704	60.5	9.4	410	2	Q9VXS4	DROME	Q9VXS4	drosophila	777	60	9.3	346	2	Q8B6T3	EUDL	Q8B6T3	eudromia el
705	60.5	9.4	412	2	Q4RRU8	TETNG	Q4RRU8	tetraodon n	778	60	9.3	346	2	Q8M805	9COLU	Q8M805	streptopeli
706	60.5	9.4	416	2	Q4S7R5	TETNG	Q4S7R5	tetraodon n	779	60	9.3	359	1	WNT8A	BRARE	WNT8A	brachydanio
707	60.5	9.4	420	1	BMP2	TETNG	Q80482	tetraodon n	780	60	9.3	361	2	Q848K8	9BACT	Q848K8	uncultured
708	60.5	9.4	425	2	Q4S0H1	TETNG	Q4S0H1	tetraodon n	781	60	9.3	363	1	PGLR	ASPPA	PGLR	aspergillus
709	60.5	9.4	452	2	Q9LTH8	ARATH	Q9LTH8	arabidopsis	782	60	9.3	372	2	Q5EPB2	NEIGO	Q5EPB2	neisseria g
710	60.5	9.4	494	2	Q852S7	9CARY	Q852S7	suaeda japo	783	60	9.3	378	1	PGLR	PENEN	PGLR	penicillium
711	60.5	9.4	503	2	Q3BKV1	9HEPC	Q3BKV1	hepatitis c	784	60	9.3	379	2	Q9S4U3	SELRU	Q9S4U3	selenomonas
712	60.5	9.4	527	2	Q7TNK4	MOUSE	Q7TNK4	mus musculus	785	60	9.3	383	1	SNIP1	MOUSE	SNIP1	mouse
713	60.5	9.4	553	2	Q495L1	HUMAN	Q495L1	homo sapien	786	60	9.3	383	1	Q3V106	MOUSE	Q3V106	m adult mal
714	60.5	9.4	553	2	Q495L1	HUMAN	Q495L1	homo sapien	787	60	9.3	395	2	Q7K742	CABEL	Q7K742	caenorhabdi
715	60.5	9.4	584	2	Q4IA69	GIBBE	Q4IA69	gibberella	788	60	9.3	400	2	Q9U8B1	9TRYP	Q9U8B1	trypanosoma
716	60.5	9.4	622	2	Q9W3C4	DROME	Q9W3C4	drosophila	789	60	9.3	407	2	Q9NXX2	HUMAN	Q9NXX2	homo sapien
717	60.5	9.4	627	2	P74489	SYNY3	P74489	synecocyst	790	60	9.3	418	1	PPA6	MOUSE	PPA6	mouse
718	60.5	9.4	640	1	SPT10	YEAST	P35208	saccharomyc	791	60	9.3	418	1	Q3TNE2	MOUSE	Q3TNE2	mouse
719	60.5	9.4	655	2	Q705H8	HPV43	Q705H8	human papil	792	60	9.3	424	2	Q86UY1	HUMAN	Q86UY1	homo sapien
720	60.5	9.4	659	2	Q9SU58	DROME	Q9SU58	drosophila	793	60	9.3	435	2	Q5LKK1	SILPO	Q5LKK1	silicibacte
721	60.5	9.4	664	2	Q5N008	CRYNE	Q5N008	cryptococcu	794	60	9.3	445	2	Q38YD5	LACSS	Q38YD5	lactobacill
722	60.5	9.4	664	2	Q5KBC9	CRYNE	Q5KBC9	cryptococcu	795	60	9.3	450	2	Q4UF91	THEAN	Q4UF91	theileria a
723	60.5	9.4	746	2	Q4ORX8	DESAC	Q4ORX8	desulfuromo	796	60	9.3	462	2	Q4V791	XENTR	Q4V791	xenopus tro
724	60.5	9.4	751	2	Q3HKG4	RHOS4	Q3HKG4	rhodobacter	797	60	9.3	464	2	Q9JJR1	MOUSE	Q9JJR1	mus musculus
725	60.5	9.4	807	1	YNPF	ECOLI	P77783	escherichia	798	60	9.3	467	2	Q60Q96	CAEBR	Q60Q96	caenorhabdi
726	60.5	9.4	808	2	Q6EW77	ECOLI	Q6EW77	escherichia	799	60	9.3	494	2	Q2ULV3	ASPOR	Q2ULV3	aspergillus
727	60.5	9.4	808	2	Q7ADN3	ECO57	Q7ADN3	escherichia	800	60	9.3	495	2	Q2UUP9	ASPOR	Q2UUP9	aspergillus
728	60.5	9.4	808	2	Q8CW17	ECOL6	Q8CW17	escherichia	801	60	9.3	530	2	Q5D5K3	ALV	Q5D5K3	avian leuko
729	60.5	9.4	817	2	Q8DCT9	VIBVU	Q8DCT9	vibrio vuln	802	60	9.3	533	2	Q5D5K2	ALV	Q5D5K2	avian leuko
730	60.5	9.4	819	2	Q7MH12	VIBVU	Q7MH12	vibrio vuln	803	60	9.3	533	2	Q5D5K2	ALV	Q5D5K2	avian leuko
731	60.5	9.4	879	2	Q8IM68	PLAF7	Q8IM68	plasmodium	804	60	9.3	548	2	Q7U124	MYCBO	Q7U124	mycobacteri
732	60.5	9.4	914	2	Q85SQ7	ORYSA	Q85SQ7	oryza sativ	805	60	9.3	555	2	Q2X5W6	9GAMM	Q2X5W6	shewanella
733	60.5	9.4	1006	2	Q2X8S2	PSEPU	Q2X8S2	pseudomonas	806	60	9.3	555	2	Q2ZSX0	SHEPU	Q2ZSX0	shewanella
734	60.5	9.4	1019	1	LFC	CARRO	Q26422	c limulus l	807	60	9.3	559	1	Q3Q9M1	9GAMM	Q3Q9M1	shewanella
735	60.5	9.4	1055	2	Q8OS37	9VIRU	Q8OS37	una virus.	808	60	9.3	565	2	Q4SHE1	TETNG	Q4SHE1	tetraodon n
736	60.5	9.4	1265	2	Q2JTG4	9CYAN	Q2JTG4	cyanobacter	809	60	9.3	610	2	Q5ZLS5	CHICK	Q5ZLS5	gallus gall
737	60.5	9.4	1362	2	Q6Q114	RAT	Q6Q114	rattus norv	810	60	9.3	614	1	Y268	CHLMU	Y268	chlamydia m
738	60.5	9.4	1710	2	Q7RBL5	PLAYO	Q7RBL5	plasmodium	811	60	9.3	636	2	Q4WCS1	ASPFU	Q4WCS1	aspergillus
739	60.5	9.4	1974	2	Q21281	CABEL	Q21281	caenorhabdi	812	60	9.3	644	2	Q6NUU9	HUMAN	Q6NUU9	homo sapien
740	60.5	9.4	2104	2	Q964N4	CABEL	Q964N4	caenorhabdi	813	60	9.3	647	2	Q4RES8	TETNG	Q4RES8	tetraodon n
741	60.5	9.4	2104	2	Q964N4	CABEL	Q964N4	caenorhabdi	814	60	9.3	656	2	Q4H332	CIOIN	Q4H332	ciona intes
742	60.5	9.4	2239	2	Q8IBW8	PLAF7	Q8IBW8	plasmodium	815	60	9.3	683	2	Q3JV89	BURP1	Q3JV89	burkholderi
743	60.5	9.4	2353	2	Q7M560	BRARE	Q7M560	brachydanio	816	60	9.3	725	2	Q6MBT5	PARUM	Q6MBT5	parachlamyd
744	60.5	9.4	4006	2	Q4S7X0	TETNG	Q4S7X0	tetraodon n	817	60	9.3	734	2	Q3TYU8	MOUSE	Q3TYU8	mus musculu
745	60.5	9.4	5138	2	Q9ZW94	ARATH	Q9ZW94	arabidopsis	818	60	9.3	746	2	Q4Q1E3	LEIMA	Q4Q1E3	leishmania
746	60	9.3	53	2	Q3BS46	XANC5	Q3BS46	xanthomonas	819	60	9.3	795	2	Q2QPR8	ORYSA	Q2QPR8	oryza sativ
747	60	9.3	67	1	YHFD	BACSU	Q07602	bacillus su	820	60	9.3	812	2	Q4SKQ4	TETNG	Q4SKQ4	tetraodon n
748	60	9.3	74	2	Q7UY67	RHOBA	Q7UY67	rhodopirell	821	60	9.3	825	1	SE5	RAT	SE5	rattus norv
749	60	9.3	89	2	Q6UMG9	HUMAN	Q6UMG9	homo sapien	822	60	9.3	843	2	Q7XQC6	ORYSA	Q7XQC6	oryza sativ
750	60	9.3	139	2	Q6DFZ6	BRARE	Q6DFZ6	brachydanio	823	60	9.3	896	2	Q6FEG8	BRARE	Q6FEG8	brachydanio
751	60	9.3	166	2	Q66TW3	9DIPT	Q66TW3	culicoides	824	60	9.3	903	2	Q6P9F4	HUMAN	Q6P9F4	homo sapien
752	60	9.3	197	2	Q4SNJ2	TETNG	Q4SNJ2	tetraodon n	825	60	9.3	903	2	Q8TDY4	HUMAN	Q8TDY4	homo sapien
753	60	9.3	209	2	Q659J2	HYDMA	Q659J2	hydra magni	826	60	9.3	903	2	Q6P949	BRARE	Q6P949	brachydanio
754	60	9.3	230	2	Q4SNJ1	TETNG	Q4SNJ1	tetraodon n	827	60	9.3	903	2	Q6P949	BRARE	Q6P949	brachydanio
755	60	9.3	231	2	Q82547	CITSI	Q82547	citrus sine	828	60	9.3	979	2	Q3GSA1	9GAMM	Q3GSA1	psychrobact
756	60	9.3	241	2	Q69RGI	ORYSA	Q69RGI	oryza sativ	829	60	9.3	1020	2	Q9C0D4	HUMAN	Q9C0D4	homo sapien
757	60	9.3	254	2	Q35Q78	9BRAD	Q35Q78	bradyrhizob	830	60	9.3	1069	2	Q67WC7	ORYSA	Q67WC7	oryza sativ
758	60	9.3	263	2	Q8CGG4	MOUSE	Q8CGG4	mus musculus	831	60	9.3	1193	2	Q4QGS0	LEIMA	Q4QGS0	leishmania
759	60	9.3	284	2	Q8WN82	BOVIN	Q8WN82	bos taurus	832	60	9.3	1254	2	Q6K517	ORYSA	Q6K517	oryza sativ
760	60	9.3	293	2	Q2TTT1	ECOLI	Q2TTT1	escherichia	833	60	9.3	1337	2	Q4RKW0	TETNG	Q4RKW0	tetraodon n
761	60	9.3	294	2	Q4WRZ3	ASPFU	Q4WRZ3	aspergillus	834	60	9.3	1455	2	Q4SBY5	TETNG	Q4SBY5	tetraodon n

835	60	9.3	1551	2	Q3UIX6_MOUSE	Q3ulx6 mus musculus	908	59.5	9.2	698	2	Q3BEC0_9TRYP	Q3BEC0 trypanosoma
836	60	9.3	1554	1	JADIC_MOUSE	F41230 mus musculus	909	59.5	9.2	768	2	Q61SD3_CAEBR	Q61sd3 caenorhabdi
837	60	9.3	1869	2	Q93809_MAGGR	Q93809 magnaporth	910	59.5	9.2	772	2	Q4WKQ8_ASFPU	Q4wkq8 aspergillus
838	60	9.3	2157	2	Q4SDX1_TETNG	Q4sdx1 tetraodon n	911	59.5	9.2	779	1	SREKJ7_BOVIN	Q2kj77 bos taurus
839	60	9.3	3038	1	LKNS_ASPE	Q98a5 aspergillus	912	59.5	9.2	866	1	SREC2_HUMAN	Q98g6 homo sapien
840	60	9.3	3161	2	O54511_YEREN	O54511 yerenia en	913	59.5	9.2	866	2	Q58A83_HUMAN	Q58a83 homo sapien
841	60	9.3	4823	2	Q93321_FUGRU	Q93321 fugu rubrip	914	59.5	9.2	870	1	SULP1_MOUSE	Q8K07 mus musculus
842	59.5	9.2	94	2	Q75150_ORYSA	Q75150 oryza sativ	915	59.5	9.2	946	2	Q3ED56_ARATH	Q3ed56 arabidopsis
843	59.5	9.2	104	1	RK25_PEA	P11892 pisum sativ	916	59.5	9.2	952	2	Q8NIT8_NEUCR	Q8nit8 neuropept
844	59.5	9.2	107	2	Q57ND5_SALCH	O57nd5 salmonella	917	59.5	9.2	977	2	Q4P2N9_USTWA	Q4p2n9 ustilago ma
845	59.5	9.2	110	2	Q562P5_ARATH	O562p5 arabidopsis	918	59.5	9.2	983	1	GLNE_PROAC	O6a94 propionibac
846	59.5	9.2	111	2	Q25104_HIRNI	Q25104 hirudo nipp	919	59.5	9.2	1006	2	Q7BJU9_PSEPU	Q7bj99 pseudomonas
847	59.5	9.2	120	2	Q6XHY7_DROYA	Q6xhy7 drosophila	920	59.5	9.2	1006	2	Q8BEH0_PSEPK	Q8BEH0 pseudomonas
848	59.5	9.2	120	2	Q9VMB9_DROME	Q9vmb9 drosophila	921	59.5	9.2	1019	2	Q8T9S1_TACTR	Q8t9s1 tachypleus
849	59.5	9.2	140	2	Q84J66_ORYSA	Q84j66 oryza sativ	922	59.5	9.2	1020	1	ACAI_ARATH	Q37145 arabidopsis
850	59.5	9.2	154	1	RNAS8_MIOTA	O8ep27 miopithecus	923	59.5	9.2	1079	2	Q6ZPZ0_MOUSE	Q6zpz0 mus musculus
851	59.5	9.2	154	2	Q86NN8_DROME	O86nn8 drosophila	924	59.5	9.2	1243	2	Q7Z8F3_TRIRE	Q7z8f3 trichoderma
852	59.5	9.2	155	2	Q9JKN8_MUSPA	Q9jkn8 mus pahari	925	59.5	9.2	1313	2	Q8XRR8_RALSO	Q8xrr8 ralsconia e
853	59.5	9.2	158	2	Q647G8_ARAHY	Q647g8 arachis hyp	926	59.5	9.2	1449	2	Q9U1I2_DROME	Q9u1i2 drosophila
854	59.5	9.2	158	2	Q3VOS5_MOUSE	Q3vos5 mus musculus	927	59.5	9.2	1462	2	Q9U1I3_DROME	Q9u1i3 drosophila
855	59.5	9.2	160	1	HSPB6_HUMAN	O14588 homo sapien	928	59.5	9.2	1671	2	Q571L9_MOUSE	Q571l9 mus musculus
856	59.5	9.2	160	2	O6NVI3_HUMAN	O6nvi3 homo sapien	929	59.5	9.2	1869	2	Q59FG1_HUMAN	Q59fg1 homo sapien
857	59.5	9.2	183	1	RM32_YEAST	P25348 saccharomyc	930	59.5	9.2	2114	1	MYO9B_MOUSE	Q9qy96 mus musculus
858	59.5	9.2	210	1	BAR2_CHITE	P02851 chironomus	931	59.5	9.2	2222	1	CACIB_RAT	Q07652 rattus norv
859	59.5	9.2	220	2	Q5XYR8_BORGA	O5xyr8 borrelia ga	932	59.5	9.2	2224	2	Q9NYZ6_HUMAN	Q9nyz6 homo sapien
860	59.5	9.2	226	2	Q21128_CAEBL	O21128 caenorhabdi	933	59.5	9.2	2251	2	Q5VZB6_HUMAN	Q5vzb6 homo sapien
861	59.5	9.2	239	2	Q2X1F0_9GAMM	Q2x1f0 shewanella	934	59.5	9.2	2259	1	CACIE_EBIBT	Q02343 cryocolagus
862	59.5	9.2	239	2	Q2ZU35_SHEPU	Q2zu35 shewanella	935	59.5	9.2	2270	2	Q5VZB8_HUMAN	Q5vzb8 homo sapien
863	59.5	9.2	240	2	Q855Y4_9CAUD	Q855y4 mycobacteri	936	59.5	9.2	2272	1	CACIE_MOUSE	Q61290 mus musculus
864	59.5	9.2	248	2	Q41IQ5_GIBZE	O41iq5 gibberella	937	59.5	9.2	2295	2	Q923K6_RAT	Q923k6 rattus norv
865	59.5	9.2	252	2	Q7YTD2_SACKO	Q7ytd2 saccolossu	938	59.5	9.2	2312	1	CACIE_HUMAN	Q15878 homo sapien
866	59.5	9.2	258	2	Q94GT3_ORYSA	Q94gt3 oryza sativ	939	59.5	9.2	2313	2	Q5VZB7_HUMAN	Q5vzb7 homo sapien
867	59.5	9.2	258	2	Q7XGM7_ORYSA	Q7xgm7 oryza sativ	940	59.5	9.2	2382	2	Q9B1I9_DROME	Q9b1i9 drosophila
868	59.5	9.2	259	2	Q2QNF4_ORYSA	Q2qnf4 oryza sativ	941	59.5	9.2	2409	2	Q960G6_DROME	Q960g6 drosophila
869	59.5	9.2	260	2	Q86Y18_HUMAN	O86y18 homo sapien	942	59.5	9.2	3034	1	CELK1_MOUSE	Q35161 mus musculus
870	59.5	9.2	265	2	Q5M8K0_XENTR	O5m8k0 xenopus tro	943	59.5	9.2	3312	1	CELK3_HUMAN	Q9nyf7 homo sapien
871	59.5	9.2	293	2	Q6FOI6_CANGA	O6foi6 candida gla	944	59.5	9.2	3689	2	Q7PPF9_ANOGA	Q7ppf9 anopheles g
872	59.5	9.2	343	1	Q05937_YEAST	O05937 saccharomyc	945	59.5	9.2	4186	2	Q5Y190_HUMAN	Q5y190 homo sapien
873	59.5	9.2	359	1	FIX2_RHILE	P07748 rhizobium l	946	59	9.2	65	2	Q6BZL3_DEBHA	Q6bzl3 debaryomyce
874	59.5	9.2	366	2	Q6ATF0_ORYSA	O6atf0 oryza sativ	947	59	9.2	82	2	Q2NP17_NPVHC	Q2np17 hyphantria
875	59.5	9.2	368	1	CAAL_PSEPK	O88nv0 pseudomonas	948	59	9.2	102	2	Q9SNM2_PENMO	Q9snm2 penaeus mon
876	59.5	9.2	381	2	Q98A22_RHILO	O98a22 rhizobium l	949	59	9.2	109	2	Q6IG96_DROME	Q6ig96 drosophila
877	59.5	9.2	388	2	Q54G98_DICDI	O54g98 dictyosteli	950	59	9.2	115	2	Q3HNA5_9GEMI	Q3hna5 tobacco lea
878	59.5	9.2	409	2	Q94CL7_ARATH	O94cl7 arabidopsis	951	59	9.2	155	2	Q9JUG8_MUSCR	Q9jkg8 mus caroli
879	59.5	9.2	420	2	Q98NE5_RHILO	O98nb5 rhizobium l	952	59	9.2	157	2	Q9XTV5_CABEL	Q9xtv5 caenorhabdi
880	59.5	9.2	422	2	Q9MOH0_ARATH	Q9moh0 arabidopsis	953	59	9.2	158	2	Q43M16_SOLUS	Q43m16 solibacter
881	59.5	9.2	436	2	Q4SBN4_TETNG	O4sbn4 tetraodon n	954	59	9.2	158	2	Q9CTX4_MOUSE	Q9ctx4 mus musculus
882	59.5	9.2	427	1	CREA_ASFNG	O05620 aspergillus	955	59	9.2	160	1	ECF_HUMAN	P12724 homo sapien
883	59.5	9.2	428	2	Q4VB70_BRARE	O4vb70 brachydanio	956	59	9.2	160	1	PCP_PONPY	P47781 pongo pygma
884	59.5	9.2	446	2	Q6EB41_HUMAN	O6eb41 homo sapien	957	59	9.2	160	2	Q4VBC1_HUMAN	Q4vbc1 homo sapien
885	59.5	9.2	447	1	TBL2_HUMAN	O9yp43 homo sapien	958	59	9.2	171	2	Q22Q2_9GAMM	Q22q2 shewanella
886	59.5	9.2	447	2	Q5RDY0_PONPY	Q5rdy0 pongo pygma	959	59	9.2	171	2	Q22Q2_9GAMM	Q22q2 shewanella
887	59.5	9.2	493	2	Q84SA4_ASSTR	O84sa4 aster tripo	960	59	9.2	175	2	Q2NTQ1_SODGL	Q2ntq1 sodalis glo
888	59.5	9.2	503	2	Q3BKW0_9HEPC	Q3bkw0 hepaticis c	961	59	9.2	178	2	Q6AVC1_ORYSA	Q6avc1 oryza sativ
889	59.5	9.2	510	2	Q4AE31_FUGRU	O4ae31 fugu rubrip	962	59	9.2	193	1	PERP_HUMAN	Q6efx8 homo sapien
890	59.5	9.2	510	2	Q90WM4_FUGRU	O90wm4 fugu rubrip	963	59	9.2	199	2	Q34Z51_9GAMM	Q34z51 alkalilimni
891	59.5	9.2	514	2	Q7PBJ7_ANOGA	O7ppj7 anopheles g	964	59	9.2	227	2	Q7KPV6_LUCUC	Q7kpvy lucilia cup
892	59.5	9.2	514	2	Q65BEC1_ORYSA	O65be4 oryza sativ	965	59	9.2	230	2	Q2ZLQ3_SHEPU	Q2zlg3 shewanella
893	59.5	9.2	533	2	Q6EBC1_LUPAL	O6ebc1 lupinus alb	966	59	9.2	238	2	Q46G98_METBA	Q46ge7 xenopus lae
894	59.5	9.2	543	2	Q754G6_ASAGO	O754g6 ashbya goss	967	59	9.2	245	2	Q7XV53_ORYSA	Q7xv53 oryza sativ
895	59.5	9.2	561	2	Q3F2A4_9BURK	Q3f2a4 burkholderi	968	59	9.2	259	2	Q5CPE3_CRYPV	Q5cpe3 cryptospori
896	59.5	9.2	572	2	Q80XH4_MOUSE	O80xh4 mus musculus	969	59	9.2	272	2	Q2QWC6_ORYSA	Q2qwc6 oryza sativ
897	59.5	9.2	575	2	Q4D2L5_TRYCR	O4d2l5 trypanosoma	970	59	9.2	280	2	Q448M1_SOLUS	Q448m1 solibacter
898	59.5	9.2	592	1	TLLZ2_HUMAN	O9bwv7 homo sapien	971	59	9.2	284	2	Q801F0_XENLA	Q801f0 xenopus lae
899	59.5	9.2	594	2	Q9P4A3_EMENI	O9p4a3 emerigella	972	59	9.2	296	2	Q66KB7_XENLA	Q66ke7 xenopus lae
900	59.5	9.2	594	2	Q5B7V8_EMENI	O5b7v8 aspergillus	973	59	9.2	307	2	Q4ZM71_PSEU2	Q4zm71 pseudomonas
901	59.5	9.2	605	2	Q5DU24_MOUSE	O5du24 mus musculus	974	59	9.2	314	2	Q8S835_ORYSA	Q8s835 oryza sativ
902	59.5	9.2	622	2	Q7ZWK0_XENLA	O7zwk0 xenopus lae	975	59	9.2	319	2	Q3Q4R7_9GAMM	Q3q4r7 shewanella
903	59.5	9.2	633	1	MUTL_PSEAE	O9hul8 pseudomonas	976	59	9.2	321	2	Q2QYP4_ORYSA	Q2qyp4 oryza sativ
904	59.5	9.2	659	2	Q34LH5_RHOPA	Q34lh5 rhodopseudo	977	59	9.2	328	2	Q68DU4_HUMAN	Q68du4 homo sapien
905	59.5	9.2	666	2	Q9SPL4_MACIN	O9spl4 macadamia i	978	59	9.2	332	2	Q85EE8_9GALL	Q85ee8 penelopina
906	59.5	9.2	698	2	Q9UV14_EMENI	O9uv14 emerigella	979	59	9.2	346	2	Q7HXQ7_PSADE	Q7hxq7 psarocolius
907	59.5	9.2	698	2	Q5B961_EMENI	O5b961 aspergillus	980	59	9.2	346	2	Q8HJ63_APALIS	Q8hj63 apalis flav



981	59	9.2	346	2	Q8HN67	acryllium v	Q8hn67	acryllium v	1054	59	9.2	716	2	Q7M1Q5	ORYSA	Q7m1q5	oryza sativ
982	59	9.2	346	2	Q8LVW0	geothlypis	Q8lvw0	geothlypis	1055	59	9.2	730	1	IF2	BACHD	Q9Ka77	bacillus ha
983	59	9.2	346	2	Q8M801	streptopeli	Q8m801	streptopeli	1056	59	9.2	745	2	Q4S190	TETNG	Q4s190	tetraodon n
984	59	9.2	346	2	Q8M810	streptopeli	Q8m810	streptopeli	1057	59	9.2	802	1	NAB3	YEAST	P38996	saccharomyc
985	59	9.2	346	2	Q8SEF0	psarocolius	Q8sef0	psarocolius	1058	59	9.2	832	2	Q7Z9H9	SCHPO	P38996	schizosacch
986	59	9.2	346	2	Q8SIR3	carduelis p	Q8sir3	carduelis p	1059	59	9.2	837	1	PHLD	MOUSE	O70362	mus musculus
987	59	9.2	346	2	Q8W7C4	dendragapus	Q8w7c4	dendragapus	1060	59	9.2	842	2	Q7TNZ4	MOUSE	Q7tnz4	mus musculus
988	59	9.2	346	2	Q957Y6	anomalopter	Q957y6	anomalopter	1061	59	9.2	842	2	Q8R4J2	MOUSE	Q8r4j2	mus musculus
989	59	9.2	346	2	Q958B7	pteronemia	Q958b7	pteronemia	1062	59	9.2	842	2	Q8VCU2	MOUSE	Q8vcu2	mus musculus
990	59	9.2	346	2	Q9G8K1	geothlypis	Q9g8k1	geothlypis	1063	59	9.2	842	2	Q9DBH3	MOUSE	Q9dbh3	mus musculus
991	59	9.2	346	2	Q9G8M6	carduelis p	Q9g8m6	carduelis p	1064	59	9.2	846	2	Q2LAE0	LOCOMI	Q2lae0	locusta mig
992	59	9.2	346	2	Q9G8N1	eremophila	Q9g8n1	eremophila	1065	59	9.2	857	2	Q3GVH5	ACTO	Q3gvh5	nocardioid
993	59	9.2	346	2	Q9ML60	numme	Q9ml60	numida mele	1066	59	9.2	860	2	Q8S6M6	ORYSA	Q8s6m6	oryza sativ
994	59	9.2	346	2	Q9ML67	dendragapus	Q9ml67	dendragapus	1067	59	9.2	871	1	SULF1	HUMAN	Q81wu6	homo sapien
995	59	9.2	346	2	Q9ML72	centrocercu	Q9ml72	centrocercu	1068	59	9.2	871	2	Q7Z2W2	HUMAN	Q7z2w2	homo sapien
996	59	9.2	346	2	Q8M7Z9	streptopeli	Q8m7z9	streptopeli	1069	59	9.2	874	2	Q4SDF0	TETNG	Q4sdf0	tetraodon n
997	59	9.2	346	2	Q8M808	streptopeli	Q8m808	streptopeli	1070	59	9.2	895	2	Q802U7	BRARE	Q802u7	brachydania
998	59	9.2	346	2	Q8SK79	psarocolius	Q8sk79	psarocolius	1071	59	9.2	975	2	Q8W2U4	ORYSA	Q8w2u4	oryza sativ
999	59	9.2	346	2	Q9ML71	corurnix au	Q9ml71	corurnix au	1072	59	9.2	986	2	Q9DW99	RCVMV	Q9dw99	rat cytoMeg
1000	59	9.2	348	2	Q3T078	bos taurus	Q3t078	bos taurus	1073	59	9.2	1009	2	Q4STN5	TETNG	Q4stn5	tetraodon n
1001	59	9.2	357	2	Q2PEX9	trifolium p	Q2pex9	trifolium p	1074	59	9.2	1018	2	Q7SFB6	ASHGO	Q7sfb6	ashbya gos
1002	59	9.2	359	2	Q9GRG4	toxoplasma	Q9grg4	toxoplasma	1075	59	9.2	1046	2	Q4E275	TRYCR	Q4e275	trypanosoma
1003	59	9.2	369	2	Q4TGD6	tetraodon n	Q4tgd6	tetraodon n	1076	59	9.2	1059	2	Q7XE41	ORYSA	Q7xe41	oryza sativ
1004	59	9.2	372	2	Q5JIV7	pyrococcus	Q5jiv7	pyrococcus	1077	59	9.2	1064	1	JMJ2A	MOUSE	Q8bw72	mus musculus
1005	59	9.2	381	2	Q2R2Q3	oryza sativ	Q2r2q3	oryza sativ	1078	59	9.2	1082	2	Q4CNR9	TRYCR	Q4cnr9	trypanosoma
1006	59	9.2	399	2	Q3WUF6	mesorhizobi	Q3wuf6	mesorhizobi	1079	59	9.2	1130	2	Q4SVS4	TETNG	Q4svs4	tetraodon n
1007	59	9.2	401	2	Q67XK9	arabidopsis	Q67xk9	arabidopsis	1080	59	9.2	1149	2	Q4S2V5	TETNG	Q4s2v5	tetraodon n
1008	59	9.2	402	2	Q99037	trichoderma	Q99037	trichoderma	1081	59	9.2	1185	1	STB5L	MOUSE	Q5cdqr4	mus musculus
1009	59	9.2	402	2	Q99022	trichoderma	Q99022	trichoderma	1082	59	9.2	1423	1	SSH2	MOUSE	Q5gw75	mus musculus
1010	59	9.2	402	2	Q99038	trichoderma	Q99038	trichoderma	1083	59	9.2	1551	2	Q4S523	TETNG	Q4s523	tetraodon n
1011	59	9.2	404	2	Q2LAG2	ctenopharyn	Q2lag2	ctenopharyn	1084	59	9.2	1724	2	Q4RMC8	TETNG	Q4rnc8	tetraodon n
1012	59	9.2	409	2	Q6AWY1	oryza sativ	Q6awy1	oryza sativ	1085	59	9.2	1942	2	Q4DY12	TRYCR	Q4dy12	trypanosoma
1013	59	9.2	412	2	Q93811	arabidopsis	Q93811	arabidopsis	1086	59	9.2	2135	2	O61077	PLAFA	O61077	plasmodium
1014	59	9.2	427	2	Q4XYG5	xenopus tro	Q4xyg5	xenopus tro	1087	59	9.2	2162	2	Q9NYZ5	HUMAN	Q9nyz5	homo sapien
1015	59	9.2	429	2	Q9W6U3	fugu rubrip	Q9w6u3	fugu rubrip	1088	59	9.2	2559	2	Q4RGT6	TETNG	Q4rgt6	tetraodon n
1016	59	9.2	429	2	Q413E3	gibberella	Q413e3	gibberella	1089	59	9.2	2639	1	PDZK3	HUMAN	O15018	homo sapien
1017	59	9.2	433	2	Q413E3	gibberella	Q413e3	gibberella	1090	59	9.2	2839	2	Q9VAD3	DROME	Q9vad3	drosophila
1018	59	9.2	437	2	Q44555	caenorhabdi	Q44555	caenorhabdi	1091	59	9.2	3609	2	Q9KRV0	DROME	Q9krv0	drosophila
1019	59	9.2	439	2	Q5P447	azoarcus sp	Q5p447	azoarcus sp	1092	59	9.2	3657	2	Q99ND0	MOUSE	Q99nd0	mus musculus
1020	59	9.2	441	2	Q3E9Z2	arabidopsis	Q3e9z2	arabidopsis	1093	59	9.2	5374	2	Q5FIW8	LACAC	Q5fiw8	lactobacill
1021	59	9.2	453	2	Q2KXN6	borav	Q2kxn6	borav	1094	58.5	9.1	66	2	Q74CU7	GEOSL	Q74cu7	geobacter s
1022	59	9.2	465	2	Q31VLO	RHOS4	Q31vlo	rhodobacter	1095	58.5	9.1	88	2	Q3W4Q0	ACTO	Q3w4q0	frankia sp.
1023	59	9.2	468	2	Q4SAMS	TETNG	Q4sams	tetraodon n	1096	58.5	9.1	114	2	O6N3A0	BHOPA	O6n3a0	rhodopseudo
1024	59	9.2	473	2	Q4SAMS	TETNG	Q4sams	tetraodon n	1097	58.5	9.1	114	2	Q19441	CABEL	Q19441	caenorhabdi
1025	59	9.2	479	2	Q4SAMS	TETNG	Q4sams	tetraodon n	1098	58.5	9.1	115	2	Q19441	CABEL	Q19441	caenorhabdi
1026	59	9.2	491	1	ZN655	HUMAN	Q4f9r6	human immu	1099	58.5	9.1	147	2	Q5IU48	HORVD	Q5iu48	hordeum vul
1027	59	9.2	500	2	Q4F9R6	9HIV1	Q4f9r6	human immu	1100	58.5	9.1	149	2	Q654C9	ORYSA	Q654c9	oryza sativ
1028	59	9.2	509	1	TSSP	MOUSE	Q9qxe5	mus musculu	1101	58.5	9.1	151	2	Q8TEC6	HUMAN	Q8tec6	homo sapien
1029	59	9.2	509	2	Q5SZ30	MOUSE	Q5sz30	mus musculu	1102	58.5	9.1	162	2	Q9Y9C2	APERPE	Q9y9c2	aeropyrum p
1030	59	9.2	518	2	Q9LIH4	STRCO	Q9lih4	streptomyce	1103	58.5	9.1	169	2	O5L8A0	BACFN	O5l8a0	bacteroides
1031	59	9.2	539	2	Q7RC79	PLAYO	Q7rc79	plasmodium	1104	58.5	9.1	169	2	Q4LNK0	BACFR	Q4lnk0	bacteroides
1032	59	9.2	540	2	Q33UJ9	9GAMM	Q33uj9	shewanella	1105	58.5	9.1	171	2	Q6YV86	ORYSA	Q6yv86	oryza sativ
1033	59	9.2	551	2	Q4BBL9	BURVI	Q4bb19	burkholderi	1106	58.5	9.1	183	2	Q96U87	NEUCR	Q96u87	neurospora
1034	59	9.2	553	2	Q3P2V7	9GAMM	Q3p2v7	shewanella	1107	58.5	9.1	214	2	Q82E90	STRAW	Q82e90	streptomyce
1035	59	9.2	574	2	Q87N55	VBIPA	Q87n55	vibrio para	1108	58.5	9.1	225	2	Q95JZ5	MACFA	Q95jz5	macaca fasc
1036	59	9.2	576	2	Q9VD52	DROME	Q9vd52	drosophila	1109	58.5	9.1	230	2	Q9UJV6	HUMAN	Q9ujv6	homo sapien
1037	59	9.2	579	2	Q8C393	MOUSE	Q8c393	mus musculu	1110	58.5	9.1	232	2	Q3MAL3	ANAVT	Q3mal3	anabaena va
1038	59	9.2	579	2	Q9WVIO	MOUSE	Q9wvio	mus musculu	1111	58.5	9.1	237	2	Q612S9	CABBR	Q612s9	caenorhabdi
1039	59	9.2	603	2	Q02302	PSESP	Q02302	pseudomonas	1112	58.5	9.1	255	2	Q3KPM5	XENLA	Q3kpm5	xenopus lae
1040	59	9.2	605	2	Q5DTV1	MOUSE	Q5dtv1	mus musculu	1113	58.5	9.1	263	2	Q3KFJ3	PSEPP	Q3kfm3	pseudomonas
1041	59	9.2	614	2	Q4VPT6	MYXXA	Q4vpt6	myxococcus	1114	58.5	9.1	267	2	Q84SX4	ORYSA	Q84sx4	oryza sativ
1042	59	9.2	633	2	Q3H5A9	9ACTO	Q3h5a9	nocardioid	1115	58.5	9.1	267	2	Q4SUL6	TETNG	Q4sul6	tetraodon n
1043	59	9.2	637	2	Q6PA32	XENLA	Q6pa32	xenopus lae	1116	58.5	9.1	280	2	Q37050	SIVCZ	Q37050	chimpanzee
1044	59	9.2	644	2	Q44DN7	CHRLS	Q44dn7	chromohalob	1117	58.5	9.1	285	2	Q6DJC8	XENLA	Q6djc8	xenopus lae
1045	59	9.2	646	2	Q30TT1	THIDN	Q30tt1	thiomicrosp	1118	58.5	9.1	302	2	Q7YTG9	CABEL	Q7ytg9	caenorhabdi
1046	59	9.2	651	2	Q2VJ88	9PAPI	Q2vj88	human papil	1119	58.5	9.1	303	2	Q3H6M6	9ACTO	Q3h6m6	nocardioid
1047	59	9.2	660	1	CXCC1	MOUSE	Q9cww7	mus musculu	1120	58.5	9.1	310	2	Q4WY17	ASPFU	Q4wy17	aspergillus
1048	59	9.2	660	2	Q3UIZ4	MOUSE	Q3uiz4	mus musculu	1121	58.5	9.1	311	2	Q4RQB2	TETNG	Q4rgb2	tetraodon n
1049	59	9.2	660	2	Q541B1	MOUSE	Q541b1	mus musculu	1122	58.5	9.1	324	2	Q3FN61	9BURK	Q3fn61	rhodotera
1050	59	9.2	666	2	Q9SPL5	MACIN	Q9spl5	macadamia i	1123	58.5	9.1	329	2	Q2LAB5	MOUSE	Q2lae5	mus musculus
1051	59	9.2	676	2	Q46A10	METBA	Q46a10	methanosarc	1124	58.5	9.1	340	2	Q4EON7	TRYCR	Q4e0n7	trypanosoma
1052	59	9.2	693	2	Q4RAX0	TETNG	Q4rax0	tetraodon n	1125	58.5	9.1	368	2	Q95WF7	ACRMI	Q95wf7	acropora mi
1053	59	9.2	714	2	Q3V0C1	m adult mal	Q3v0c1	m adult mal	1126	58.5	9.1	368	2	Q68FU6	RAT	Q68fu6	rattus norv



1127	58.5	9.1	371	2	Q389J9_9TRYP	Q389j9	trypanosoma	1200	58.5	9.1	3454	2	Q7Y1G0_ORYSA	Q7Y1g0	oryza sativ
1128	58.5	9.1	406	2	Q72ZY9_PETMA	Q72zy9	petromyzon	1201	58.5	9.1	3767	1	MUA3_CABEL	P34576	caenorhabdi
1129	58.5	9.1	414	2	Q8U217_9PAPI	Q8u217	phocoena sp	1202	58.5	9.1	5146	2	Q8SPM4_BOVIN	P34576	bos taurus
1130	58.5	9.1	416	2	Q4H3S1_CIOIN	Q4h3e1	ciona intes	1203	58	9.0	46	2	Q86B29_9CAEN	Q86b29	reishia cla
1131	58.5	9.1	416	2	Q80731_ARATH	Q80731	arabidopsis	1204	58	9.0	73	2	Q5Y4U8_AGEOR	Q5y4u8	agelena ori
1132	58.5	9.1	419	2	Q2NRG2_SODGL	Q2nrg2	sodalis gio	1205	58	9.0	92	2	Q8SKY9_DROME	Q8sky9	drosophila
1133	58.5	9.1	420	2	Q804S3_FUGRU	Q804s3	fugu rubrip	1206	58	9.0	96	2	Q61JUT6_DROME	Q61j16	drosophila
1134	58.5	9.1	422	2	Q804S3_FUGRU	Q804s3	paralichthy	1207	58	9.0	105	2	Q6K2T3_ORYSA	Q6k2t3	oryza sativ
1135	58.5	9.1	439	2	Q3SEH3_PARTE	Q3seh3	paramemius	1208	58	9.0	114	2	P74050_SVNY3	P74050	synecocyst
1136	58.5	9.1	439	2	Q417L1_KINRA	Q417l1	kineococcus	1209	58	9.0	122	2	Q2K382_RHJET	Q2k382	rhizobium e
1137	58.5	9.1	447	2	Q95RA7_DROME	Q95ra7	drosophila	1210	58	9.0	123	2	Q2RLJ3_MOOTH	Q2rlj3	moorella th
1138	58.5	9.1	456	2	Q9RAH1_HUMAN	Q9rahl	homo sapien	1211	58	9.0	123	2	Q6D9N6_ERWCT	Q6d9n6	erwinia car
1139	58.5	9.1	461	2	Q6GQK7_XENLA	Q6gqk7	xenopus lae	1212	58	9.0	126	2	Q61JH5_DROME	Q61j15	drosophila
1140	58.5	9.1	462	2	Q2R0J2_ORYSA	Q2r0j2	oryza sativ	1213	58	9.0	128	2	Q50E33_9MURI	Q50e33	arvicanthhis
1141	58.5	9.1	472	2	Q6ETN5_ORYSA	Q6etn5	oryza sativ	1214	58	9.0	128	2	Q50E34_9MURI	Q50e34	arvicanthhis
1142	58.5	9.1	476	2	Q4Q1J2_LEIMA	Q4q1j2	leishmania	1215	58	9.0	145	1	RLJ5_MYCHJ	Q4a819	mycoplasma
1143	58.5	9.1	478	2	Q440Y3_SOLUS	Q440y3	solibacter	1216	58	9.0	145	1	RLJ5_MYCHJ	Q4aaf8	mycoplasma
1144	58.5	9.1	486	2	Q2RP04_RHOKU	Q2rpu4	rhodospirill	1217	58	9.0	136	2	Q7RUI5_NEUCR	Q7rui5	neurospora
1145	58.5	9.1	496	2	Q7S6G4_NEUCR	Q7s6g4	neurospora	1218	58	9.0	141	2	Q8QLK9_9NUCL	Q8qlk9	mamestra p
1146	58.5	9.1	509	2	Q8PKL3_XANAC	Q8pkl3	xanthomonas	1219	58	9.0	143	2	Q9YCH7_AERPE	Q9ych7	aeropyrum p
1147	58.5	9.1	556	2	Q54WV4_DICDI	Q54wv4	dictyosteli	1220	58	9.0	145	1	RLJ5_MYCHJ	Q4a819	mycoplasma
1148	58.5	9.1	561	2	Q9X9P8_STRTE	Q9x9p8	streptomyce	1221	58	9.0	145	1	RLJ5_MYCHJ	Q4aaf8	mycoplasma
1149	58.5	9.1	569	2	Q6A2B2_9RETR	Q6a2b2	avian endog	1222	58	9.0	150	2	Q6ZVM6_HUMAN	Q6zvm6	homo sapien
1150	58.5	9.1	582	2	Q7UX40_RHOBA	Q7ux40	rhodopirell	1223	58	9.0	150	2	Q63831_MEUGE	Q63831	melospiza g
1151	58.5	9.1	630	2	Q7Q460_ANOGA	Q7q460	anophelies g	1224	58	9.0	153	2	Q6VVG3_ANOGA	Q6vvg3	anophelies g
1152	58.5	9.1	637	2	Q7UL95_RHOBA	Q7ul95	rhodopirell	1225	58	9.0	153	2	Q6VVG4_ANOGA	Q6vvg4	anophelies g
1153	58.5	9.1	642	2	Q4HZG6_GIBZE	Q4h2g6	gibberella	1226	58	9.0	154	2	Q9NEH6_DROME	Q9neh6	drosophila
1154	58.5	9.1	642	2	Q3SYX4_BOVIN	Q3syx4	bos taurus	1227	58	9.0	154	2	Q4SA33_TETNG	Q4sa33	tetraodon n
1155	58.5	9.1	645	2	Q52KS4_XENLA	Q52ks4	xenopus lae	1228	58	9.0	155	2	Q2S577_9CNID	Q2s577	nematostell
1156	58.5	9.1	658	2	Q2N8M5_9SPHN	Q2n8m5	erythrobaet	1229	58	9.0	155	2	Q5GAM2_RAT	Q5gam2	rattus norv
1157	58.5	9.1	659	2	Q371D1_RHOPA	Q371d1	rhodopseudo	1230	58	9.0	155	2	Q9R125_MOUSE	Q9r125	mus musculus
1158	58.5	9.1	659	2	Q52128_XENLA	Q52128	xenopus lae	1231	58	9.0	155	2	Q9R127_RAT	Q9r127	rattus norv
1159	58.5	9.1	699	2	Q5KFX2_CRYNE	Q5kfx2	cryptococcu	1232	58	9.0	159	2	Q9FPB0_ORYSA	Q9fpb0	oryza sativ
1160	58.5	9.1	720	1	DOCK9_RAT	Q63603	rattus norv	1233	58	9.0	169	2	Q60EA7_ORYSA	Q60ea7	oryza sativ
1161	58.5	9.1	720	2	Q4RSX3_TETNG	Q4rsx3	tetraodon n	1234	58	9.0	170	2	Q3Q0D7_9GAMM	Q3q0d7	shewanella
1162	58.5	9.1	742	2	Q4P890_USTMA	Q4p890	ustilago ma	1235	58	9.0	171	2	Q3STC5_9GAMM	Q3stc5	shewanella
1163	58.5	9.1	761	2	Q9SLQ2_MACFA	Q9slq2	macaca fasc	1236	58	9.0	171	2	Q5S881_9PSED	Q5s881	pseudomonas
1164	58.5	9.1	792	2	Q3JIK9_BURP1	Q3jik9	burkholderi	1237	58	9.0	172	2	Q5TV92_ANOGA	Q5tv92	anophelies g
1165	58.5	9.1	820	2	Q55W58_CRYNE	Q55w58	cryptococcu	1238	58	9.0	172	2	Q7XY01_CHLS6	Q7xyv1	chlorarachn
1166	58.5	9.1	820	2	Q5KK36_CRYNE	Q5kk36	cryptococcu	1239	58	9.0	175	2	Q2SNC3_9GAMM	Q2snc3	habella che
1167	58.5	9.1	825	2	Q216K7_9DELT	Q216k7	uncultured	1240	58	9.0	180	2	Q7XEP3_ORYSA	Q7xep3	oryza sativ
1168	58.5	9.1	870	1	SULF1_RAT	Q8vi60	rattus norv	1241	58	9.0	186	2	Q7YEP87_COWPX	Q7yep87	cowpox viru
1169	58.5	9.1	874	1	EGFL4_RAT	Q9qyp0	rattus norv	1242	58	9.0	192	2	Q36EC1_9GAMM	Q36ec1	shewanella
1170	58.5	9.1	911	2	Q4X1S9_ASFPFU	Q4x1s9	aspergillus	1243	58	9.0	193	2	Q351L7_9GAMM	Q351l7	alkalilimni
1171	58.5	9.1	922	2	Q8BPR4_MOUSE	Q8bpr4	mus musculus	1244	58	9.0	200	2	Q2TE04_9HYME	Q2te04	spathieus sp
1172	58.5	9.1	922	2	Q8K2D7_MOUSE	Q8k2d7	mus musculus	1245	58	9.0	203	2	Q3FQC3_9BURK	Q3fcq3	rhodofera
1173	58.5	9.1	924	2	Q8BNE1_MOUSE	Q8bne1	m 12 days e	1246	58	9.0	205	2	Q4Y4M6_PLACH	Q4y4m6	plasmodium
1174	58.5	9.1	927	2	Q7Q0N1_ANOGA	Q7q0n1	anophelies g	1247	58	9.0	218	2	Q3USA2_MOUSE	Q3usa2	mus musculus
1175	58.5	9.1	952	2	Q6A005_MOUSE	Q6a005	mus musculus	1248	58	9.0	219	2	Q2R312_ORYSA	Q2r312	oryza sativ
1176	58.5	9.1	960	2	Q4S187_TETNG	Q4s187	tetraodon n	1249	58	9.0	222	2	Q61GT3_CABBR	Q61gt3	caenorhabdi
1177	58.5	9.1	971	2	Q751Y2_ORYSA	Q751y2	oryza sativ	1250	58	9.0	230	2	Q7R8X0_PLAYO	Q7r8x0	plasmodium
1178	58.5	9.1	996	2	Q6BM64_DEBHA	Q6bm64	debaromyce	1251	58	9.0	233	2	Q8NJJ6_PONPY	Q8nj16	pongo pygma
1179	58.5	9.1	1002	2	Q6AVJ4_ORYSA	Q6avj4	oryza sativ	1252	58	9.0	233	2	Q8NJJ7_PONPY	Q8nj10	pongo pygma
1180	58.5	9.1	1002	2	Q7QU52_RHOBA	Q7qu52	rhodopirell	1253	58	9.0	233	2	Q8MJ10_PONPY	Q8mj10	pongo pygma
1181	58.5	9.1	1019	1	LFC_TACTR	P28175	tachypleus	1254	58	9.0	245	2	Q4RM34_TETNG	Q4rm34	tetraodon n
1182	58.5	9.1	1060	2	Q5B600_EMENI	Q5b600	aspergillus	1255	58	9.0	248	2	Q9SL34_ARATH	Q9sl34	arabidopsis
1183	58.5	9.1	1100	2	Q2SUL9_BURTH	Q2sul9	burkholderi	1256	58	9.0	259	2	Q8MKQ6_DROME	Q8mkq6	drosophila
1184	58.5	9.1	1107	2	Q4TB26_TETNG	Q4tb26	tetraodon n	1257	58	9.0	268	2	Q96N84_HUMAN	Q96n84	homo sapien
1185	58.5	9.1	1238	2	Q74808_SCHPO	Q74808	schizosacch	1258	58	9.0	283	2	Q37051_SIVCZ	Q37051	chimpazee
1186	58.5	9.1	1363	2	Q2UUR2_ASPOR	Q2uur2	aspergillus	1259	58	9.0	284	2	Q4S4X5_TETNG	Q4s4x5	tetraodon n
1187	58.5	9.1	1426	2	Q4Q868_LEIMA	Q4q868	leishmania	1260	58	9.0	285	2	Q5PSP7_XENLA	Q5p5p7	xenopus lae
1188	58.5	9.1	1467	2	Q4T699_TETNG	Q4t699	tetraodon n	1261	58	9.0	289	2	Q75D76_ASHGO	Q75d76	ashbya goss
1189	58.5	9.1	1474	2	Q3SQG4_BURP1	Q3sqg4	burkholderi	1262	58	9.0	295	2	Q34V57_9GAMM	Q34v57	alkalilimni
1190	58.5	9.1	1610	2	Q4S5Z3_TETNG	Q4s5z3	burkholderi	1263	58	9.0	298	2	Q6UVV4_PSEAK	Q6uvv4	pseudodocl
1191	58.5	9.1	1637	2	Q9XSV8_BOVIN	Q9xsv8	bos taurus	1264	58	9.0	309	2	Q4V9A2_BRARE	Q4v9a2	brachydanio
1192	58.5	9.1	1673	2	Q5B614_EMENI	Q5b614	aspergillus	1265	58	9.0	330	2	Q8DLU4_XYNEL	Q8dlu4	synecococc
1193	58.5	9.1	1724	2	Q751X6_ORYSA	Q751x6	oryza sativ	1266	58	9.0	332	2	Q6K1C8_9GALL	Q6k1c8	mitu toment
1194	58.5	9.1	1726	2	Q5B614_EMENI	Q5b614	aspergillus	1267	58	9.0	332	2	Q6K1C9_9GALL	Q6k1c9	mitu toment
1195	58.5	9.1	1761	2	Q86XN2_HUMAN	Q86xn2	homo sapien	1268	58	9.0	332	2	Q8SEB1_PAUPA	Q8seeb1	pauzi pauxi
1196	58.5	9.1	2282	1	ZAN_RABIT	P57999	oryctolagus	1269	58	9.0	332	2	Q8SEEB_OREDE	Q8seeb	oreophasia
1197	58.5	9.1	2330	1	EGFL4_MOUSE	P60882	mus musculus	1270	58	9.0	335	2	Q8HCJ6_MOTFL	Q8hcj6	motacilla f
1198	58.5	9.1	2386	1	EGFL4_HUMAN	Q7z7m0	homo sapien	1271	58	9.0	341	2	Q674B4_9CORV	Q674b4	lanioturdus
1199	58.5	9.1	2783	2	Q4Q1Z5_LEIMA	Q4q1z9	leishmania	1272	58	9.0	343	2	Q7Y6Z6_PASIL	Q7y6z6	passerella

1273	58	9.0	343	2	Q7Y869_PASIL	Q7Y869 passerella	1346	58	9.0	346	2	Q8LXD1_9ICTE	Q8Lxd1 psarocolius
1274	58	9.0	343	2	Q7Y113_9EMBE	Q7Y113 papilo chlo	1347	58	9.0	346	2	Q8M2V5_9EMBE	Q8m2v5 parocaria co
1275	58	9.0	343	2	Q7Y114_PASIL	Q7Y114 passerella	1348	58	9.0	346	2	Q8M2W2_1CTVI	Q8m2w2 icteria vir
1276	58	9.0	343	2	Q7Y115_PASIL	Q7Y115 passerella	1349	58	9.0	346	2	Q8M2W9_9EMBE	Q8m2w9 emberiza ep
1277	58	9.0	343	2	Q7Y116_PASIL	Q7Y116 passerella	1350	58	9.0	346	2	Q8M2X4_9EMBE	Q8m2x4 chloroepinga
1278	58	9.0	343	2	Q7Y117_PASIL	Q7Y117 passerella	1351	58	9.0	346	2	Q8M2X9_9EMBE	Q8m2x9 callamospiza
1279	58	9.0	343	2	Q7Y118_PASIL	Q7Y118 passerella	1352	58	9.0	346	2	Q8M2Y2_9EMBE	Q8m2y2 atlappetes s
1280	58	9.0	343	2	Q7Y119_PASIL	Q7Y119 passerella	1353	58	9.0	346	2	Q8M2Y3_9EMBE	Q8m2y3 atlapetes s
1281	58	9.0	343	2	Q7Y120_9EMBE	Q7Y120 zontotrichia	1354	58	9.0	346	2	Q8M456_9EMBE	Q8m456 zontotrichia
1282	58	9.0	343	2	Q7Y121_SPIAR	Q7Y121 spizella ar	1355	58	9.0	346	2	Q8SE19_9ICTE	Q8se19 psarocolius
1283	58	9.0	343	2	Q7Y122_PASIL	Q7Y122 passerella	1356	58	9.0	346	2	Q8SEU3_9ICTE	Q8seu3 psarocolius
1284	58	9.0	343	2	Q7Y123_PASIL	Q7Y123 passerella	1357	58	9.0	346	2	Q8SIR5_9PASE	Q8sir5 petronia de
1285	58	9.0	343	2	Q7Y124_PASIL	Q7Y124 passerella	1358	58	9.0	346	2	Q8SIS4_9PASE	Q8sis4 quelea quel
1286	58	9.0	345	2	Q8CMH5_SYNEL	Q8cmh5 synechococc	1359	58	9.0	346	2	Q8SK74_9ICTE	Q8sk74 gymnostinop
1287	58	9.0	345	2	Q8CM18_SYNEL	Q8cm18 synechococc	1360	58	9.0	346	2	Q8SK75_9ICTE	Q8sk75 gymnostinop
1288	58	9.0	345	2	Q8DKD0_SYNEL	Q8dkd0 synechococc	1361	58	9.0	346	2	Q8SK77_9ICTE	Q8sk77 gymnostinop
1289	58	9.0	345	2	Q8DMA6_SYNEL	Q8dma6 synechococc	1362	58	9.0	346	2	Q8SK78_PSADE	Q8sk78 psarocolius
1290	58	9.0	345	2	Q8G8L2_9EMBE	Q8g8l2 haplospiza	1363	58	9.0	346	2	Q8SK80_PSADE	Q8sk80 psarocolius
1291	58	9.0	346	1	NU2M_ANAC	Q63767 anas acuta	1364	58	9.0	346	2	Q8SK81_PSADE	Q8sk81 psarocolius
1292	58	9.0	346	1	NU2M_ANAM	Q63794 anas americ	1365	58	9.0	346	2	Q8SK82_9ICTE	Q8sk82 psarocolius
1293	58	9.0	346	1	NU2M_ANACA	Q63796 anas capens	1366	58	9.0	346	2	Q8SK83_9ICTE	Q8sk83 psarocolius
1294	58	9.0	346	1	NU2M_ANAFA	Q63797 anas falcat	1367	58	9.0	346	2	Q8SK89_9CORV	Q8s0a9 viroclanius
1295	58	9.0	346	1	NU2M_ANAFO	Q63775 anas formos	1368	58	9.0	346	2	Q8SK83_9ICTE	Q8sk83 psarocolius
1296	58	9.0	346	1	NU2M_ANAPE	Q63798 anas penelo	1369	58	9.0	346	2	Q8SK85_9ICTE	Q8sk85 ammodramus
1297	58	9.0	346	1	NU2M_STRCA	Q21398 struthio ca	1370	58	9.0	346	2	Q8G8K6_9EMBE	Q8g8k6 ammodramus
1298	58	9.0	346	2	Q674V2_PODCA	Q674v2 podocoryne	1371	58	9.0	346	2	Q8G8K8_9EMBE	Q8g8k8 pipilo fusc
1299	58	9.0	346	2	Q8DKX8_SYNEL	Q8dkx8 synechococc	1372	58	9.0	346	2	Q8G8L0_MELMO	Q8g8l0 melospiza m
1300	58	9.0	346	2	Q63768_ANAAU	Q63768 anas auchla	1373	58	9.0	346	2	Q8G8L0_SPIBR	Q8g8l0 spizella br
1301	58	9.0	346	2	Q63769_ANAAU	Q63769 anas auchla	1374	58	9.0	346	2	Q8G8M9_9FRIN	Q8g8m9 peucedramus
1302	58	9.0	346	2	Q63771_ANACH	Q63771 anas chlozo	1375	58	9.0	346	2	Q8G8M9_9FRIN	Q8g8m9 peucedramus
1303	58	9.0	346	2	Q63772_9AVES	Q63772 anas caroli	1376	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1304	58	9.0	346	2	Q63773_9AVES	Q63773 anas cyano	1377	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1305	58	9.0	346	2	Q63774_9AVES	Q63774 anas erythr	1378	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1306	58	9.0	346	2	Q63777_9AVES	Q63777 anas hotten	1379	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1307	58	9.0	346	2	Q63779_9AVES	Q63779 anas platat	1380	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1308	58	9.0	346	2	Q63780_9AVES	Q63780 anas puna	1381	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1309	58	9.0	346	2	Q63781_9AVES	Q63781 anas querqu	1382	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1310	58	9.0	346	2	Q63782_9AVES	Q63782 anas smithi	1383	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1311	58	9.0	346	2	Q63783_9AVES	Q63783 specularia	1384	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1312	58	9.0	346	2	Q63784_9AVES	Q63784 anas sparsa	1385	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1313	58	9.0	346	2	Q63785_9AVES	Q63785 anas superc	1386	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1314	58	9.0	346	2	Q63790_9AVES	Q63790 aescornis	1387	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1315	58	9.0	346	2	Q63793_9AVES	Q63793 lophonetta	1388	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1316	58	9.0	346	2	Q63802_9AVES	Q63802 sarkidiorni	1389	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1317	58	9.0	346	2	Q63804_9AVES	Q63804 tadorna tad	1390	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1318	58	9.0	346	2	Q63955_9AVES	Q63955 anas zonorh	1391	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1319	58	9.0	346	2	Q63967_9AVES	Q63967 anas bahame	1392	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1320	58	9.0	346	2	Q63970_9AVES	Q63970 anas flavir	1393	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1321	58	9.0	346	2	Q63975_9AVES	Q63975 anas gibber	1394	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1322	58	9.0	346	2	Q63978_9AVES	Q63978 anas clypea	1395	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1323	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1396	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1324	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1397	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1325	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1398	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1326	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1399	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1327	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1400	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1328	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1401	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1329	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1402	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1330	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1403	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1331	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1404	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1332	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1405	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1333	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1406	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1334	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1407	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1335	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1408	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1336	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1409	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1337	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1410	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1338	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1411	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1339	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1412	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1340	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1413	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1341	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1414	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1342	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1415	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1343	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1416	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1344	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1417	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius
1345	58	9.0	346	2	Q63983_9AVES	Q63983 anas luzoni	1418	58	9.0	346	2	Q8G8K3_9ICTE	Q8g8k3 psarocolius

1419	58	9.0	472	2	Q4RGH9_TETNG	Q4rgh9 tetraodon n
1420	58	9.0	479	2	Q8DIU5_SYNEL	Q8diu5 synecococc
1421	58	9.0	484	2	Q9AQK9_9BACT	Q9aak9 prevotella
1422	58	9.0	487	1	CSN1_XENLA	Q6nts xenopus lae
1423	58	9.0	489	2	Q3UZO0_BURP1	Q3iqz0 burkholderi
1424	58	9.0	492	2	Q5PFM1_GLUOX	Q5fpm1 gluconobact
1425	58	9.0	504	2	Q8BIF4_MOUSE	Q8bif4 mus musculus
1426	58	9.0	521	2	Q7SXB6_BRARE	Q7sxb6 brachydanio
1427	58	9.0	536	2	Q9SPJ5_DICDI	Q9spj5 dictyosteli
1428	58	9.0	543	2	Q67SV0_SYMTH	Q67sv0 symbiobacte
1429	58	9.0	544	2	Q33OX7_9GAMM	Q33qx7 shewanella
1430	58	9.0	545	2	Q2W9X9_MAGSA	Q2w9x9 magnetospir
1431	58	9.0	552	2	Q8DHL8_SYNEL	Q8dhl8 synecococc
1432	58	9.0	569	2	Q4QDG9_LEIMA	Q4qdg9 leishmania
1433	58	9.0	572	1	MPIP3_XENLA	P30311 xenopus lae
1434	58	9.0	585	2	Q9YHU3_FUGRU	Q9yhu3 fugu rubrip
1435	58	9.0	588	2	Q4P2X7_USTWA	Q4px7 ustilago ma
1436	58	9.0	588	2	Q55ZA9_CRYNE	Q55za9 cryptococcu
1437	58	9.0	589	1	ZN131_PONPY	Q5rau9 pongo pygma
1438	58	9.0	596	2	Q5RAL5_PONPY	Q5ral5 pongo pygma
1439	58	9.0	602	2	Q3UZ32_MOUSE	Q3uz32 mus musculus
1440	58	9.0	603	2	Q22787_ARATH	Q22787 arabidopsis
1441	58	9.0	603	2	Q4RSD5_TETNG	Q4rsd5 tetraodon n
1442	58	9.0	606	2	Q3TDM4_MOUSE	Q3tdw4 mus musculus
1443	58	9.0	610	2	Q8CC52_MOUSE	Q8cc52 mus musculus
1444	58	9.0	629	2	Q4QOQ4_LEIMA	Q4qoq4 leishmania
1445	58	9.0	635	2	Q3NCR3_9PROT	Q3ncr3 nitrosomona
1446	58	9.0	654	2	Q4H828_9DELO	Q4h828 deinococcus
1447	58	9.0	673	2	Q6PLT6_CANGA	Q6plt6 candida gla
1448	58	9.0	679	2	Q6NNW4_DROME	Q6nnw4 drosophila
1449	58	9.0	694	2	Q8DAH0_ARATH	Q8dah0 vibrio vuln
1450	58	9.0	706	2	Q8DAH0_VIBU	Q8dah0 vibrio vuln
1451	58	9.0	707	2	Q39912_GONPO	Q39912 gonyaulax p
1452	58	9.0	709	2	Q4DPE5_TRYCR	Q4dpe5 trypanosoma
1453	58	9.0	727	2	Q4TCA2_TETNG	Q4tca2 tetraodon n
1454	58	9.0	743	2	Q9SVR9_DROME	Q9svr9 drosophila
1455	58	9.0	744	2	Q9VD23_DROME	Q9vd23 drosophila
1456	58	9.0	764	2	Q3FKL8_9BURK	Q3fkl8 rhodospirax
1457	58	9.0	783	2	Q3UAU1_MOUSE	Q3uau1 mus musculus
1458	58	9.0	786	2	Q6A167_PEA	Q6a167 pisum sativ
1459	58	9.0	806	2	Q9FGM0_ARATH	Q9fgm0 arabidopsis
1460	58	9.0	810	2	Q6GUA3_MOUSE	Q6gua3 mus musculus
1461	58	9.0	828	2	Q4QAE1_LEIMA	Q4qae1 leishmania
1462	58	9.0	838	1	POSTN_MOUSE	Q62009 mus musculus
1463	58	9.0	841	2	Q5RBR3_PONPY	Q5rbr3 pongo pygma
1464	58	9.0	852	2	Q4MWV8_9SEPU	Q4mwv8 aspergillus
1465	58	9.0	908	2	Q675V8_9UROC	Q675v8 oikopleura
1466	58	9.0	909	2	Q4T520_TETNG	Q4t520 tetraodon n
1467	58	9.0	919	2	Q7L665_HUMAN	Q7l665 homo sapien
1468	58	9.0	919	2	Q75KM8_HUMAN	Q75km8 homo sapien
1469	58	9.0	921	2	Q75KM9_HUMAN	Q75km9 homo sapien
1470	58	9.0	941	2	Q9Y4C2_HUMAN	Q9y4c2 homo sapien
1471	58	9.0	962	2	Q61ZN8_CABER	Q61zn8 caenorhabdi
1472	58	9.0	994	2	Q8R381_MOUSE	Q8r381 mus musculus
1473	58	9.0	998	1	EPHA7_HUMAN	Q15375 homo sapien
1474	58	9.0	998	1	EPHA7_MOUSE	Q61772 mus musculus
1475	58	9.0	998	1	EPHA7_RAT	P54759 rattus norv
1476	58	9.0	998	2	Q8BSU8_MOUSE	Q8bsu8 mus musculus
1477	58	9.0	1023	1	PHF8_MOUSE	Q80tj7 mus musculus
1478	58	9.0	1037	1	ULK2_MOUSE	Q9qv01 mus musculus
1479	58	9.0	1037	2	Q3UG39_MOUSE	Q3ug39 mus musculus
1480	58	9.0	1037	2	Q3UIJ5_MOUSE	Q3uij5 mus musculus
1481	58	9.0	1060	2	Q3JG41_BURP1	Q3jg41 burkholderi
1482	58	9.0	1118	2	Q5SUB4_MOUSE	Q5sub4 mus musculus
1483	58	9.0	1129	2	Q4WZF0_ASEPU	Q4wzf0 aspergillus
1484	58	9.0	1131	2	Q7RWF1_NEUCR	Q7rwf1 neurospora
1485	58	9.0	1186	1	STBSL_HUMAN	Q9y2k9 homo sapien
1486	58	9.0	1205	2	Q3JRH4_BURP1	Q3jrh4 burkholderi
1487	58	9.0	1206	2	Q2XG17_PSEPU	Q2xg17 pseudomonas
1488	58	9.0	1292	2	Q9NJA5_BABBO	Q9nja5 babesia bov
1489	58	9.0	1423	1	SSH2_HUMAN	Q76176 homo sapien
1490	58	9.0	1514	2	Q6NN49_DROME	Q6nn49 drosophila
1491	58	9.0	1514	2	Q9NBK9_DROME	Q9nbk9 drosophila

1492	58	9.0	1514	2	Q9VUN0_DROME	Q9vun0 drosophila
1493	58	9.0	1639	1	LAMC1_DROME	P15215 drosophila
1494	58	9.0	1639	2	Q5BI30_DROME	Q5bi30 drosophila
1495	58	9.0	1739	2	Q4SRN8_TETNG	Q4arn8 tetraodon n
1496	58	9.0	1965	2	Q6FRD9_CANGA	Q6frd9 candida gla
1497	58	9.0	2101	2	Q61RX2_CABER	G61rx2 caenorhabdi
1498	58	9.0	2396	2	Q2YV00_STAAB	Q2yv00 staphylococ
1499	58	9.0	3550	2	Q9JUN2_MOUSE	Q9jjn2 mus musculus
1500	58	9.0	5376	1	ZAN_MOUSE	O88799 mus musculus

RESULT 1

Q6UXB2\_HUMAN PRELIMINARY; PRT; 119 AA.

ID Q6UXB2\_HUMAN

AC Q6UXB2;

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.

DT 21-FEB-2006, entry version 11.

DE DMC (VEGF co-regulated chemokine 1 precursor).

GN Name=VCCI; ORFNames=UNQ473;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=22887236; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H., Yanaura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D., Wood W.I., Godowski P.J., Gray A.M.;

RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."

RL Genome Res. 13:2265-2270(2003).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Lung and heart;

| RA | Medline=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M., Ussid T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S., Krzywicki M.I., Skalek U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;|  |  |  | | --- | --- | --- | | RT | "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." |  | | RL | Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). |  | | RN | [3] |  | | RP | NUCLEOTIDE SEQUENCE. |  | | RC | TISSUE=Lung and heart; |  | | RG | NIH MGC Project; |  | | RL | Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases. |  | |

```
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Weinstein E.J., Head R., Griggs D., Sun D., Westlin M., Mazzarella R.;
RT "Expression of VCC-1, a Novel Angiogenic Chemokine, Promotes Tumor
RL Growth.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RW [5]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Lung and heart;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY358433; AAQ88799.1; -; mRNA.
DR EMBL; BC112095; AAL12096.1; -; mRNA.
DR EMBL; AY598464; AAU04875.1; -; mRNA.
DR EMBL; BC093946; AAH93946.1; -; mRNA.
DR Ensembl; ENSG0000189377; Homo sapiens.
KW Signal.
FT SIGNAL 1 22 Potential.
FT CHAIN 23 119 VEGF co-regulated chemokine 1.
SQ SEQUENCE 119 AA; 13819 MW; F2D2FD68E847CC9B CRC64;

Query Match 100.0%; Score 644; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 9.3e-59;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLLLLPLMLSMWSSSLNPGVARGHRDRGQSRRLWLGSGGCECKDWFLRAP 60
DB 1 MKVLISLLLLPLMLSMWSSSLNPGVARGHRDRGQSRRLWLGSGGCECKDWFLRAP 60
QY 61 RRKFTVSGLPKQPCDHFHFGKGNVKTQRHQRHHRKPNKHSRACQOFLKQQLRSFALPL 119
DB 61 RRKFTVSGLPKQPCDHFHFGKGNVKTQRHQRHHRKPNKHSRACQOFLKQQLRSFALPL 119

RESULT 2
QY Q5UW37 MOUSE PRELIMINARY; PRT; 119 AA.
AC Q5UW37;
DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DT VEGF co-regulated chemokine 1 precursor.
DE Name=BC024561; Synonyms=Vccl1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Weinstein E.J., Head R., Griggs D., Sun D., Westlin M., Mazzarella R.;
RT "Expression of VCC-1, a Novel Angiogenic Chemokine, Promotes Tumor
RL Growth.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY598463; AAU04874.1; -; mRNA.
DR MGI; MGI:2387642; BC024561.
KW Signal.
FT SIGNAL 1 22 Potential.
FT CHAIN 23 119 VEGF co-regulated chemokine 1.
SQ SEQUENCE 119 AA; 13627 MW; 314BA9416EC40D9E CRC64;

Query Match 70.8%; Score 456; DB 2; Length 119;
Best Local Similarity 71.4%; Pred. No. 3e-39;
Matches 85; Conservative 9; Mismatches 25; Indels 0; Gaps 0;
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```
QY 1 MKVLISLLLLPLMLSMWSSSLNPGVARGHRDRGQSRRLWLGSGGCECKDWFLRAP 60
DB 1 MKVLISLLLLPLMLSMWSSSLNPGVARGHRDRGQSRRLWLGSGGCECKDWFLRAP 60
QY 61 RRKFTVSGLPKQPCDHFHFGKGNVKTQRHQRHHRKPNKHSRACQOFLKQQLRSFALPL 119
DB 61 RRKFTVSGLPKQPCDHFHFGKGNVKTQRHQRHHRKPNKHSRACQOFLKQQLRSFALPL 119

RESULT 3
QY Q8R3U6 MOUSE PRELIMINARY; PRT; 128 AA.
AC Q8R3U6;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE CDNA sequence BC024561.
GN Name=BC024561;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Weinstein E.J., Head R., Griggs D., Sun D., Westlin M., Mazzarella R.;
RT "Expression of VCC-1, a Novel Angiogenic Chemokine, Promotes Tumor
RL Growth.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC024561; AAH24561.1; -; mRNA.
DR Ensembl; ENSMUSG0000060188; Mus musculus.
DR MGI; MGI:2387642; BC024561.
SQ SEQUENCE 128 AA; 14043 MW; CCE67DA04D23D7DF CRC64;

Query Match 50.0%; Score 322; DB 2; Length 128;
Best Local Similarity 70.9%; Pred. No. 2.6e-25;
Matches 61; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 MKVLISLLLLPLMLSMWSSSLNPGVARGHRDRGQSRRLWLGSGGCECKDWFLRAP 60
DB 1 MKVLISLLLLPLMLSMWSSSLNPGVARGHRDRGQSRRLWLGSGGCECKDWFLRAP 60
QY 61 RRKFTVSGLPKQPCDHFHFGKGNVKTQRHQRHHRKPNKHSRACQOFLKQQLRSFALPL 119
DB 61 RRKFTVSGLPKQPCDHFHFGKGNVKTQRHQRHHRKPNKHSRACQOFLKQQLRSFALPL 119

RESULT 4
QY Q8R3U6 MOUSE PRELIMINARY; PRT; 128 AA.
AC Q8R3U6;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE CDNA sequence BC024561.
GN Name=BC024561;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Weinstein E.J., Head R., Griggs D., Sun D., Westlin M., Mazzarella R.;
RT "Expression of VCC-1, a Novel Angiogenic Chemokine, Promotes Tumor
RL Growth.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC024561; AAH24561.1; -; mRNA.
DR Ensembl; ENSMUSG0000060188; Mus musculus.
DR MGI; MGI:2387642; BC024561.
SQ SEQUENCE 128 AA; 14043 MW; CCE67DA04D23D7DF CRC64;

Query Match 50.0%; Score 322; DB 2; Length 128;
Best Local Similarity 70.9%; Pred. No. 2.6e-25;
Matches 61; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 MKVLISLLLLPLMLSMWSSSLNPGVARGHRDRGQSRRLWLGSGGCECKDWFLRAP 60
DB 1 MKVLISLLLLPLMLSMWSSSLNPGVARGHRDRGQSRRLWLGSGGCECKDWFLRAP 60
QY 61 RRKFTVSGLPKQPCDHFHFGKGNVKTQRHQRHHRKPNKHSRACQOFLKQQLRSFALPL 119
DB 61 RRKFTVSGLPKQPCDHFHFGKGNVKTQRHQRHHRKPNKHSRACQOFLKQQLRSFALPL 119
```

61 KRKATAVLGPPRKQCPCDHHVKGREK 86

## RESULT 4

Q52VJ8_CIOIN	PRELIMINARY;	PRT;	170 AA.
ID	Q52VJ8_CIOIN		
AC	Q52VJ8;		
DT	24-MAY-2005,		integrated into UniProtKB/TrEMBL.
DT	24-MAY-2005,		sequence version 1.
DT	07-FEB-2006,		entry version 2.
DE	Secreted protein (Fragment).		
DE	Secreted protein (Fragment).		
GN	Name=S7;		
OS	Ciona intestinalis.		
OC	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;		
OC	Phlebobranchia; Clonidae; Clona.		
OX	NCBI TaxID=7719;		

## RN [1]

RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=14;  
RC Khalturin K., Kuern U., Pinnow N., Bosch T.C.G.;  
RA "Towards a molecular code for individuality in the absence of MHC:  
RT screening for individually variable genes in the urochordate *Ciona*  
RT intestinalis.";   
RT Dev. Comp. Immunol. 0:0-0(2005).  
CC -----  
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CC -----  
DR EMBL; AY895028; AAY19463.1; -; mRNA.  
DR NON\_TER 1  
FT 170  
FT 170  
SQ SEQUENCE 170 AA; 19396 MW; 57776EDA757E2FFE CRC64;

Query Match	Score 81:	DB 2:	Length 170:
12.6%			

Query Match	12.8%	Score 01, SS 2, Length 170,
Best Local Similarity	27.9%;	Pred. NO. 3.7;
Matches 31;	Conservative 15;	Mismatches 37;
Indels 28;	Gaps 5;	

**Qy** 1 MKVLI-----SSLLILLPLMLMSWVSSLNPGVARGHRRDQGASRRWLQEGQE 49  
|::|| :| ||||: : | || : |  
**Db** 1 MRILLIILTIIVSFATQSLSLPLLLPRLPs-----RSSCSRGCSNAHCVRG--V 51

**Qy** 50 CECKDWFLR-----APRRKFMVTSGLPKKQCPCDHF--GNVKTRHQH 92  
||| : || | : : : : : : : : : :  
**Db** 52 CECURYFTRGLGCVADSAVFSGTGLTVRSPDCGYKCIGKARCERFERH 108  
||| : || | : : : : : : : : : :

## RESULT 5

Q52VK0_CIOIN	PRELIMINARY;	PRT; 170 AA.
ID Q52VK0_CIOIN		
AC Q52VK0;		
DT 24-MAY-2005,	integrated into UniProtKB/TrEMBL.	
DT 24-MAY-2005,	sequence version 1.	
DT 07-FEB-2006,	entry version 2.	
DE	Secreted protein (Fragment).	
GN Name=S7;		
OS	Ciona intestinalis.	
OC Eukaryota; Metazoa;	Chordata; Urochordata; Ascidiacea; Enterogona;	
OC Phlebobranchia; Cionidae;	Ciona.	
OX NCBI TaxID=7719;		

```

OX      NCBI_TaxID=1113,
RN      [1]

```

RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=13;  
RA Khatluri K., Kuern U., Pinnow N., Bosch T.C.G.;  
RT "Towards a molecular code for individuality in the absence of MHC:  
RT screening for individually variable genes in the urochordate *Ciona*  
RT *intestinalis*.";  
RL Dev. Comp. Immunol. 0:0-0(2005).  
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CC -----  
DR EMBL: AY895026; AAV19461.1; -; mRNA.  
FT NON TER 1

FT	NON TER	170	170
SQ	SEQUENCE	170 AA;	19468 MW; 54140ED9161E2FFE CRC64;

Query Match 12.6% Score 81; DB 2; Length 170;

Best Local Similarity 27.9%; Pred.No. 3.7; Indels 28; Gaps 5;  
Matches 31; Conservative 15; Mismatches 37;

Qy 1 MKVLI-----SSLILLPLMLMSVSSLPNGVARGHRDRGQASRRWLQEGQE 49  
     |   |||  |   |||  |   |   |   |   |   |   |   |   |  
Db 1 MRILILLIIIVSFATSQLSLIPLLPRLPS-----RSSCSRGESNAHCRVG-V 51

Qy 50 CEKDWFLR-----APRRKFTMTVSGLPKKCPCDHPFK--GNVKTRHQRH 92  
     |   |   |   |   |   |   |   |   |   |   |   |   |   |  
Db 52 CENRYPTRLGVCAADRSAVFGTGLTVASPCCGYNKICIGKARCSPERFH 102  
     |   |   |   |   |   |   |   |   |   |   |   |   |   |

## RESULT 6

[illegible]

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ENBL: AY895024; AAY19459.1; -: mRNA.

DR InterPro: IPR006210: EGF.

DR InterPro: IPR0000742; EGF 3.

DK InterPro: IPR00742; EGF-like repeat; IPR00742; EGF-like repeat; DB InterPro: IPR013032; EGF-like repeat; IPR013032; EGF-like repeat

DK INCEFTIO; IFR013032; EGF\_like\_1eg:  
 DR SMART: SM00181: EGF: 4

DR SMARI; SM00181; EGF; 4.  
DR PROSITE, PS01196. EGF 3. UNKNOWN 5

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DR PROSITE; PS01186; EGF_2; UNKNOWN_5
DB PROSITE; PSE0026; EGF_3; 4

```

DR	PROSTITE; PS50026; EGF 3; 4.
ET	NON TER 207 207

FT	NON TER	397	397
SEQUENCE		307 22.	11555 MW.
CC			712C82E0EB01A97E CBC64.

Query Match

Best Local Similarity	27.9%;	Pred. No. 8.6;
Matches	31; Conservative	15; Mismatches 37; Indels 28; Gaps 5;

**QY** 1 MKVLI-----SSLLILLPLMLMSWVSSSLNPGVARGHRDQGASRRWLQEGQE 49  
|::|| :| | ||| : : | | | : |  
**db** 1 MRILLIILQIVSTASQLSLLPPLLPRPS-----RSSCRGCEENAHKRVG--V 51

50 CECYTWELP-----APPPKEMTVSGIPKKOCPDHEK--GNVKKTRHQPH 92

QY 50 CECNDWFLR-----AFRRKNFMIVSGLEKNQCCECHFR--GNVKNYKHAQNH 32

## RESULT 7

Q3CNY9 ALTAT  
ID Q3CNY9 ALTAT PRELIMINARY; PRT; 487 AA.

AC Q3CNY9;

DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.

DT 22-NOV-2005, sequence version 1.

DT 07-FEB-2006, entry version 3.

DE Outer membrane efflux protein precursor.

GN ORFNames=Pat1DRAFT 2339;  
DE Outer membrane efflux protein precursor;  
GN

GN OKFNAMIB=FACTIDNFI\_2333;



```
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR013032; EGF like reg.
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF00628; PHD; 1.
DR SMART; SM00249; PHD; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
DR PROSITE; PS00016; ZF_PHD_2; 1.
SQ SEQUENCE 188 AA; 21463 MW; 94330032F8B9274F5 CRC64;

Query Match 12.5%; Score 80.5; DB 2; Length 188;
Best Local Similarity 30.5%; Pred. No. 4.6;
Matches 25; Conservative 11; Mismatches 29; Indels 17; Gaps 6;

QY 49 ECB-KDWF-----LRAPRRKFTMTVSLPKKQCF-CDHFKNVKKTRQRRHR-----KPNK 98
Db 22 ECDICKDFHSGCVQVEHH---AADIVYHCNCPPIHGYPYMKKNNWRRHDYTEPND 78

QY 99 HSRACQ-----FLKQCQLRSFA 116
Db 79 GTRPVQAGTAVFVKELQARSFA 100

RESULT 10
QSRHD1 BRARE PRELIMINARY; PRT; 613 AA.
AC QSRHD1
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 21-DEC-2004, sequence version 1.
DE Novel protein (Sb:cb414) (Fragment).
GN Names=si:dkay-10506.2; Synonyms=DKEY-10506.2;
GN ORFNames=DKEY-10506.2-001;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Felan S.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL; BX537168; CA112074.1; -; Genomic DNA.
DR Ensembl; ENSDARG0000018111; Danio rerio.
DR ZFIN; ZDB-GENE-030131-9829; si:dkay-10506.2.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR013032; EGF like reg.
DR InterPro; IPR013129; TF_JmJC.
DR InterPro; IPR003347; TF_JmJC_AAH.
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF02373; JmJC; 1.
DR Pfam; PF00628; PHD; 1.
DR SMART; SM00558; JmJC; 1.
DR SMART; SM00249; PHD; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
DR PROSITE; PS00016; ZF_PHD_2; 1.
FT NON_TER 613
SQ SEQUENCE 613 AA; 70705 MW; 2F1F9F998C60F138 CRC64;

Query Match 12.5%; Score 80.5; DB 2; Length 613;
Best Local Similarity 30.5%; Pred. No. 15;
Matches 25; Conservative 11; Mismatches 29; Indels 17; Gaps 6;

QY 49 ECB-KDWF-----LRAPRRKFTMTVSLPKKQCF-CDHFKNVKKTRQRRHR-----KPNK 98
Db 22 ECDICKDFHSGCVQVEHH---AADIVYHCNCPPIHGYPYMKKNNWRRHDYTEPND 78
```

```
QY 99 HSRACQ-----FLKQCQLRSFA 116
Db 79 GTRPVQAGTAVFVKELQARSFA 100

RESULT 11
Q4BU62 BURVI PRELIMINARY; PRT; 844 AA.
AC Q4BU62
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Aldehyde dehydrogenase.
GN ORFNames=Bcep1808DRAFT_7356;
OS Burkholderia vietnamiensis G4.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=269482;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G4;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Burkholderia
RT vietnamiensis G4.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G4;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer P., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia vietnamiensis
RT G4.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G4;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
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CC
CC EMBL; AAHE02000001; EAM33087.1; -; Genomic DNA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002086; Ald_DH.
DR Pfam; PF00171; Aldedh; 1.
DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
SQ SEQUENCE 844 AA; 94149 MW; F0DE2BCBDB076A2 CRC64;

Query Match 12.4%; Score 80; DB 2; Length 844;
Best Local Similarity 27.4%; Pred. No. 23;
Matches 26; Conservative 10; Mismatches 37; Indels 22; Gaps 2;

QY 24 LNPGVARGHRDGRQASRRWLQGGQCECKDFLAPRRKFTMTVSLPKKQCFCDHFKN 83
Db 215 VRPLVRRAVRARDPADHREVR-----RASREARLVRDGLPRAGCRPD----- 256

QY 84 VKKTRHQRHRRKPKNHSRACQQLKQCQLRSFALP 118
Db 257 ----RDVAHRRPRRRHAPARQGRGRCAALRAAGRP 287

RESULT 12
```

```
Q61TA9 CAEBR
ID Q61TA9_CAEBR PRELIMINARY; PRT; 662 AA.
AC Q61TA9;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Hypothetical protein CBG05828 (Fragment).
GN Name=CBG05828;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
ON NCBI_TaxID=6238;
RX PubMed=14624247; DOI=10.1371/journal.pbio.0000045;
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AF16;
RA Stein L.D., Bao Z., Blasiar D., Blumenthal T., Brent M.R., Chen N.,
RA Chinwalla A., Clarke L., Clee C., Coghlan A., Coulson A.,
RA D'Eustachio P., Fitch D.H.A., Fulton L.A., Fulton R.E.,
RA Griffiths-Jones S., Harris T.W., Hillier L.W., Kamath R.,
RA Kuwabara P.E., Mardis E.R., Marra M.A., Miner T.L., Minx P.,
RA Mullikin J.C., Plumb R.W., Rogers J., Schein J.E., Sohrmann M.,
RA Spieth J., Stajich J.E., Wei C., Willey D., Wilson R.K., Durbin R.,
RA Waterston R.H.;
RT "The genome sequence of Caenorhabditis briggsae: a platform for
RT comparative genomics."
RL PLOS Biol. 1:166-192(2003).
CC -!- CAUTION: The sequence shown here is derived from an
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CC -----
DR EMBL; CAAC01000028; CAE61852.1; -; Genomic DNA.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0045872; F:metal ion binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR006121; HeavyMe transpt.
DR InterPro; IPR001841; ZnF_RING.
DR PROSITE; PS01047; HMA_1; UNKNOWN_1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00899; ZF_RING_2; 1.
DR Complete proteome; Hypothetical protein; Metal-binding; Zinc;
KW Zinc-finger.
FT NON_TER 1 662
FT NON_TER 662 662
SQ SEQUENCE 662 AA; 78226 MW; 56012PFF3E9AAA0B CRC64;

Query Match 12.3%; Score 79.5; DB 2; Length 662;
Best Local Similarity 29.9%; Pred. No. 20;
Matches 20; Conservative 14; Mismatches 32; Indels 1; Gaps 1;

QY 32 HDRGQASRRWLQEGGCECKDWFAPRRKFMVTSGLPKKQCPDHFKNVKTTRHQ 91
: ||| ||| : : : : : : : : : : : : : : : : : : : : : : : :
DB 125 NWRGASQKWLAPRLKDEKWRAPRCYYILANRLCSDCILDDHQHGLVKSLHQL 184
: ||| ||| : : : : : : : : : : : : : : : : : : : : : : : :

QY 92 HHRKPK 98
DB 185 EY-TPEK 190

RESULT 13
Q52VJ5 CIOIN
ID Q52VJ5_CIOIN PRELIMINARY; PRT; 170 AA.
AC Q52VJ5;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Secreted protein (Fragment).
GN Name=S7;
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Cloniidae; Ciona.
ON NCBI_TaxID=7719;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=15;
RA Khalturin K., Kuern U., Pinnow N., Bosch T.C.G.;
RT "Towards a molecular code for individuality in the absence of MHC:
RT screening for individually variable genes in the urochordate Ciona
RT intestinalis."
RL Dev. Comp. Immunol. 0:0-0(2005).
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CC -----
DR EMBL; AY895031; AAV19466.1; -; mRNA.
FT NON_TER 1 170
FT NON_TER 170 170
SQ SEQUENCE 170 AA; 19492 MW; 5A0D96FC112C52DA CRC64;

Query Match 12.0%; Score 77.5; DB 2; Length 170;
Best Local Similarity 27.7%; Pred. No. 8.4;
Matches 31; Conservative 16; Mismatches 38; Indels 27; Gaps 5;

QY 1 MKVLI-----SSLLLLPLMLSMYSVSSINPGVARGHRDRGQASRRWLQEGGQE 49
: ||| ||| : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 MRILILIIQIVSFTASQSLPLLLPLPLPS-----RSSCSRGCKSNHCRVG--V 51
: ||| ||| : : : : : : : : : : : : : : : : : : : : : : : :

QY 50 CECKDWFIL-----APRRKFMVTSGLPKKQCPDHFKNVKTTRHQHRRK 95
: ||| ||| : : : : : : : : : : : : : : : : : : : : : : : :
DB 52 CECNRYTRGLYSCVADRSVFSCTGLTVRSTDCGNK-CIGKARCFERQ 102
: ||| ||| : : : : : : : : : : : : : : : : : : : : : : : :
```

## RESULT 14

```
Q6NDV5 RHOPA
ID Q6NDV5 RHOPA PRELIMINARY; PRT; 192 AA.
AC Q6NDV5;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Hypothetical protein.
DE Hypothetical protein.
GN OrderedLocusNames=RPAP7;
OS Rhodopseudomonas palustris.
OG Plasmid RPAP.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopseudomonas.
ON NCBI_TaxID=1076;
RX [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobet C., Torres y Torres J.L., Peres C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RT "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodopseudomonas palustris."
RL Nat. Biotechnol. 22:55-61(2004).
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CC -----
DR EMBL; BX571964; CAE25444.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein; Plasmid.
SQ SEQUENCE 192 AA; 23263 MW; 8D49063CA9701CA0 CRC64;

Query Match 12.0%; Score 77.5; DB 2; Length 192;
Best Local Similarity 28.4%; Pred. No. 9.5;
Matches 25; Conservative 14; Mismatches 30; Indels 19; Gaps 5;

QY 26 PGVARGHRDRGQASRRWLQEGGCECKDWFAPRRKFMVTSGLPKKQCPDHFKNV 85
: ||| ||| : : : : : : : : : : : : : : : : : : : : : : : :
```





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OM protein - protein search, using sw model

Run on: August 3, 2006, 09:54:47 ; Search time 26 Seconds  
(without alignments)  
400.621 Million cell updates/sec

Title: US-10-015-967-2

Perfect score: 644

Sequence: 1 MKVLISLLLLPLMLMSV.....SRACQQLKCOLRSPALPL 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents\_AA:\*

1: /EMC\_Celerra\_SID33/ptodata/2/iaa/5\_COMB.pep:\*

2: /EMC\_Celerra\_SID33/ptodata/2/iaa/6\_COMB.pep:\*

3: /EMC\_Celerra\_SID33/ptodata/2/iaa/7\_COMB.pep:\*

4: /EMC\_Celerra\_SID33/ptodata/2/iaa/H\_COMB.pep:\*

5: /EMC\_Celerra\_SID33/ptodata/2/iaa/PCUR\_COMB.pep:\*

6: /EMC\_Celerra\_SID33/ptodata/2/iaa/RE\_COMB.pep:\*

7: /EMC\_Celerra\_SID33/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	644	100.0	119	2	US-09-991-181-165
2	644	100.0	119	2	US-09-990-444-165
3	644	100.0	119	2	US-09-997-333-165
4	644	100.0	119	2	US-09-992-598-165
5	644	100.0	119	2	US-09-989-735-165
6	644	100.0	119	3	US-09-989-726-165
7	644	100.0	119	3	US-09-997-514-165
8	644	100.0	119	3	US-09-989-728-165
9	644	100.0	119	3	US-09-997-349-165
10	644	100.0	119	3	US-09-997-653-165
11	644	100.0	119	3	US-09-989-293A-165
12	610	94.7	112	2	US-09-621-976-3926
13	84.5	13.1	620	2	US-09-252-991A-17301
14	76	11.8	456	2	US-09-248-796A-19808
15	74	11.5	131	2	US-09-248-796A-23977
16	74	11.5	629	2	US-09-252-991A-16777
17	73.5	11.4	66	2	US-09-497-822C-14
18	73.5	11.4	70	1	US-07-737-736B-3
19	72.5	11.3	724	2	US-09-252-991A-28517
20	72.5	11.3	752	2	US-10-104-047-2991
21	72	11.2	689	2	US-09-252-991A-19258
22	71.5	11.1	108	2	US-09-350-933A-92
23	70.5	10.9	146	2	US-09-893-737-42
24	70.5	10.9	420	2	US-09-252-991A-27610
25	70	10.9	188	1	US-08-469-427A-11
26	70	10.9	188	1	US-08-609-443B-11

188	1	US-08-569-063C-11	Sequence 11, Appl
188	2	US-08-795-430-57	Sequence 57, Appl
188	2	US-08-851-896-11	Sequence 11, Appl
188	2	US-09-355-700-57	Sequence 57, Appl
188	2	US-09-431-888-6	Sequence 6, Appl
188	2	US-08-671-573B-56	Sequence 56, Appl
188	2	US-09-438-046-12	Sequence 12, Appl
188	2	US-09-631-092B-56	Sequence 56, Appl
188	2	US-09-468-647A-107	Sequence 107, Appl
188	2	US-09-534-376A-57	Sequence 57, Appl
188	2	US-09-214-982-34	Sequence 34, Appl
188	2	US-09-795-006A-117	Sequence 117, Appl
626	2	US-09-252-991A-30510	Sequence 30510, A
446	1	US-08-307-444A-5	Sequence 5, Appl
446	1	US-08-587-389-5	Sequence 5, Appl
456	1	US-08-307-444A-3	Sequence 3, Appl
456	1	US-08-307-444A-4	Sequence 4, Appl
456	1	US-08-587-389-3	Sequence 3, Appl
456	1	US-08-587-389-4	Sequence 4, Appl
475	1	US-08-307-444A-1	Sequence 1, Appl
475	1	US-08-307-444A-2	Sequence 2, Appl
475	1	US-08-587-389-1	Sequence 1, Appl
475	1	US-08-587-389-2	Sequence 2, Appl
476	1	US-08-014-723-1	Sequence 1, Appl
476	1	US-08-014-723-2	Sequence 2, Appl
476	1	US-08-014-723-18	Sequence 18, Appl
476	1	US-08-110-011A-1	Sequence 1, Appl
476	1	US-08-110-011A-2	Sequence 2, Appl
476	1	US-08-110-011A-18	Sequence 18, Appl
494	1	US-08-014-723-14	Sequence 14, Appl
494	1	US-08-014-723-16	Sequence 16, Appl
494	1	US-08-110-011A-14	Sequence 14, Appl
494	1	US-08-110-011A-16	Sequence 16, Appl
497	1	US-08-312-870-3	Sequence 3, Appl
497	2	US-09-331-793-4	Sequence 4, Appl
498	1	US-08-733-564-2	Sequence 2, Appl
516	2	US-09-509-994-1	Sequence 1, Appl
516	2	US-09-509-994-2	Sequence 2, Appl
568	2	US-09-252-991A-27039	Sequence 27039, A
575	1	US-08-261-206A-59	Sequence 59, Appl
575	1	US-08-312-870-1	Sequence 1, Appl
575	1	US-08-170-290A-54	Sequence 54, Appl
575	2	US-09-880-484D-2	Sequence 2, Appl
575	2	US-10-438-648-2	Sequence 2, Appl
575	2	US-09-949-002-296	Sequence 296, Appl
575	7	5466668-6	Patent No. 5466668
682	2	US-09-949-002-436	Sequence 436, Appl
229	2	US-09-252-991A-24867	Sequence 24867, A
261	2	US-09-252-991A-21486	Sequence 21486, A
1077	2	US-10-104-047-2291	Sequence 2291, Ap
427	2	US-08-764-870-11	Sequence 11, Appl
427	2	US-09-949-016-5933	Sequence 5933, Ap
427	2	US-09-509-482D-12	Sequence 12, Appl
450	2	US-09-509-482D-10	Sequence 10, Appl
455	2	US-09-949-016-9487	Sequence 9487, Ap
477	2	US-09-509-482D-9	Sequence 9, Appl
451	2	US-09-252-991A-25804	Sequence 25804, A
613	2	US-09-252-991A-22424	Sequence 22424, A
863	2	US-09-252-991A-21831	Sequence 21831, A
521	2	US-09-252-991A-25430	Sequence 25430, A
690	2	US-09-252-991A-16715	Sequence 16715, A
298	2	US-09-252-991A-18133	Sequence 18133, A
1798	2	US-09-561-709B-11	Sequence 11, Appl
209	2	US-09-252-991A-21256	Sequence 21256, A
333	2	US-09-252-991A-18431	Sequence 18431, A
423	2	US-09-919-497-86	Sequence 86, Appl
178	2	US-09-252-991A-32482	Sequence 32482, A
518	2	US-09-252-991A-25203	Sequence 25203, A
106	2	US-09-950-933A-95	Sequence 96, Appl
201	2	US-09-252-991A-23308	Sequence 23308, A
279	2	US-09-252-991A-24954	Sequence 24954, A
342	2	US-09-252-991A-23254	Sequence 23254, A
190	2	US-09-252-991A-19049	Sequence 19049, A

100	65	10.1	274	2	US-09-252-991A-19575	Sequence 19575, A	173	60.5	9.4	188	2	US-09-252-991A-22379	Sequence 22379, A
101	65	10.1	407	2	US-09-252-991A-25732	Sequence 25732, A	174	60.5	9.4	210	1	US-08-770-379-1	Sequence 1, Appl
102	65	10.1	629	2	US-09-949-016-7746	Sequence 7746, Ap	175	60.5	9.4	210	2	US-09-230-637-23	Sequence 23, Appl
103	65	10.1	1798	2	US-09-845-583A-8	Sequence 8, Appl	176	60.5	9.4	278	2	US-09-252-991A-20792	Sequence 20792, A
104	65	10.1	1798	2	US-09-917-254-87	Sequence 87, Appl	177	60.5	9.4	297	2	US-09-252-991A-18170	Sequence 18170, A
105	64.5	10.0	235	2	US-09-949-016-7903	Sequence 7903, Ap	178	60.5	9.4	462	2	US-09-252-991A-20410	Sequence 20410, A
106	64.5	10.0	382	2	US-09-252-991A-28833	Sequence 28833, A	179	60.5	9.4	471	2	US-09-252-991A-19620	Sequence 19620, A
107	64.5	10.0	525	2	US-09-252-991A-17506	Sequence 17506, A	180	60.5	9.4	487	2	US-09-252-991A-29118	Sequence 29118, A
108	64.5	10.0	593	2	US-09-252-991A-31061	Sequence 31061, A	181	60.5	9.4	504	2	US-09-252-991A-22272	Sequence 22272, A
109	64.5	10.0	921	2	US-09-252-991A-17504	Sequence 17504, A	182	60.5	9.4	535	2	US-09-252-991A-18410	Sequence 18410, A
110	64	9.9	132	2	US-09-270-767-59725	Sequence 59725, A	183	60.5	9.4	541	2	US-09-252-991A-17206	Sequence 17206, A
111	64	9.9	154	2	US-09-270-767-44301	Sequence 44301, A	184	60.5	9.4	894	2	US-09-252-991A-30397	Sequence 30397, A
112	64	9.9	214	2	US-09-963-156A-1	Sequence 1, Appl	185	60.5	9.4	1019	1	US-08-296-014A-4	Sequence 4, Appl
113	64	9.9	366	2	US-09-252-991A-23504	Sequence 23504, A	186	60.5	9.4	1019	1	US-08-596-405-4	Sequence 4, Appl
114	64	9.9	460	3	US-09-958-359-26	Sequence 26, Appl	187	60.5	9.4	1019	1	US-08-877-620-4	Sequence 4, Appl
115	64	9.9	1854	2	US-09-949-016-11625	Sequence 11625, A	188	60.5	9.4	1019	2	US-09-287-368-4	Sequence 4, Appl
116	63.5	9.9	106	2	US-09-950-933A-79	Sequence 79, Appl	189	60.5	9.4	1019	2	US-09-636-795-4	Sequence 4, Appl
117	63.5	9.9	148	2	US-09-252-991A-18652	Sequence 18652, A	190	60.5	9.4	1019	2	US-10-183-992-8	Sequence 8, Appl
118	63	9.8	267	2	US-09-252-991A-23411	Sequence 23411, A	191	60	9.3	80	2	US-09-270-767-37893	Sequence 37893, A
119	63	9.8	302	2	US-09-252-991A-25724	Sequence 25724, A	192	60	9.3	80	2	US-09-270-767-37893	Sequence 37893, A
120	63	9.8	371	2	US-09-538-092-630	Sequence 630, App	193	60	9.3	170	2	US-09-270-767-37893	Sequence 37893, A
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122	62.5	9.7	403	2	US-09-949-016-7412	Sequence 7412, Ap	195	60	9.3	612	2	US-09-252-991A-30072	Sequence 30072, A
123	62.5	9.7	414	1	US-08-255-471-9	Sequence 9, Appl	196	60	9.3	636	2	US-09-252-991A-30707	Sequence 30707, A
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125	62	9.6	116	2	US-07-757-022B-38	Sequence 98, Appl	198	60	9.3	903	2	US-10-104-047-2951	Sequence 2951, Ap
126	62	9.6	116	2	US-07-757-022B-110	Sequence 110, App	199	60	9.3	932	2	US-09-252-991A-26175	Sequence 26175, A
127	62	9.6	116	2	US-07-757-022B-120	Sequence 120, App	200	60	9.3	932	1	US-08-450-332-2	Sequence 2, Appl
128	62	9.6	116	2	US-07-757-022B-138	Sequence 138, App	201	60	9.3	3038	1	US-08-637-640-2	Sequence 2, Appl
129	62	9.6	116	3	US-10-124-557-98	Sequence 98, Appl	202	60	9.3	3038	1	US-09-004-406C-2	Sequence 2, Appl
130	62	9.6	116	3	US-10-124-557-110	Sequence 110, App	203	59.5	9.2	104	2	US-09-732-210-464	Sequence 464, App
131	62	9.6	116	3	US-10-124-557-138	Sequence 138, App	204	59.5	9.2	154	2	US-09-270-767-42472	Sequence 42472, A
132	62	9.6	116	3	US-09-252-991A-17166	Sequence 17166, A	205	59.5	9.2	179	2	US-09-252-991A-26223	Sequence 26223, A
133	62	9.6	151	2	US-09-252-991A-21747	Sequence 21747, A	206	59.5	9.2	254	2	US-09-270-767-46094	Sequence 46094, A
134	62	9.6	959	2	US-07-757-022B-74	Sequence 74, Appl	207	59.5	9.2	297	2	US-09-252-991A-26587	Sequence 26587, A
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136	62	9.6	1270	2	US-07-757-022B-44	Sequence 44, Appl	209	59.5	9.2	356	2	US-09-252-991A-26571	Sequence 26571, A
137	62	9.6	1270	2	US-07-757-022B-44	Sequence 44, Appl	210	59.5	9.2	447	2	US-09-981-181-369	Sequence 369, App
138	62	9.6	1270	3	US-10-124-557-44	Sequence 44, Appl	211	59.5	9.2	447	2	US-09-990-444-369	Sequence 369, App
139	62	9.6	1670	2	US-09-949-016-5883	Sequence 5883, Ap	212	59.5	9.2	447	2	US-09-997-333-369	Sequence 369, App
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141	61.5	9.5	121	2	US-09-513-999C-4364	Sequence 4364, Ap	214	59.5	9.2	447	2	US-09-989-735-369	Sequence 369, App
142	61.5	9.5	226	2	US-09-252-991A-27728	Sequence 27728, A	215	59.5	9.2	447	3	US-09-989-726-369	Sequence 369, App
143	61.5	9.5	232	1	US-08-824-996-9	Sequence 9, Appl	216	59.5	9.2	447	3	US-09-987-514-369	Sequence 369, App
144	61.5	9.5	232	2	US-08-463-968-5	Sequence 5, Appl	217	59.5	9.2	447	3	US-09-989-728-369	Sequence 369, App
145	61.5	9.5	244	2	US-09-252-991A-30138	Sequence 30138, A	218	59.5	9.2	447	3	US-09-997-349-369	Sequence 369, App
146	61.5	9.5	249	2	US-09-252-991A-32292	Sequence 32292, A	219	59.5	9.2	447	3	US-09-997-653-369	Sequence 369, App
147	61.5	9.5	252	1	US-08-052-205-9	Sequence 9, Appl	220	59.5	9.2	491	2	US-09-989-293A-369	Sequence 369, App
148	61.5	9.5	252	1	US-08-595-974-9	Sequence 9, Appl	221	59.5	9.2	491	2	US-09-328-352-5438	Sequence 5438, Ap
149	61.5	9.5	269	2	US-09-252-991A-26344	Sequence 26344, A	222	59.5	9.2	529	2	US-09-252-991A-18245	Sequence 18245, A
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151	61.5	9.5	369	1	US-08-052-205-4	Sequence 4, Appl	224	59.5	9.2	591	2	US-09-252-991A-20951	Sequence 20951, A
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157	61.5	9.5	691	2	US-10-282-162-20	Sequence 20, Appl	230	59	9.2	180	2	US-09-949-016-10723	Sequence 10723, A
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159	61.5	9.5	694	2	US-09-313-942-22	Sequence 22, Appl	232	59	9.2	193	2	US-09-370-838-206	Sequence 206, App
160	61.5	9.5	694	2	US-10-282-162-18	Sequence 18, Appl	233	59	9.2	197	2	US-09-854-133-206	Sequence 206, App
161	61.5	9.5	694	2	US-10-282-162-22	Sequence 22, Appl	234	59	9.2	197	2	US-09-673-395A-514	Sequence 514, App
162	61	9.5	71	2	US-09-894-882-125	Sequence 125, App	235	59	9.2	228	2	US-09-643-597-174	Sequence 174, App
163	61	9.5	136	2	US-09-513-999C-7844	Sequence 7844, Ap	236	59	9.2	238	2	US-09-480-884A-174	Sequence 174, App
164	61	9.5	161	2	US-09-252-991A-30023	Sequence 30023, A	237	59	9.2	238	2	US-09-542-615A-174	Sequence 174, App
165	61	9.5	339	2	US-10-101-464A-899	Sequence 899, App	238	59	9.2	238	2	US-09-606-421B-174	Sequence 174, App
166	61	9.5	428	2	US-09-252-991A-25955	Sequence 25955, A	239	59	9.2	238	2	US-09-466-396A-174	Sequence 174, App
167	61	9.5	1014	2	US-09-762-724-2	Sequence 2, Appl	240	59	9.2	238	2	US-09-476-496A-174	Sequence 174, App
168	60.5	9.4	90	2	US-09-252-991A-28743	Sequence 28743, A	241	59	9.2	238	2	US-09-630-940B-174	Sequence 174, App
169	60.5	9.4	106	2	US-09-950-933A-78	Sequence 78, Appl	242	59	9.2	238	2	US-10-007-700-174	Sequence 174, App
170	60.5	9.4	115	2	US-09-270-767-33388	Sequence 33388, A	243	59	9.2	238	2	US-09-252-991A-28573	Sequence 28573, A
171	60.5	9.4	115	2	US-09-270-767-48605	Sequence 48605, A	244	59	9.2	259	2	US-09-270-767-56884	Sequence 56884, A
172	60.5	9.4	162	2	US-09-328-352-5594	Sequence 5594, Ap	245	59	9.2	305	2		

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247	59	9.2	372	2	US-09-252-991A-32717	Sequence 32717, A	320	58	9.0	998	1	US-08-449-645A-17	Sequence 17, Appl
248	59	9.2	402	2	US-09-029-755C-5	Sequence 5, Appli	321	58	9.0	998	1	US-08-702-367A-17	Sequence 17, Appl
249	59	9.2	402	2	US-09-252-991A-24729	Sequence 24729, A	322	58	9.0	998	2	US-08-368-776A-2	Sequence 2, Appli
250	59	9.2	416	2	US-09-270-767-41646	Sequence 41646, A	323	58	9.0	998	2	US-09-949-016-6501	Sequence 6501, Ap
251	59	9.2	487	2	US-09-252-991A-18280	Sequence 18280, A	324	58	9.0	998	2	US-09-378-759-17	Sequence 17, Appl
252	59	9.2	780	2	US-09-252-991A-18846	Sequence 18846, A	325	58	9.0	998	5	US-10-073-064-2	Sequence 2, Appli
253	59	9.2	871	2	US-09-773-426A-3	Sequence 3, Appli	326	58	9.0	998	5	PCT-US95-04681-17	Sequence 17, Appl
254	59	9.2	871	2	US-10-314-881-3	Sequence 3, Appli	327	58	9.0	998	5	PCT-US96-00419-2	Sequence 2, Appli
255	59	9.2	871	2	US-09-495-823-3	Sequence 3, Appli	328	58	9.0	1005	2	US-09-949-016-9901	Sequence 9901, Ap
256	59	9.2	871	3	US-10-426-776-11	Sequence 11, Appl	329	58	9.0	1037	2	US-09-428-711A-21	Sequence 21, Appl
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259	59	9.2	1608	2	US-09-964-956-61	Sequence 61, Appl	332	58	9.0	2955	1	US-08-443-260-3	Sequence 3, Appli
260	59	9.2	1611	2	US-09-668-673B-16	Sequence 16, Appl	333	58	9.0	2955	2	US-08-442-805A-3	Sequence 3, Appli
261	59	9.2	1611	2	US-10-389-532-16	Sequence 16, Appl	334	58	9.0	2955	2	US-08-443-900A-3	Sequence 3, Appli
262	59	9.2	1788	2	US-09-964-956-60	Sequence 60, Appl	335	58	9.0	2955	2	US-08-444-818-124	Sequence 124, App
263	59	9.2	2641	2	US-09-964-956-63	Sequence 63, Appl	336	58	9.0	2955	2	US-08-249-843-3	Sequence 3, Appli
264	59	9.2	2811	2	US-09-964-956-27	Sequence 27, Appl	337	58	9.0	2995	2	US-08-444-818-138	Sequence 138, App
265	59	9.2	2814	2	US-09-964-956-25	Sequence 25, Appl	338	58	9.0	3011	1	US-08-833-678A-6	Sequence 6, Appli
266	58.5	9.1	81	2	US-09-621-976-6450	Sequence 6450, Ap	339	58	9.0	3011	2	US-08-444-818-177	Sequence 177, App
267	58.5	9.1	132	2	US-09-270-767-32010	Sequence 32010, A	340	58	9.0	3011	2	US-08-529-169A-6	Sequence 6, Appli
268	58.5	9.1	132	2	US-09-270-767-47227	Sequence 47227, A	341	58	9.0	3011	2	US-09-483-793-6	Sequence 6, Appli
269	58.5	9.1	138	2	US-09-252-991A-20349	Sequence 20349, A	342	58	9.0	3011	3	US-10-232-643-6	Sequence 6, Appli
270	58.5	9.1	170	2	US-09-252-991A-16827	Sequence 16827, A	343	57.5	8.9	128	2	US-09-252-991A-32567	Sequence 32567, A
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272	58.5	9.1	184	2	US-09-270-767-47196	Sequence 47196, A	345	57.5	8.9	145	2	US-09-270-767-54459	Sequence 54459, A
273	58.5	9.1	185	2	US-09-252-991A-21225	Sequence 21225, A	346	57.5	8.9	217	2	US-09-602-543-5	Sequence 5, Appli
274	58.5	9.1	198	2	US-09-252-991A-22691	Sequence 22691, A	347	57.5	8.9	218	2	US-09-252-991A-19579	Sequence 19579, A
275	58.5	9.1	208	2	US-09-252-991A-23874	Sequence 23874, A	348	57.5	8.9	231	2	US-09-252-991A-27366	Sequence 27366, A
276	58.5	9.1	302	2	US-09-252-991A-24042	Sequence 24042, A	349	57.5	8.9	232	2	US-08-807-992B-4	Sequence 4, Appli
277	58.5	9.1	328	2	US-09-252-991A-26593	Sequence 26593, A	350	57.5	8.9	235	2	US-09-602-543-4	Sequence 4, Appli
278	58.5	9.1	346	2	US-09-252-991A-26988	Sequence 26988, A	351	57.5	8.9	237	2	US-09-252-991A-18254	Sequence 18254, A
279	58.5	9.1	366	2	US-09-252-991A-22528	Sequence 22528, A	352	57.5	8.9	248	2	US-09-252-991A-30679	Sequence 30679, A
280	58.5	9.1	392	2	US-09-252-991A-27219	Sequence 27219, A	353	57.5	8.9	296	2	US-09-252-991A-17538	Sequence 17538, A
281	58.5	9.1	404	2	US-10-375-693-26	Sequence 26, Appl	354	57.5	8.9	377	2	US-09-252-991A-24649	Sequence 24649, A
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283	58.5	9.1	430	2	US-09-252-991A-33661	Sequence 32661, A	356	57.5	8.9	432	2	US-09-227-613-9	Sequence 9, Appli
284	58.5	9.1	430	2	US-10-029-180-32	Sequence 32, Appl	357	57.5	8.9	432	2	US-10-191-513A-9	Sequence 9, Appli
285	58.5	9.1	431	2	US-09-270-767-45143	Sequence 45143, A	358	57.5	8.9	465	2	US-09-439-261-40	Sequence 40, Appl
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287	58.5	9.1	490	2	US-10-183-992-2	Sequence 2, Appli	360	57.5	8.9	465	2	US-10-191-513A-38	Sequence 38, Appl
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289	58.5	9.1	977	2	US-09-252-991A-16655	Sequence 16655, A	362	57.5	8.9	564	2	US-09-252-991A-26890	Sequence 26890, A
290	58.5	9.1	1019	2	US-10-183-992-4	Sequence 4, Appli	363	57.5	8.9	709	2	US-08-937-067-12	Sequence 12, Appl
291	58.5	9.1	1101	2	US-09-561-709B-5	Sequence 5, Appli	364	57.5	8.9	890	3	US-09-958-359-34	Sequence 34, Appl
292	58.5	9.1	1761	2	US-09-561-709B-1	Sequence 1, Appli	365	57.5	8.9	955	2	US-10-094-749-2652	Sequence 2652, Ap
293	58	9.0	160	2	US-08-444-818-18	Sequence 18, Appl	366	57.5	8.9	1083	1	US-08-296-014A-2	Sequence 2, Appli
294	58	9.0	186	1	US-08-089-458B-6	Sequence 6, Appli	367	57.5	8.9	1083	1	US-08-596-405-2	Sequence 2, Appli
295	58	9.0	202	2	US-10-104-047-3917	Sequence 3917, Ap	368	57.5	8.9	1083	1	US-08-877-620-2	Sequence 2, Appli
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298	58	9.0	268	2	US-10-094-749-3060	Sequence 3060, Ap	371	57.5	8.9	1083	2	US-10-183-992-6	Sequence 6, Appli
299	58	9.0	276	2	US-09-252-991A-18128	Sequence 18128, A	372	57.5	8.9	2120	2	US-09-949-016-9768	Sequence 9768, Ap
300	58	9.0	394	2	US-09-949-016-6716	Sequence 6716, Ap	373	57	8.9	119	2	US-09-950-933A-63	Sequence 63, Appl
301	58	9.0	410	2	US-09-252-991A-30570	Sequence 30570, A	374	57	8.9	144	2	US-09-180-100-21	Sequence 21, Appl
302	58	9.0	427	2	US-09-949-016-9842	Sequence 9842, Ap	375	57	8.9	144	2	US-09-252-991A-21500	Sequence 21500, A
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305	58	9.0	530	2	US-09-252-991A-28311	Sequence 28311, A	378	57	8.9	156	2	US-10-031-607-9	Sequence 9, Appli
306	58	9.0	610	2	US-08-368-776A-3	Sequence 3, Appli	379	57	8.9	159	2	US-09-180-100-23	Sequence 23, Appl
307	58	9.0	610	3	US-10-073-064-3	Sequence 3, Appli	380	57	8.9	159	2	US-09-949-713-23	Sequence 23, Appl
308	58	9.0	610	5	PCT-US96-00419-3	Sequence 3, Appli	381	57	8.9	185	2	US-09-252-991A-17220	Sequence 17220, A
309	58	9.0	626	2	US-08-368-776A-5	Sequence 5, Appli	382	57	8.9	195	2	US-10-031-607-11	Sequence 11, Appl
310	58	9.0	626	5	US-10-073-064-5	Sequence 5, Appli	383	57	8.9	197	2	US-08-974-022-49	Sequence 49, Appl
311	58	9.0	626	5	PCT-US96-00419-5	Sequence 5, Appli	384	57	8.9	197	2	US-08-795-445A-49	Sequence 49, Appl
312	58	9.0	739	2	US-08-444-818-148	Sequence 148, App	385	57	8.9	197	2	US-08-974-186-49	Sequence 49, Appl
313	58	9.0	794	2	US-09-949-016-9883	Sequence 9883, Ap	386	57	8.9	197	2	US-08-795-446B-49	Sequence 49, Appl
314	58	9.0	811	1	US-08-426-627-2	Sequence 2, Appli	387	57	8.9	197	2	US-08-706-945D-135	Sequence 135, App
315	58	9.0	811	1	US-08-426-627-22	Sequence 22, Appl	388	57	8.9	197	2	US-08-577-788C-49	Sequence 49, Appl
316	58	9.0	993	2	US-08-368-776A-11	Sequence 11, Appl	389	57	8.9	197	2	US-08-577-788C-49	Sequence 49, Appl
317	58	9.0	993	3	US-10-073-064-11	Sequence 11, Appl	390	57	8.9	197	3	US-09-613-591F-132	Sequence 132, Appl
318	58	9.0	994	2	US-08-368-776A-12	Sequence 12, Appl	391	57	8.9	203	2	US-10-031-607-10	Sequence 10, Appl

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393	57	8.9	217	2	US-09-252-991A-28385	Sequence 28385, A	466	56	8.7	165	1	US-08-350-884-82	Sequence 82, Appl
394	57	8.9	218	2	US-09-252-991A-26852	Sequence 26852, A	467	56	8.7	165	1	US-08-709-173-82	Sequence 82, Appl
395	57	8.9	232	2	US-09-533-310B-4	Sequence 4, Appli	468	56	8.7	165	1	US-08-709-177-82	Sequence 82, Appl
396	57	8.9	235	2	US-09-489-039A-7180	Sequence 7180, Ap	469	56	8.7	174	2	US-09-854-133-426	Sequence 426, App
397	57	8.9	239	2	US-09-252-991A-32603	Sequence 32603, A	470	56	8.7	221	2	US-09-252-991A-31566	Sequence 31566, A
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399	57	8.9	289	2	US-09-042-785A-11	Sequence 11, Appl	472	56	8.7	297	2	US-09-252-991A-21551	Sequence 21551, A
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405	57	8.9	376	2	US-09-949-713-22	Sequence 22, Appl	478	56	8.7	313	1	US-08-487-231-45	Sequence 45, Appl
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407	57	8.9	416	2	US-09-487-558B-80	Sequence 80, Appl	480	56	8.7	313	2	US-09-201-912-45	Sequence 45, Appl
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411	57	8.9	508	2	US-09-949-016-9414	Sequence 9414, Ap	484	56	8.7	416	2	US-09-949-016-11669	Sequence 11669, A
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413	57	8.9	564	2	US-08-939-106-15	Sequence 15, Appl	486	56	8.7	417	2	US-09-690-359-20	Sequence 20, Appl
414	57	8.9	564	2	US-09-442-102-15	Sequence 15, Appl	487	56	8.7	417	5	PCT-US92-06965A-25	Sequence 25, Appl
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416	57	8.9	592	2	US-10-438-339-8	Sequence 8, Appl	489	56	8.7	422	2	US-10-104-047-2882	Sequence 2882, Ap
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419	57	8.9	790	2	US-09-252-991A-23247	Sequence 23247, A	492	56	8.7	428	2	US-09-905-125A-142	Sequence 142, App
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421	57	8.9	812	2	US-10-104-047-2027	Sequence 2027, Ap	494	56	8.7	428	2	US-09-906-700-142	Sequence 142, App
422	57	8.9	878	2	US-09-252-991A-31974	Sequence 31974, A	495	56	8.7	428	2	US-03-903-603A-142	Sequence 142, App
423	57	8.9	976	1	US-08-449-645A-18	Sequence 18, Appl	496	56	8.7	428	2	US-03-904-920A-142	Sequence 142, App
424	57	8.9	976	1	US-08-702-367A-18	Sequence 18, Appl	497	56	8.7	428	2	US-09-909-064-142	Sequence 142, App
425	57	8.9	976	2	US-09-949-016-6499	Sequence 6499, Ap	498	56	8.7	428	2	US-09-905-381A-142	Sequence 142, App
426	57	8.9	976	2	US-09-378-759-18	Sequence 18, Appl	499	56	8.7	428	2	US-09-906-618-142	Sequence 142, App
427	57	8.9	976	5	PCT-US95-04681-18	Sequence 18, Appl	500	56	8.7	428	2	US-09-906-646-142	Sequence 142, App
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433	57	8.9	3287	1	US-08-477-451-7	Sequence 7, Appli	506	56	8.7	428	3	US-09-907-841-142	Sequence 142, App
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439	56.5	8.8	241	2	US-09-252-991A-32534	Sequence 32534, A	512	56	8.7	465	2	US-09-483-799-2	Sequence 2, Appli
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444	56.5	8.8	326	2	US-09-252-991A-18751	Sequence 18751, A	517	56	8.7	521	2	US-09-252-991A-26010	Sequence 26010, A
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446	56.5	8.8	340	2	US-09-940-244-402	Sequence 402, App	519	56	8.7	581	2	US-08-270-767-56754	Sequence 56754, A
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449	56.5	8.8	418	2	US-08-795-430-13	Sequence 13, Appl	522	56	8.7	590	2	US-09-370-838-187	Sequence 187, App
450	56.5	8.8	418	2	US-09-355-700-13	Sequence 13, Appl	523	56	8.7	595	2	US-09-252-991A-18995	Sequence 18995, A
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452	56.5	8.8	447	2	US-09-482-273-128	Sequence 128, App	525	56	8.7	595	2	US-09-854-133-187	Sequence 187, App
453	56.5	8.8	451	2	US-09-949-016-9567	Sequence 9567, Ap	526	56	8.7	610	2	US-09-949-016-6945	Sequence 6945, Ap
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455	56.5	8.8	539	2	US-09-252-991A-27717	Sequence 27717, A	528	56	8.7	631	2	US-09-483-799-1	Sequence 1, Appli
456	56.5	8.8	602	2	US-09-489-039A-11694	Sequence 11694, A	529	56	8.7	631	3	US-10-232-643-1	Sequence 1, Appli
457	56.5	8.8	720	2	US-09-252-991A-26650	Sequence 26650, A	530	56	8.7	632	2	US-09-929-955-29	Sequence 29, Appl
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459	56.5	8.8	774	2	US-09-948-429C-69	Sequence 69, Appl	532	56	8.7	632	3	US-10-307-047-12	Sequence 12, Appl
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463	56	8.7	156	2	US-09-252-991A-32450	Sequence 32450, A	536	56	8.7	685	2	US-09-107-433-3433	Sequence 3433, Ap
464	56	8.7	160	2	US-09-270-767-37669	Sequence 37669, A	537	56	8.7				

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539	56	8.7	686	2	US-09-881-654-2	Sequence 2, Appli	612	56	8.7	1161	2	US-09-193-043-99	Sequence 99, Appli
540	56	8.7	686	2	US-10-637-323-2	Sequence 2, Appli	613	56	8.7	1161	2	US-09-688-307A-2	Sequence 2, Appli
541	56	8.7	686	2	US-09-929-955-17	Sequence 17, Appli	614	56	8.7	1161	2	US-09-688-307A-99	Sequence 99, Appli
542	56	8.7	686	2	US-09-929-955-31	Sequence 31, Appli	615	56	8.7	1161	2	US-09-350-253-2	Sequence 2, Appli
543	56	8.7	686	2	US-09-929-955-32	Sequence 32, Appli	616	56	8.7	1161	2	US-09-350-253-99	Sequence 99, Appli
544	56	8.7	686	2	US-09-929-955-43	Sequence 43, Appli	617	56	8.7	1247	2	US-09-404-627-2	Sequence 2, Appli
545	56	8.7	686	2	US-09-929-955-44	Sequence 44, Appli	618	56	8.7	1771	2	US-09-721-479B-2	Sequence 2, Appli
546	56	8.7	686	2	US-09-929-955-45	Sequence 45, Appli	619	56	8.7	1771	2	US-09-721-479B-9	Sequence 9, Appli
547	56	8.7	686	2	US-09-929-955-46	Sequence 46, Appli	620	56	8.7	1771	2	US-09-721-479B-11	Sequence 11, Appli
548	56	8.7	686	2	US-09-929-955-47	Sequence 47, Appli	621	56	8.7	1771	2	US-09-721-479B-11	Sequence 11, Appli
549	56	8.7	686	2	US-09-929-955-48	Sequence 48, Appli	622	56	8.7	1786	2	US-08-444-818-54	Sequence 54, Appli
550	56	8.7	686	2	US-09-929-955-49	Sequence 49, Appli	623	56	8.7	1799	2	US-09-845-583A-6	Sequence 6, Appli
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555	56	8.7	686	2	US-09-930-591-6	Sequence 6, Appli	628	56	8.7	2261	2	US-08-444-818-66	Sequence 66, Appli
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557	56	8.7	686	2	US-09-930-591-8	Sequence 8, Appli	630	56	8.7	2703	1	US-08-185-433-19	Sequence 19, Appli
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594	56	8.7	949	2	US-09-404-627-4	Sequence 4, Appli	667	55.5	8.6	269	1	US-08-125-077-14	Sequence 14, Appli
595	56	8.7	1021	1	US-07-910-760-12	Sequence 12, Appli	668	55.5	8.6	278	2	US-09-252-991A-28712	Sequence 28712, A
596	56	8.7	1021	1	US-08-440-519-12	Sequence 12, Appli	669	55.5	8.6	309	2	US-09-252-991A-23189	Sequence 23189, A
597	56	8.7	1021	2	US-08-440-549-12	Sequence 12, Appli	670	55.5	8.6	328	2	US-09-252-991A-26345	Sequence 26345, A
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603	56	8.7	1161	1	US-08-485-618-99	Sequence 99, Appli	676	55.5	8.6	434	2	US-08-558-135-3	Sequence 3, Appli
604	56	8.7	1161	1	US-08-362-652-2	Sequence 2, Appli	677	55.5	8.6	461	2	US-09-949-016-8839	Sequence 8839, Ap
605	56	8.7	1161	1	US-08-605-672-2	Sequence 2, Appli	678	55.5	8.6	495	2	US-09-252-991A-21489	Sequence 21489, A
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608	56	8.7	1161	1	US-08-482-293A-99	Sequence 99, Appli	681	55.5	8.6	532	2	US-10-094-749-2041	Sequence 2041, Ap
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610	56	8.7	1161	1	US-08-943-363-99	Sequence 99, Appli	683	55.5	8.6	630	2	US-09-252-991A-26324	Sequence 26324, A

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685	55.5	8.6	715	2	US-10-104-047-3385	Sequence 3385, Ap	758	1890	2	US-09-004-838-88	Sequence 88, Appli
686	55.5	8.6	822	2	US-09-252-991A-21920	Sequence 21920, A	759	76	2	US-09-749-637A-68	Sequence 68, Appli
687	55.5	8.6	2237	1	US-08-455-543A-48	Sequence 48, Appl	760	138	2	US-09-252-991A-26969	Sequence 26969, A
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693	55.5	8.6	2339	1	US-08-455-543A-47	Sequence 47, Appl	766	164	2	US-09-252-991A-21892	Sequence 21892, A
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701	55	8.5	72	2	US-09-894-882-338	Sequence 338, App	774	232	2	US-09-574-708A-10	Sequence 10, Appl
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705	55	8.5	177	2	US-09-492-709A-369	Sequence 369, App	778	232	2	US-09-795-006A-147	Sequence 147, App
706	55	8.5	181	2	US-09-780-717-23	Sequence 23, Appl	779	232	2	US-09-495-468-7	Sequence 7, Appli
707	55	8.5	260	2	US-09-252-991A-26958	Sequence 26958, A	780	232	2	US-09-219-442-7	Sequence 7, Appli
708	55	8.5	267	2	US-09-252-991A-18758	Sequence 18758, A	781	270	2	US-09-252-991A-24974	Sequence 24974, A
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711	55	8.5	344	2	US-09-252-991A-22486	Sequence 22486, A	784	305	2	US-08-558-135-6	Sequence 6, Appli
712	55	8.5	347	2	US-09-543-681A-6173	Sequence 6173, Ap	785	309	2	US-09-248-796A-26183	Sequence 26183, A
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732	55	8.5	438	2	US-09-799-978-12	Sequence 12, Appl	805	562	2	US-10-104-047-3214	Sequence 3214, Ap
733	55	8.5	441	2	US-09-252-991A-24012	Sequence 24012, A	806	562	2	US-08-252-991A-28765	Sequence 28765, A
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738	55	8.5	614	2	US-09-252-991A-20210	Sequence 20210, A	811	592	2	US-09-252-991A-18124	Sequence 18124, A
739	55	8.5	666	2	US-09-252-991A-17462	Sequence 17462, A	812	598	2	US-08-949-016-6699	Sequence 6699, Ap
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741	55	8.5	686	1	US-08-350-884-70	Sequence 70, Appl	814	631	2	US-09-128-314-2	Sequence 2, Appli
742	55	8.5	686	1	US-08-709-173-70	Sequence 70, Appl	815	636	2	US-09-252-991A-32429	Sequence 32429, A
743	55	8.5	686	1	US-08-709-177-70	Sequence 70, Appl	816	654	2	US-09-252-991A-25801	Sequence 25801, A
744	55	8.5	797	2	US-09-422-999B-8	Sequence 8, Appli	817	654	2	US-09-252-991A-18483	Sequence 18483, A
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746	55	8.5	841	1	US-08-709-173-86	Sequence 86, Appl	819	659	2	US-08-188-281B-14	Sequence 14, Appl
747	55	8.5	841	1	US-08-709-177-86	Sequence 86, Appl	820	687	1	PCT-US94-07280-14	Sequence 14, Appl
748	55	8.5	841	1	US-09-252-991A-24162	Sequence 24162, A	821	687	5	PCT-US95-01087-14	Sequence 14, Appl
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751	55	8.5	1147	1	US-08-735-893-3	Sequence 3, Appli	824	971	2	US-09-690-359-52	Sequence 52, Appl
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833	54.5	8.5	1342	2	US-09-561-709B-13	Sequence 13, Appl	906	54	8.4	341	2	US-09-029-045-12	Sequence 12, Appl
834	54.5	8.5	1411	2	US-09-252-991A-28408	Sequence 28408, A	907	54	8.4	341	2	US-09-435-321-12	Sequence 12, Appl
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836	54.5	8.5	1648	5	PCT-US94-07280-12	Sequence 12, Appl	909	54	8.4	347	2	US-09-227-613-40	Sequence 40, Appl
837	54.5	8.5	1648	5	PCT-US95-01087-12	Sequence 12, Appl	910	54	8.4	347	2	US-10-191-513A-40	Sequence 40, Appl
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840	54.5	8.5	2546	2	US-09-949-016-9500	Sequence 9500, Ap	913	54	8.4	355	2	US-08-834-033A-6	Sequence 6, Appli
841	54.5	8.5	2546	2	US-09-949-016-9501	Sequence 9501, Ap	914	54	8.4	355	2	US-09-363-574-5	Sequence 5, Appli
842	54.5	8.5	2573	2	US-09-252-991A-27553	Sequence 25753, A	915	54	8.4	355	2	US-09-363-526-5	Sequence 5, Appli
843	54.5	8.5	2894	1	US-08-466-975A-23	Sequence 23, Appl	916	54	8.4	359	1	US-08-976-074-5	Sequence 5, Appli
844	54.5	8.5	2894	1	US-08-391-671A-23	Sequence 23, Appl	917	54	8.4	359	1	US-08-083-741-5	Sequence 5, Appli
845	54.5	8.5	2894	2	US-08-467-902A-23	Sequence 23, Appl	918	54	8.4	359	2	US-08-976-166A-5	Sequence 5, Appli
846	54.5	8.5	2894	2	US-09-275-265-23	Sequence 23, Appl	919	54	8.4	360	2	US-09-252-991A-17551	Sequence 17551, A
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854	54.5	8.5	3011	2	US-09-952-572-9	Sequence 9, Appli	927	54	8.4	437	2	US-09-489-039A-8958	Sequence 8958, Ap
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857	54.5	8.5	3011	5	PCT-US94-07280-1	Sequence 1, Appli	930	54	8.4	457	1	US-08-833-610-4	Sequence 4, Appli
858	54.5	8.5	3011	5	PCT-US95-01087-1	Sequence 1, Appli	931	54	8.4	457	2	US-08-834-033A-2	Sequence 2, Appli
859	54.5	8.5	3011	5	PCT-US95-01087-1	Sequence 1, Appli	932	54	8.4	457	2	US-08-834-033A-14	Sequence 14, Appl
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862	54	8.4	94	2	US-09-252-991A-28217	Sequence 28217, A	935	54	8.4	457	2	US-09-330-235-18	Sequence 18, Appl
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864	54	8.4	106	2	US-09-950-933A-70	Sequence 70, Appl	937	54	8.4	458	2	US-09-439-261-10	Sequence 10, Appl
865	54	8.4	120	2	US-10-104-047-2417	Sequence 2417, Ap	938	54	8.4	458	2	US-09-439-261-44	Sequence 44, Appl
866	54	8.4	140	2	US-10-094-749-1769	Sequence 1769, Ap	939	54	8.4	458	2	US-09-227-613-11	Sequence 11, Appl
867	54	8.4	177	2	US-09-252-991A-22998	Sequence 22998, A	940	54	8.4	458	2	US-09-227-613-41	Sequence 41, Appl
868	54	8.4	179	2	US-09-252-991A-27201	Sequence 27201, A	941	54	8.4	458	2	US-10-191-513A-11	Sequence 11, Appl
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872	54	8.4	184	2	US-08-481-985B-83	Sequence 83, Appl	945	54	8.4	481	2	US-09-252-991A-31018	Sequence 31018, A
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875	54	8.4	206	2	US-09-252-991A-31591	Sequence 31591, A	948	54	8.4	524	1	US-08-447-500-24	Sequence 24, Appl
876	54	8.4	226	2	US-09-252-991A-30602	Sequence 30602, A	949	54	8.4	524	1	US-08-453-866-24	Sequence 24, Appl
877	54	8.4	250	2	US-09-502-540-13813	Sequence 13813, A	950	54	8.4	524	1	US-08-185-359-24	Sequence 24, Appl
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879	54	8.4	260	2	US-09-008-271A-7	Sequence 7, Appli	952	54	8.4	614	2	US-09-017-706-9	Sequence 9, Appli
880	54	8.4	260	2	US-09-618-259-7	Sequence 7, Appli	953	54	8.4	614	2	US-09-017-706-10	Sequence 10, Appl
881	54	8.4	260	2	US-09-368-415-7	Sequence 7, Appli	954	54	8.4	614	2	US-09-017-706-11	Sequence 11, Appl
882	54	8.4	260	2	US-09-999-833A-395	Sequence 395, App	955	54	8.4	614	2	US-09-017-706-12	Sequence 12, Appl
883	54	8.4	260	2	US-10-020-445A-395	Sequence 395, App	956	54	8.4	614	2	US-09-017-706-13	Sequence 13, Appl
884	54	8.4	260	2	US-09-978-189-395	Sequence 395, App	957	54	8.4	614	2	US-09-017-706-14	Sequence 14, Appl
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886	54	8.4	260	3	US-08-915-659A-7	Sequence 7, Appli	959	54	8.4	644	2	US-09-252-991A-27860	Sequence 27860, A
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890	54	8.4	260	3	US-10-013-917A-395	Sequence 395, App	963	54	8.4	669	2	US-10-226-296-3	Sequence 3, Appli
891	54	8.4	262	2	US-09-252-991A-21401	Sequence 21401, A	964	54	8.4	694	2	US-10-226-296-3	Sequence 3, Appli
892	54	8.4	293	2	US-08-328-352-5522	Sequence 5522, Ap	965	54	8.4	760	2	US-09-252-991A-19869	Sequence 19869, A
893	54	8.4	272	1	US-08-887-997B-2	Sequence 2, Appli	966	54	8.4	779	1	US-08-426-627-4	Sequence 4, Appli
894	54	8.4	275	3	US-09-336-271C-72	Sequence 72, Appl	967	54	8.4	779	1	US-08-426-627-24	Sequence 24, Appl
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896	54	8.4	287	2	US-09-252-991A-29475	Sequence 29475, A	969	54	8.4	817	2	US-09-508-377-68	Sequence 68, Appl
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899	54	8.4	311	2	US-08-481-985B-69	Sequence 69, Appl	972	54	8.4	837	1	US-08-426-627-23	Sequence 23, Appl
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902	54	8.4	323	2	US-09-227-613-17	Sequence 17, Appl	975	54	8.4				

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987	53.5	8.3	145	2	US-09-919-497-68	Sequence 68, Appl	1060	53.5	8.3	706	1	US-09-461-657B-3	Sequence 3, Appli
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994	53.5	8.3	179	2	US-09-992-095B-36	Sequence 36, Appl	1067	53.5	8.3	1024	2	US-09-562-737-46	Sequence 46, Appl
995	53.5	8.3	179	3	US-10-000-986A-36	Sequence 36, Appl	1068	53.5	8.3	1171	1	US-08-445-135-1	Sequence 1, Appli
996	53.5	8.3	197	2	US-09-252-991A-32294	Sequence 32294, A	1069	53.5	8.3	1311	2	US-07-757-022B-42	Sequence 42, Appl
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1007	53.5	8.3	268	2	US-09-610-651-22	Sequence 22, Appl	1080	53.5	8.3	1719	2	US-10-024-450-4	Sequence 4, Appli
1008	53.5	8.3	268	2	US-09-345-373-22	Sequence 22, Appl	1081	53.5	8.3	1719	2	US-10-142-650-1	Sequence 1, Appli
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1149	53	8.2	1025	1	US-08-567-680A-4	Sequence 4, Appl	1222	52.5	8.2	592	2	US-09-996-620-14	Sequence 14, Appl
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1153	53	8.2	2627	1	US-09-060-836-3	Sequence 3, Appl	1226	52.5	8.2	611	1	US-08-677-049-2	Sequence 2, Appl
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 644; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 8e-69;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-990-444-165
; Sequence 165, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C19
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; CURRENT FILING DATE: 2001-11-14
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 2; Length 119;  
Best Local Similarity 100.0%; Pred. No. 8e-69;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLSSLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQBGQCECECKWFLRAP 60  
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Db 61 RKFWTVSGLPKKQCPCHDFKGNVKKTRHORHHRKPNKHSRACQOFLKOCQLRSFALPL 119

## RESULT 4

US-09-992-598-165  
; Sequence 165, Application US/09992598  
; Patent No. 6956108  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC20  
; CURRENT APPLICATION NUMBER: US/09/992,598  
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; PRIOR APPLICATION NUMBER: 60/049787  
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62 PRIOR FILING DATE: 1998-07-07  
63 PRIOR APPLICATION NUMBER: 60/091982  
64 PRIOR FILING DATE: 1998-07-07  
65 PRIOR APPLICATION NUMBER: 60/092182  
66 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 2; Length 119;  
Best Local Similarity 100.0%; Pred. No. 86-69;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 5  
US-09-989-735-165  
; Sequence 165, Application US/09989735  
; Patent No. 6972185  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
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; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC61  
; CURRENT APPLICATION NUMBER: US/09/989,735  
; CURRENT FILING DATE: 2001-11-19  
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-09
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Query Match 100.0%; Score 644; DB 2; Length 119;  
Best Local Similarity 100.0%; Pred. No. 8e-69;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKVLISLLLLLLPLMLMSVSSSLNPGVARGHRRGQASRWLQGGQCECKDWFLRAP 60
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Db 61 RRFKMTVSLPKKQPCDHPKGNVKKTRHQRHKKPKHSRAQQFLKQQLRSFALPL 119

## RESULT 6

US-09-989-726-165  
; Sequence 165, Application US/09989726  
; Patent No. 7018811  
; GENERAL INFORMATION:  
; APPLICANT: Aekhenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tuma, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P27301C60  
; CURRENT APPLICATION NUMBER: US/09/989, 726  
; CURRENT FILING DATE: 2001-11-19  
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; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
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; APPLICANT: Eaton, Dan L.  
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; APPLICANT: Williams, P. Mickey  
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; APPLICANT: Zhang, Zemin  
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RESULT 8  
US-09-989-728-165

Sequence 165, Application US/09989728  
Patent No. 7029873  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
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APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C72  
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54 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 3; Length 119;  
Best Local Similarity 100.0%; Pred. No. 8e-69; Mismatches 0; Indels 0; Gaps 0;  
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## RESULT 9

US-09-997-349-165  
; Sequence 165, Application US/09997349  
; Patent No. 7034106  
; GENERAL INFORMATION:

1 APPLICANT: Ashkenazi, Avi J.  
2 APPLICANT: Baker, Kevin P.  
3 APPLICANT: Botstein, David  
4 APPLICANT: Desnoyers, Luc  
5 APPLICANT: Eaton, Dan L.  
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22 APPLICANT: Williams, P. Mickey  
23 APPLICANT: Wood, William I.  
24 APPLICANT: Zhang, Zemin  
25 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
26 FILE OF INVENTION: Acids Encoding the Same  
27 FILE REFERENCE: P2730PIC37  
28 CURRENT APPLICATION NUMBER: US/09/997,349  
29 CURRENT FILING DATE: 2001-11-15  
30 PRIOR APPLICATION NUMBER: 60/049787  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 3; Length 119;

Best Local Similarity 100.0%; Pred. No. 8e-69;

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RESULT 10

US-09-997-653-165

; Sequence 165, Application US/09997653

; Patent No. 7034122

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

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APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C38  
CURRENT APPLICATION NUMBER: US/09/997,653  
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PRIORITY FILING DATE: 1998-06-24

;; PRIOR APPLICATION NUMBER: 60/090444  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090445  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090472  
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;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
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;; PRIOR FILING DATE: 1998-07-01  
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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 3; Length 119;

Best Local Similarity 100.0%; Pred. No. 9e-69;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKVLISLLLLPLMLMSVSSLPNGVARGHRDRGQASRRWLQSGGQCECKDWFLRAP 60

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Db 61 RRKFTVSGLPKKQPCDHFKNVKKTRHQRHHRKPKHSHSRACQQLKQCQLRSFALPL 119

RESULT 11

US-09-989-293A-165

; Sequence 165, Application US/09989293A

; Patent No. 7034136

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kljavin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: P2730P1C66  
;; CURRENT APPLICATION NUMBER: US/09/989,293A  
;; CURRENT FILING DATE: 2001-11-20  
;; PRIOR APPLICATION NUMBER: 60/049787  
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;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

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; Sequence 3926, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm

; SEQ ID NO 3926  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -22...-1  
US-09-621-976-3926

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DB 61 RKKFTVSGLPKKQCPCHDFKGNVKKTRHQRHRRKPKHSHSRACQQLKQCOL 112

RESULT 13  
US-09-252-991A-17301  
; Sequence 17301, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 17301  
; LENGTH: 620  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-17301

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DB 538 ARSHDRGQQRDHNRRRPHREGROORE--DQYRREPHR-----GR 576  
QY 84 VKKTRHQRHRRKPKHSHSRACQQLKQCOL 111  
DB 577 RQORDHQ-HRRRPHREGROQRDQHRQC 603

RESULT 14  
US-09-248-796A-19808  
; Sequence 19808, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstein et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 19808  
; LENGTH: 456  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-19808

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QY 112 LRSFALP 118  
DB 328 -RGFARP 333

RESULT 15  
US-09-248-796A-23977  
; Sequence 23977, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstein et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 23977  
; LENGTH: 131  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-23977

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QY 104 QQFLKQCOLRSFALP 118  
DB 79 QQVHQQTQLRTFSQP 93

Search completed: August 3, 2006, 09:56:24  
Job time : 43 secs

GenCore version 5.1.1.9

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OM protein - protein search, using sw model

Run on: August 3, 2006, 10:12:44 ; Search time 184 Seconds  
(without alignments)  
299.579 Million cell updates/sec

Title: US-10-015-967-2

Perfect score: 644

Sequence: 1 MKVLISLLLLPLMLMSNV.....SRACQFLKQCLRSFALPL 119

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Published Applications AA Main:\*

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
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- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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564	644	100.0	119	4	US-10-174-587-140
628	644	100.0	119	4	US-10-063-742-26
734	644	100.0	119	4	US-10-412-548-2
744	644	100.0	119	5	US-10-972-317-26
745	644	100.0	119	5	US-10-886-040-2
746	644	100.0	119	5	US-10-820-474A-94
748	644	100.0	119	5	US-10-950-374-165
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756	644	100.0	119	5	US-10-986-403-284
757	644	100.0	119	5	US-10-986-405-290
758	644	100.0	119	5	US-10-986-405-335
759	644	100.0	119	5	US-10-986-405-339
760	644	100.0	119	5	US-10-986-405-362
763	644	100.0	119	6	US-11-102-240-26
764	644	100.0	119	6	US-11-103-195-26
765	548	85.1	97	4	US-10-412-548-3
766	527	81.8	93	3	US-09-814-123-59
767	527	81.8	93	4	US-10-649-857-59
768	456	70.8	119	4	US-10-412-548-5
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770	296	46.0	64	3	US-09-814-122-39
771	296	46.0	64	4	US-10-649-857-39
772	81.5	12.7	248	6	US-11-096-568A-2923

773	77.5	12.0	364	4	US-10-437-963-163690	Sequence 163690,
774	75	11.6	1817	4	US-10-437-963-139845	Sequence 139845,
775	74	11.5	231	4	US-10-424-599-262198	Sequence 262198,
776	74	11.5	308	4	US-10-424-599-263933	Sequence 263933,
777	73.5	11.4	66	5	US-10-886-384-14	Sequence 14, Appl
778	73.5	11.4	439	6	US-11-087-099-4346	Sequence 4346, Ap
779	73.5	11.4	440	5	US-10-732-923-19499	Sequence 19499, A
780	73	11.3	172	4	US-10-425-115-306551	Sequence 306551,
781	73	11.3	759	4	US-10-437-963-126585	Sequence 126585,
782	72.5	11.3	101	4	US-10-437-963-170821	Sequence 170821,
783	72.5	11.3	752	4	US-10-104-047-2991	Sequence 2991, Ap
784	72.5	11.3	752	6	US-11-072-512-2391	Sequence 2391, Ap
785	72.5	11.3	3313	3	US-09-737-149-29	Sequence 29, Appl
786	72.5	11.3	3313	4	US-10-038-854-69	Sequence 69, Appl
787	72.5	11.3	3313	4	US-10-701-283-29	Sequence 29, Appl
788	71.5	11.1	108	3	US-09-950-933A-92	Sequence 92, Appl
789	71.5	11.1	651	5	US-10-650-274-106	Sequence 106, App
790	71.5	11.1	863	4	US-10-437-963-188081	Sequence 188081,
791	71.5	11.1	978	4	US-10-437-963-150739	Sequence 150739,
792	71	11.0	188	5	US-10-868-577A-8	Sequence 8, Appli
793	71	11.0	249	4	US-10-425-114-39022	Sequence 39022, A
794	71	11.0	330	4	US-10-425-114-51950	Sequence 51950, A
795	71	11.0	330	4	US-10-425-114-60309	Sequence 60309, A
796	71	11.0	330	5	US-10-450-763-55690	Sequence 55690, A
797	71	11.0	351	4	US-10-425-114-62599	Sequence 62599, A
798	71	11.0	356	4	US-10-425-114-46540	Sequence 46540, A
799	71	11.0	604	4	US-10-425-114-39423	Sequence 39423, A
800	71	11.0	758	6	US-11-096-568A-14593	Sequence 14593, A
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802	71	11.0	777	4	US-10-425-114-57846	Sequence 57846, A
803	71	11.0	1798	3	US-09-938-275-9	Sequence 9, Appli
804	71	11.0	3190	5	US-10-732-923-18448	Sequence 18448, A
805	71	11.0	3275	5	US-10-840-060-90	Sequence 90, Appl
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813	70	10.9	188	3	US-09-349-954A-6	Sequence 6, Appli
814	70	10.9	188	3	US-09-349-954A-19	Sequence 19, Appl
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816	70	10.9	188	3	US-09-907-007-6	Sequence 6, Appli
817	70	10.9	188	3	US-09-907-007-19	Sequence 19, Appl
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819	70	10.9	188	3	US-09-852-209A-10	Sequence 10, Appl
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829	70	10.9	188	4	US-10-792-480-57	Sequence 57, Appl
830	70	10.9	188	4	US-10-792-461-57	Sequence 57, Appl
831	70	10.9	188	5	US-10-772-927A-2	Sequence 2, Appli
832	70	10.9	188	5	US-10-948-736-11	Sequence 11, Appl
833	70	10.9	188	5	US-10-978-107-34	Sequence 34, Appl
834	70	10.9	188	5	US-10-924-025A-107	Sequence 107, App
835	70	10.9	188	6	US-11-064-774A-117	Sequence 117, App
836	70	10.9	188	6	US-11-075-047A-95	Sequence 95, Appl
837	70	10.9	189	4	US-10-204-070A-4	Sequence 4, Appli
838	70	10.9	216	4	US-10-264-049-3021	Sequence 3021, Ap
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842	70	10.9	1664	5	US-10-058-877-212	Sequence 212, App
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849	69.5	10.8	575	4	US-10-150-440-3	Sequence 3, Appli	922	65	10.1	501	5	US-10-473-127-370	Sequence 370, App
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851	69.5	10.8	575	4	US-10-09A-886-196	Sequence 196, App	924	65	10.1	534	5	US-10-473-127-372	Sequence 372, App
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853	69.5	10.8	575	4	US-10-373-801-29	Sequence 29, Appli	926	65	10.1	622	4	US-10-437-963-126579	Sequence 126579, A
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856	69.5	10.8	631	4	US-10-150-440-1	Sequence 1, Appli	929	65	10.1	628	5	US-10-473-127-364	Sequence 364, App
857	69.5	10.8	631	4	US-10-741-601-309	Sequence 309, App	930	65	10.1	628	5	US-10-473-127-365	Sequence 365, App
858	69.5	10.8	631	5	US-10-995-561-546	Sequence 546, App	931	65	10.1	628	5	US-10-473-127-366	Sequence 366, App
859	69.5	10.8	105	4	US-10-425-115-264686	Sequence 264686, App	932	65	10.1	628	5	US-10-473-127-368	Sequence 368, App
860	69.5	10.7	200	3	US-09-815-242-5189	Sequence 5189, App	933	65	10.1	628	5	US-10-473-127-369	Sequence 369, App
861	69.5	10.7	200	4	US-10-283-132A-43579	Sequence 43579, A	934	65	10.1	628	5	US-10-473-127-371	Sequence 371, App
862	69.5	10.7	234	5	US-10-450-763-59683	Sequence 59683, A	935	65	10.1	628	5	US-10-473-127-373	Sequence 373, App
863	69.5	10.7	430	5	US-10-739-930-5587	Sequence 5587, App	936	65	10.1	678	6	US-11-097-143-20265	Sequence 20265, A
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865	69.5	10.7	1077	4	US-10-104-047-2291	Sequence 2291, App	938	65	10.1	1269	3	US-10-437-963-142148	Sequence 142148, App
866	69.5	10.7	1077	6	US-11-072-512-2291	Sequence 2291, App	939	65	10.1	1798	3	US-09-845-583-8	Sequence 8, Appli
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870	68.5	10.6	427	6	US-11-067-321A-2	Sequence 2, Appli	943	64.5	10.0	227	4	US-10-408-765A-724	Sequence 724, App
871	68.5	10.6	427	6	US-11-156-272-12	Sequence 12, Appli	944	64.5	10.0	238	6	US-11-188-238-10275	Sequence 10275, A
872	68.5	10.6	450	6	US-11-156-272-10	Sequence 9, Appli	945	64.5	10.0	249	4	US-10-437-963-150105	Sequence 150105, A
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874	68.5	10.6	283	6	US-11-188-298-5991	Sequence 5991, App	947	64.5	10.0	338	6	US-11-096-568A-361	Sequence 361, App
875	68.5	10.6	539	4	US-10-437-963-156258	Sequence 156258, App	948	64.5	10.0	376	4	US-10-437-963-156164	Sequence 156164, A
876	68.5	10.6	849	4	US-10-425-114-47222	Sequence 47222, A	949	64.5	10.0	431	4	US-10-276-774-1563	Sequence 1563, App
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879	67.7	10.4	106	4	US-10-425-115-259981	Sequence 259981, A	952	64.5	10.0	826	4	US-10-437-963-133946	Sequence 133946, A
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881	67.7	10.4	287	6	US-11-096-568A-3206	Sequence 3207, App	954	64.5	10.0	1171	4	US-10-437-963-165935	Sequence 165935, A
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883	67.7	10.4	345	6	US-11-096-568A-3205	Sequence 3205, App	956	64	9.9	182	5	US-10-739-930-5751	Sequence 5751, App
884	67.7	10.4	345	6	US-11-096-568A-3208	Sequence 3208, App	957	64	9.9	214	3	US-09-963-156A-1	Sequence 1, Appli
885	67.7	10.4	454	6	US-11-146-428-106	Sequence 106, App	958	64	9.9	214	4	US-10-749-832-1	Sequence 1, Appli
886	67.7	10.4	475	4	US-10-369-493-23367	Sequence 23367, A	959	64	9.9	227	5	US-10-723-860-3312	Sequence 3312, App
887	67.7	10.4	475	6	US-11-087-099-2388	Sequence 2388, App	960	64	9.9	265	4	US-10-424-599-219841	Sequence 219841, A
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890	67.7	10.4	529	4	US-10-221-278-253	Sequence 253, App	963	64	9.9	485	6	US-11-087-099-9751	Sequence 9751, App
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901	66.5	10.2	238	6	US-11-087-099-10621	Sequence 10621, A	974	63.5	9.9	119	4	US-10-425-115-295087	Sequence 295087, A
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903	66.5	10.2	348	6	US-11-087-099-6269	Sequence 6269, App	976	63.5	9.9	215	4	US-10-108-260A-3350	Sequence 3350, App
904	65.5	10.2	100	4	US-10-437-963-202621	Sequence 202621, A	977	63.5	9.9	259	4	US-10-437-963-190362	Sequence 190362, A
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912	65.5	10.2	704	3	US-09-529-063-76	Sequence 76, Appli	985	63.5	9.9	441	6	US-11-129-741-2961	Sequence 2961, App
913	65.5	10.2	704	4	US-10-414-378-76	Sequence 76, Appli	986	63.5	9.9	441	6	US-11-129-741-2965	Sequence 2965, App
914	65.5	10.2	706	3	US-09-847-102A-52	Sequence 52, Appli	987	63.5	9.9	441	6	US-11-129-741-2967	Sequence 2967, App
915	65.5	10.2	706	4	US-10-285-976-49	Sequence 49, Appli	988	63.5	9.9	786	5	US-10-701-401-8	Sequence 8, Appli
916	65.5	10.2	706	4	US-10-295-027-496	Sequence 496, App	989	63.5	9.9	815	4	US-10-437-963-112487	Sequence 112487, A
917	65.5	10.2	706	4	US-10-295-027-1332	Sequence 1332, App	990	63.5	9.9	815	4	US-10-437-963-112487	Sequence 112487, A
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993	63.5	9.9	1507	4	US-10-437-963-200793	Sequence 200793,	1186	62	9.6	1270	4	US-10-124-557-44	Sequence 44, Appl
994	63.5	9.9	1598	4	US-10-437-963-112315	Sequence 112315,	1187	62	9.6	1270	6	US-11-169-232-44	Sequence 44, Appl
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996	63.5	9.9	2406	4	US-10-408-763A-1504	Sequence 1504, App	1189	62	9.6	1530	4	US-10-425-115-187278	Sequence 187278,
997	63.5	9.9	2406	5	US-10-701-401-2	Sequence 2, Appl	1190	62	9.6	1642	4	US-10-786-720-39	Sequence 39, Appl
998	63	9.8	127	4	US-10-425-114-48451	Sequence 48451, A	1191	62	9.6	1642	4	US-10-786-720-38	Sequence 38, Appl
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1002	63	9.8	295	4	US-10-425-114-60981	Sequence 60981, A	1195	61.5	9.5	121	5	US-10-473-127-270	Sequence 270, App
1003	63	9.8	332	5	US-10-723-860-2633	Sequence 2633, Ap	1196	61.5	9.5	129	4	US-10-425-115-338625	Sequence 338625,
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1005	63	9.8	343	5	US-10-450-763-54326	Sequence 54326, A	1198	61.5	9.5	232	4	US-10-060-523-9	Sequence 9, Appl
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1009	63	9.8	2343	5	US-10-330-773-904	Sequence 904, App	1202	61.5	9.5	263	4	US-10-437-963-174053	Sequence 174053,
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1011	62.5	9.7	156	3	US-09-796-753-102	Sequence 102, App	1204	61.5	9.5	341	5	US-10-511-722-21	Sequence 21, Appl
1012	62.5	9.7	156	3	US-09-796-753-118	Sequence 118, App	1205	61.5	9.5	357	5	US-10-511-722-20	Sequence 20, Appl
1013	62.5	9.7	156	4	US-10-237-535-60	Sequence 60, Appl	1206	61.5	9.5	360	3	US-09-825-561A-18	Sequence 18, Appl
1014	62.5	9.7	156	4	US-10-239-196-60	Sequence 60, Appl	1207	61.5	9.5	360	5	US-10-872-087-18	Sequence 18, Appl
1015	62.5	9.7	156	4	US-10-223-085-342	Sequence 342, App	1208	61.5	9.5	361	5	US-10-732-923-15346	Sequence 15346, A
1016	62.5	9.7	156	4	US-10-223-084-342	Sequence 342, App	1209	61.5	9.5	369	4	US-10-116-275-339	Sequence 339, App
1017	62.5	9.7	156	4	US-10-223-088-342	Sequence 342, App	1210	61.5	9.5	369	5	US-10-473-127-266	Sequence 266, App
1018	62.5	9.7	156	4	US-10-223-090-342	Sequence 342, App	1211	61.5	9.5	369	5	US-10-473-127-265	Sequence 267, App
1019	62.5	9.7	156	4	US-10-223-087-342	Sequence 342, App	1212	61.5	9.5	369	5	US-10-473-127-268	Sequence 268, App
1020	62.5	9.7	156	4	US-10-223-083-342	Sequence 342, App	1213	61.5	9.5	369	5	US-10-473-127-269	Sequence 269, App
1021	62.5	9.7	156	4	US-10-223-083-342	Sequence 342, App	1214	61.5	9.5	369	5	US-10-473-127-271	Sequence 271, App
1022	62.5	9.7	156	4	US-10-223-083-342	Sequence 342, App	1215	61.5	9.5	369	5	US-10-473-127-278	Sequence 278, App
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#### SUMMARIES

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6	527	81.8	118	6	US-10-553-436-174
7	521	80.9	94	6	US-10-553-436-173
8	521	80.9	100	6	US-10-553-436-175
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61	63.5	9.9	168	6	US-10-449-902-48083	Sequence 48083, A
62	63.5	9.9	215	7	US-11-293-697-3350	Sequence 3350, Ap
63	63.5	9.9	340	7	US-11-056-355B-10419	Sequence 10419, A
64	63.5	9.9	2392	6	US-10-540-898-907	Sequence 907, App
65	63	9.8	307	6	US-10-449-902-29497	Sequence 29497, A
66	63	9.8	464	6	US-10-449-902-53294	Sequence 53294, A
67	63	9.8	674	7	US-11-056-355B-79153	Sequence 79153, A
68	63	9.8	795	7	US-11-056-355B-79152	Sequence 79152, A
69	63	9.8	803	7	US-11-056-355B-79151	Sequence 79151, A
70	63	9.8	954	7	US-11-330-403-11849	Sequence 11849, A
71	63	9.8	2343	6	US-10-540-898-904	Sequence 904, App
72	62.5	9.7	414	7	US-11-283-329-88	Sequence 88, Appl
73	62.5	9.7	465	7	US-11-056-355B-55492	Sequence 55492, A
74	62.5	9.7	466	7	US-11-056-355B-55491	Sequence 55491, A
75	62.5	9.7	488	7	US-11-056-355B-55490	Sequence 55490, A
76	62	9.6	359	6	US-10-953-349-32049	Sequence 32049, A
77	62	9.6	359	7	US-11-056-355B-66572	Sequence 66572, A
78	62	9.6	1661	6	US-10-449-902-36756	Sequence 36756, A
79	61.5	9.5	229	6	US-11-056-355B-12823	Sequence 12823, A
80	61.5	9.5	369	6	US-10-511-937-2966	Sequence 2966, Ap
81	61	9.5	156	6	US-10-953-349-6611	Sequence 6611, Ap
82	61	9.5	156	7	US-11-056-355B-40738	Sequence 40738, A
83	61	9.5	175	7	US-11-056-355B-8053	Sequence 8053, Ap
84	61	9.5	181	6	US-10-953-349-6610	Sequence 6610, Ap
85	61	9.5	181	6	US-10-374-780A-432	Sequence 432, App
86	61	9.5	181	6	US-11-056-355B-40737	Sequence 40737, A
87	61	9.5	223	6	US-10-953-349-6609	Sequence 6609, Ap
88	61	9.5	223	7	US-11-056-355B-40736	Sequence 40736, A
89	61	9.5	463	7	US-11-056-355B-85142	Sequence 85142, A
90	61	9.5	464	7	US-11-056-355B-85141	Sequence 85141, A
91	61	9.5	491	7	US-11-056-355B-85140	Sequence 85140, A
92	60.5	9.4	106	6	US-10-953-349-7799	Sequence 7799, Ap
93	60.5	9.4	134	6	US-10-953-349-38499	Sequence 38499, A
94	60.5	9.4	134	7	US-11-056-355B-3961	Sequence 3961, Ap
95	60.5	9.4	134	7	US-11-056-355B-15231	Sequence 15231, A
96	60.5	9.4	195	6	US-10-953-349-38498	Sequence 38498, A
97	60.5	9.4	195	6	US-11-056-355B-3960	Sequence 3960, Ap
98	60.5	9.4	195	7	US-11-056-355B-15230	Sequence 15230, A
99	60.5	9.4	295	7	US-11-056-355B-5954	Sequence 5954, Ap

100	60.5	9.4	313	7	US-11-056-355B-5953	Sequence 5953, Ap	175	58	9.0	806	7	US-11-056-355B-110821	Sequence 110821,
101	60.5	9.4	318	7	US-11-056-355B-5952	Sequence 5952, Ap	176	58	9.0	815	6	US-10-953-349-8639	Sequence 8639, Ap
102	60.5	9.4	361	7	US-11-056-355B-106948	Sequence 106948,	177	58	9.0	815	7	US-11-056-355B-21131	Sequence 21131, A
103	60.5	9.4	361	7	US-11-056-355B-118187	Sequence 118187,	178	58	9.0	815	7	US-11-056-355B-99581	Sequence 99581, A
104	60.5	9.4	362	7	US-11-056-355B-87373	Sequence 87373, A	179	58	9.0	815	7	US-11-056-355B-110820	Sequence 110820,
105	60.5	9.4	396	7	US-11-289-263-7	Sequence 7, Appli	180	58	9.0	931	6	US-10-449-902-55689	Sequence 55689, A
106	60.5	9.4	452	6	US-10-953-349-5940	Sequence 5940, Ap	181	58	9.0	993	7	US-11-303-935-11	Sequence 11, Appl
107	60.5	9.4	452	7	US-11-056-355B-36211	Sequence 36211, A	182	58	9.0	994	7	US-11-303-935-12	Sequence 12, Appl
108	60.5	9.4	452	7	US-11-056-355B-36075	Sequence 36075, A	183	58	9.0	998	7	US-11-303-935-2	Sequence 2, Appli
109	60.5	9.4	463	6	US-10-953-349-5939	Sequence 5939, Ap	184	58	9.0	998	7	US-11-259-133-18	Sequence 18, Appl
110	60.5	9.4	463	6	US-11-056-355B-36210	Sequence 36210, A	185	57.5	8.9	136	6	US-10-953-349-39784	Sequence 29784, A
111	60.5	9.4	463	7	US-11-056-355B-36074	Sequence 36074, A	186	57.5	8.9	194	7	US-11-056-355B-12533	Sequence 12533, A
112	60.5	9.4	523	6	US-10-953-349-35575	Sequence 35575, A	187	57.5	8.9	194	7	US-11-056-355B-13221	Sequence 13221, A
113	60.5	9.4	808	7	US-11-330-403-18337	Sequence 18337, A	188	57.5	8.9	204	7	US-11-056-355B-12018	Sequence 12018, A
114	60.5	9.4	936	6	US-10-449-902-5526	Sequence 5526, A	189	57.5	8.9	212	7	US-11-056-355B-12532	Sequence 12532, A
116	60	9.3	150	7	US-11-330-403-686	Sequence 686, App	190	57.5	8.9	212	7	US-11-056-355B-13220	Sequence 13220, A
117	60	9.3	160	7	US-11-056-355B-6712	Sequence 6712, Ap	191	57.5	8.9	235	7	US-11-330-403-4771	Sequence 4771, Ap
118	60	9.3	165	7	US-11-056-355B-6711	Sequence 6711, Ap	192	57.5	8.9	235	7	US-11-330-403-4771	Sequence 4771, Ap
119	59.5	9.2	94	6	US-10-449-902-48319	Sequence 48319, A	193	57.5	8.9	235	7	US-11-330-403-5221	Sequence 5221, Ap
120	59.5	9.2	254	7	US-11-030-653-18	Sequence 18, Appl	194	57.5	8.9	235	7	US-11-329-868-5	Sequence 5, Appli
121	59.5	9.2	292	6	US-10-953-349-20841	Sequence 20841, A	195	57.5	8.9	236	7	US-11-056-355B-12017	Sequence 12017, A
122	59.5	9.2	292	7	US-11-056-355B-52934	Sequence 52934, A	196	57.5	8.9	236	7	US-11-330-403-18153	Sequence 18153, A
123	59.5	9.2	304	7	US-11-056-355B-2353	Sequence 2353, Ap	197	57.5	8.9	239	7	US-11-330-403-15647	Sequence 15647, A
124	59.5	9.2	330	7	US-11-056-355B-2352	Sequence 2352, Ap	198	57.5	8.9	253	7	US-11-330-403-7534	Sequence 7534, Ap
125	59.5	9.2	360	7	US-11-056-355B-2351	Sequence 2351, Ap	199	57.5	8.9	254	7	US-11-056-355B-12016	Sequence 12016, A
126	59.5	9.2	367	7	US-11-056-355B-48085	Sequence 48085, A	200	57.5	8.9	264	7	US-11-056-355B-12531	Sequence 12531, A
127	59.5	9.2	376	7	US-11-056-355B-48084	Sequence 48084, A	201	57.5	8.9	264	7	US-11-056-355B-13219	Sequence 13219, A
128	59.5	9.2	409	6	US-10-374-780A-384	Sequence 384, App	202	57.5	8.9	347	7	US-11-056-355B-41011	Sequence 41011, A
129	59.5	9.2	409	7	US-11-056-355B-48083	Sequence 48083, A	203	57.5	8.9	356	7	US-11-056-355B-41010	Sequence 41010, A
131	59.5	9.2	2224	6	US-10-829-000-14	Sequence 14, Appl	204	57.5	8.9	359	7	US-11-056-355B-41009	Sequence 41009, A
132	59.5	9.2	2312	6	US-10-829-000-12	Sequence 12, Appl	205	57.5	8.9	464	7	US-11-056-355B-46231	Sequence 46231, A
133	59	9.2	189	7	US-11-293-697-4685	Sequence 4685, Ap	206	57.5	8.9	475	7	US-11-056-355B-46230	Sequence 46230, A
134	59	9.2	193	7	US-11-105-233-146	Sequence 146, App	207	57.5	8.9	486	7	US-11-056-355B-46229	Sequence 46229, A
135	59	9.2	193	7	US-11-354-653-28	Sequence 28, Appl	208	57	8.9	136	6	US-10-449-902-42497	Sequence 42497, A
136	59	9.2	209	6	US-10-449-902-53547	Sequence 53547, A	209	57	8.9	152	7	US-11-334-081-26	Sequence 26, Appl
137	59	9.2	245	6	US-10-449-902-47213	Sequence 47213, A	210	57	8.9	153	6	US-10-953-349-30101	Sequence 30101, A
138	59	9.2	271	6	US-10-449-902-55938	Sequence 55938, A	211	57	8.9	153	7	US-11-056-355B-67454	Sequence 67454, A
139	59	9.2	558	6	US-10-449-902-40667	Sequence 40667, A	212	57	8.9	172	7	US-11-334-081-23	Sequence 23, Appl
140	59	9.2	871	7	US-11-316-132-1	Sequence 1, Appli	213	57	8.9	183	7	US-11-056-355B-4678	Sequence 4678, Ap
141	59	9.2	871	7	US-11-313-836-11	Sequence 11, Appl	214	57	8.9	211	7	US-11-334-081-44	Sequence 44, Appl
142	59	9.2	871	7	US-11-105-233-140	Sequence 140, App	215	57	8.9	231	7	US-11-056-355B-4677	Sequence 4677, Ap
143	59	9.2	998	6	US-10-449-902-50427	Sequence 50427, A	216	57	8.9	243	7	US-11-056-355B-66047	Sequence 66047, A
144	59	9.2	2162	6	US-10-829-000-13	Sequence 13, Appl	217	57	8.9	247	6	US-10-953-349-30707	Sequence 30707, A
145	58.5	9.1	149	6	US-10-449-902-51773	Sequence 51773, A	218	57	8.9	258	6	US-10-953-349-30706	Sequence 30706, A
146	58.5	9.1	189	6	US-10-449-902-40350	Sequence 40350, A	219	57	8.9	289	7	US-11-170-797-12	Sequence 12, Appl
147	58.5	9.1	239	6	US-10-953-349-24974	Sequence 24974, A	220	57	8.9	322	7	US-11-056-355B-4190	Sequence 4190, Ap
148	58.5	9.1	280	6	US-10-953-349-24973	Sequence 24973, A	221	57	8.9	324	7	US-11-056-355B-4189	Sequence 4189, Ap
149	58.5	9.1	326	6	US-10-953-349-24972	Sequence 24972, A	222	57	8.9	349	6	US-10-953-349-33572	Sequence 33572, A
150	58.5	9.1	355	7	US-11-056-355B-5510	Sequence 5510, Ap	223	57	8.9	349	7	US-11-056-355B-6931	Sequence 6931, Ap
151	58.5	9.1	355	7	US-11-056-355B-20040	Sequence 20040, A	224	57	8.9	351	7	US-11-056-355B-4188	Sequence 4188, Ap
152	58.5	9.1	416	6	US-10-953-349-4613	Sequence 4613, Ap	225	57	8.9	369	7	US-11-056-355B-78045	Sequence 78045, A
153	58.5	9.1	416	7	US-11-056-355B-39428	Sequence 39428, A	226	57	8.9	371	6	US-10-953-349-11789	Sequence 11789, A
154	58.5	9.1	448	7	US-11-056-355B-5509	Sequence 5509, Ap	227	57	8.9	371	7	US-11-056-355B-20764	Sequence 20764, A
155	58.5	9.1	448	7	US-11-056-355B-20039	Sequence 20039, A	228	57	8.9	371	7	US-11-056-355B-78544	Sequence 78544, A
156	58.5	9.1	451	6	US-10-953-349-4612	Sequence 4612, Ap	229	57	8.9	391	7	US-11-056-355B-48138	Sequence 48138, A
157	58.5	9.1	451	7	US-11-056-355B-39427	Sequence 39427, A	230	57	8.9	402	7	US-11-056-355B-78044	Sequence 78044, A
158	58.5	9.1	738	6	US-10-663-538-20	Sequence 20, Appl	231	57	8.9	404	6	US-10-953-349-11788	Sequence 11788, A
159	58.5	9.1	870	7	US-11-316-132-2	Sequence 2, Appli	232	57	8.9	404	7	US-11-056-355B-20763	Sequence 20763, A
160	58.5	9.1	3467	7	US-11-063-439-71	Sequence 71, Appl	233	57	8.9	404	7	US-11-056-355B-78543	Sequence 78543, A
161	58	9.0	72	6	US-10-449-902-34566	Sequence 34566, A	234	57	8.9	404	7	US-11-317-789A-786	Sequence 786, App
162	58	9.0	169	6	US-10-449-902-43393	Sequence 43393, A	235	57	8.9	407	7	US-11-056-355B-78043	Sequence 78043, A
163	58	9.0	248	7	US-11-056-355B-70591	Sequence 70591, A	236	57	8.9	409	6	US-10-953-349-11787	Sequence 11787, A
164	58	9.0	315	6	US-10-953-349-33865	Sequence 33865, A	237	57	8.9	409	7	US-11-056-355B-20762	Sequence 20762, A
165	58	9.0	315	7	US-11-056-355B-19463	Sequence 19463, A	238	57	8.9	409	7	US-11-056-355B-78542	Sequence 78542, A
166	58	9.0	610	7	US-11-303-935-3	Sequence 3, Appli	239	57	8.9	445	7	US-11-056-355B-8194	Sequence 8194, Ap
167	58	9.0	626	7	US-11-303-935-5	Sequence 5, Appli	240	57	8.9	463	7	US-11-056-355B-37078	Sequence 37078, A
168	58	9.0	663	6	US-10-953-349-8641	Sequence 8641, Ap	241	57	8.9	463	7	US-11-056-355B-44967	Sequence 44967, A
169	58	9.0	663	7	US-11-056-355B-21133	Sequence 21133, A	242	57	8.9	463	7	US-11-056-355B-50701	Sequence 50701, A
170	58	9.0	663	7	US-11-056-355B-99583	Sequence 99583, A	243	57	8.9	470	7	US-11-056-355B-8193	Sequence 8193, Ap
171	58	9.0	663	7	US-11-056-355B-110822	Sequence 110822,	244	57	8.9	486	7	US-11-056-355B-8192	Sequence 8192, Ap
172	58	9.0	806	6	US-10-953-349-8640	Sequence 8640, Ap	245	57	8.9	527	6	US-10-449-902-47155	Sequence 47155, A
173	58	9.0	806	7	US-11-056-355B-21132	Sequence 21132, A	246	57	8.9	578	7	US-11-056-355B-37077	Sequence 37077, A
174	58	9.0	806	7	US-11-056-355B-99582	Sequence 99582, A	247	57	8.9	578	7	US-11-056-355B-44966	Sequence 44966, A

248	57	8.9	578	7	US-11-056-355B-50700	Sequence 50700, A	321	55.5	8.6	286	6	US-10-953-349-22694	Sequence 22694, A
249	57	8.9	578	7	US-11-330-403-7904	Sequence 7904, Ap	322	55.5	8.6	312	7	US-11-174-307B-202	Sequence 202, App
250	57	8.9	578	7	US-11-330-403-13173	Sequence 13173, A	323	55.5	8.6	317	6	US-10-953-349-30064	Sequence 30064, A
251	57	8.9	579	7	US-11-330-403-1790	Sequence 1790, Ap	324	55.5	8.6	377	7	US-11-056-355B-16213	Sequence 16213, A
252	57	8.9	589	7	US-11-056-355B-37076	Sequence 37076, A	325	55.5	8.6	377	7	US-11-056-355B-67293	Sequence 67293, A
253	57	8.9	589	7	US-11-056-355B-44965	Sequence 44965, A	326	55.5	8.6	380	7	US-11-056-355B-21494	Sequence 21494, A
254	57	8.9	589	7	US-11-056-355B-50699	Sequence 50699, A	327	55.5	8.6	380	7	US-11-056-355B-102891	Sequence 102891, A
255	57	8.9	576	7	US-11-259-133-4	Sequence 4, Appli	328	55.5	8.6	380	7	US-11-056-355B-114130	Sequence 114130, A
256	57	8.9	976	7	US-11-289-102-237	Sequence 237, App	329	55.5	8.6	393	6	US-10-953-349-36844	Sequence 36844, A
257	57	8.9	1076	7	US-11-056-355B-71498	Sequence 71498, A	330	55.5	8.6	393	7	US-11-056-355B-1379	Sequence 1379, Ap
258	57	8.9	1082	7	US-11-056-355B-71497	Sequence 71497, A	331	55.5	8.6	393	7	US-11-056-355B-63651	Sequence 63651, A
259	57	8.9	1100	7	US-11-056-355B-88652	Sequence 88652, A	332	55.5	8.6	421	7	US-11-330-403-11234	Sequence 11234, A
260	57	8.9	1100	7	US-11-056-355B-92408	Sequence 92408, A	333	55.5	8.6	475	6	US-10-449-902-54998	Sequence 54998, A
261	57	8.9	1106	7	US-11-056-355B-88651	Sequence 88651, A	334	55.5	8.6	2237	6	US-11-350-336-8	Sequence 8, Appli
262	57	8.9	1106	7	US-11-056-355B-92407	Sequence 92407, A	335	55.5	8.6	2339	6	US-10-829-000-8	Sequence 8, Appli
263	57	8.9	1327	7	US-11-056-355B-71496	Sequence 71496, A	336	55.5	8.6	2339	7	US-11-350-336-4	Sequence 6, Appli
264	57	8.9	1351	7	US-11-056-355B-88650	Sequence 88650, A	337	55.5	8.6	2343	7	US-11-350-336-4	Sequence 4, Appli
265	57	8.9	1351	7	US-11-056-355B-92406	Sequence 92406, A	338	55.5	8.6	3518	7	US-11-063-439-287	Sequence 287, App
266	56.5	8.8	89	6	US-10-953-349-6270	Sequence 6270, Ap	339	55	8.5	55	7	US-11-056-355B-42043	Sequence 42043, A
267	56.5	8.8	178	7	US-11-330-403-1033	Sequence 1033, Ap	340	55	8.5	55	7	US-11-056-355B-86368	Sequence 86368, A
268	56.5	8.8	260	7	US-11-056-355B-65790	Sequence 65790, A	341	55	8.5	156	7	US-11-056-355B-19437	Sequence 19437, A
269	56.5	8.8	267	6	US-10-449-902-39874	Sequence 39874, A	342	55	8.5	177	7	US-11-056-355B-5060	Sequence 5060, Ap
270	56.5	8.8	305	6	US-10-953-349-14084	Sequence 14084, A	343	55	8.5	183	7	US-11-056-355B-12025	Sequence 12025, A
271	56.5	8.8	305	6	US-11-056-355B-56489	Sequence 56489, A	344	55	8.5	259	7	US-11-056-355B-4792	Sequence 4792, Ap
272	56.5	8.8	336	6	US-10-953-349-14083	Sequence 14083, A	345	55	8.5	263	7	US-11-056-355B-5201	Sequence 5201, Ap
273	56.5	8.8	356	7	US-11-056-355B-56488	Sequence 56488, A	346	55	8.5	285	7	US-11-056-355B-4791	Sequence 4791, Ap
274	56.5	8.8	371	6	US-10-953-349-14082	Sequence 14082, A	347	55	8.5	323	7	US-11-140-450-73	Sequence 73, Appli
275	56.5	8.8	371	7	US-11-056-355B-56487	Sequence 56487, A	348	55	8.5	326	7	US-11-056-355B-18110	Sequence 18110, A
276	56.5	8.8	385	6	US-11-293-697-3636	Sequence 3636, Ap	349	55	8.5	357	6	US-10-449-902-39153	Sequence 39153, A
277	56.5	8.8	393	6	US-10-449-902-34957	Sequence 34957, A	350	55	8.5	359	7	US-11-174-307B-4848	Sequence 4848, Ap
278	56.5	8.8	419	6	US-10-449-902-54961	Sequence 54961, A	351	55	8.5	367	7	US-11-283-329-82	Sequence 82, Appli
279	56.5	8.8	513	7	US-11-174-307B-3806	Sequence 3806, Ap	352	55	8.5	410	7	US-11-283-329-84	Sequence 84, Appli
280	56	8.7	70	6	US-10-953-349-25937	Sequence 25937, A	353	55	8.5	412	7	US-11-056-355B-9274	Sequence 9274, Ap
281	56	8.7	135	7	US-11-056-355B-37736	Sequence 37736, A	354	55	8.5	413	6	US-10-449-902-38404	Sequence 38404, A
282	56	8.7	142	6	US-10-953-349-30549	Sequence 30549, A	355	55	8.5	496	6	US-10-953-349-26964	Sequence 26964, A
283	56	8.7	145	7	US-11-056-355B-37735	Sequence 37735, A	356	55	8.5	496	7	US-11-056-355B-68057	Sequence 68057, A
284	56	8.7	147	7	US-11-056-355B-37734	Sequence 37734, A	357	55	8.5	559	6	US-10-953-349-20243	Sequence 20243, A
285	56	8.7	155	6	US-10-540-898-480	Sequence 480, App	358	55	8.5	570	6	US-10-953-349-20242	Sequence 20242, A
286	56	8.7	157	6	US-10-953-349-25384	Sequence 25384, A	359	55	8.5	586	6	US-10-449-902-42026	Sequence 42026, A
287	56	8.7	176	6	US-10-449-902-52148	Sequence 52148, A	360	55	8.5	588	6	US-10-953-349-20241	Sequence 20241, A
288	56	8.7	268	6	US-10-953-349-23748	Sequence 23748, A	361	55	8.5	724	7	US-11-330-403-7015	Sequence 7015, Ap
289	56	8.7	268	7	US-11-056-355B-56875	Sequence 56875, A	362	55	8.5	823	7	US-11-056-355B-11440	Sequence 11440, A
290	56	8.7	270	6	US-10-953-349-23747	Sequence 23747, A	363	55	8.5	831	6	US-11-056-355B-11439	Sequence 11439, A
291	56	8.7	270	7	US-11-056-355B-56874	Sequence 56874, A	364	55	8.5	834	6	US-10-953-349-9789	Sequence 9789, Ap
292	56	8.7	270	6	US-10-953-349-20672	Sequence 20672, A	365	55	8.5	854	6	US-10-953-349-9788	Sequence 9788, Ap
293	56	8.7	320	6	US-10-953-349-23746	Sequence 23746, A	366	55	8.5	862	6	US-10-449-902-52320	Sequence 52320, A
294	56	8.7	320	6	US-11-056-355B-56873	Sequence 56873, A	367	55	8.5	878	6	US-10-953-349-9787	Sequence 9787, Ap
295	56	8.7	332	6	US-10-449-902-39455	Sequence 39455, A	368	55	8.5	901	6	US-10-449-902-56454	Sequence 56454, A
296	56	8.7	332	6	US-10-449-902-51306	Sequence 51306, A	369	55	8.5	984	6	US-10-449-902-56454	Sequence 56454, A
297	56	8.7	409	7	US-11-056-355B-62067	Sequence 62067, A	370	55	8.5	1130	6	US-10-449-902-54141	Sequence 54141, A
298	56	8.7	411	7	US-10-953-349-27666	Sequence 27666, A	371	55	8.5	1357	7	US-11-330-403-13907	Sequence 13907, A
299	56	8.7	411	7	US-11-056-355B-63639	Sequence 63639, A	372	55	8.5	1366	7	US-11-056-355B-78949	Sequence 78949, A
300	56	8.7	571	7	US-11-293-697-3307	Sequence 3307, Ap	373	55	8.5	1528	7	US-11-056-355B-75257	Sequence 75257, A
301	56	8.7	610	7	US-11-056-355B-76995	Sequence 76995, A	374	55	8.5	1567	7	US-11-056-355B-75256	Sequence 75256, A
302	56	8.7	610	7	US-11-056-355B-95961	Sequence 95961, A	375	55	8.5	1583	7	US-11-056-355B-75255	Sequence 75255, A
303	56	8.7	618	7	US-11-174-307B-4078	Sequence 4078, Ap	376	55	8.5	1632	7	US-11-056-355B-78948	Sequence 78948, A
304	56	8.7	657	7	US-11-056-355B-76994	Sequence 76994, A	377	55	8.5	1691	7	US-11-056-355B-78947	Sequence 78947, A
305	56	8.7	657	7	US-11-056-355B-95960	Sequence 95960, A	378	55	8.5	1919	7	US-11-056-355B-13846	Sequence 13846, A
306	56	8.7	718	7	US-11-056-355B-76993	Sequence 76993, A	379	54.5	8.5	119	7	US-11-056-355B-13845	Sequence 13845, A
307	56	8.7	718	7	US-11-056-355B-95959	Sequence 95959, A	380	54.5	8.5	142	6	US-10-953-349-31265	Sequence 31265, A
308	56	8.7	1121	6	US-10-449-902-46558	Sequence 46558, A	381	54.5	8.5	161	7	US-11-056-355B-61382	Sequence 61382, A
309	56	8.7	182	7	US-11-131-901-6	Sequence 6, Appli	382	54.5	8.5	162	7	US-11-056-355B-51201	Sequence 51201, A
310	56	8.7	2397	6	US-10-471-571A-2832	Sequence 2832, Ap	383	54.5	8.5	178	7	US-11-330-403-4741	Sequence 4741, Ap
311	55.5	8.6	129	6	US-10-953-349-29830	Sequence 29830, A	384	54.5	8.5	179	7	US-11-293-697-4410	Sequence 4410, Ap
312	55.5	8.6	131	6	US-10-953-349-6973	Sequence 6973, Ap	385	54.5	8.5	180	7	US-11-330-403-16155	Sequence 16155, A
313	55.5	8.6	134	6	US-10-449-902-34683	Sequence 34683, A	386	54.5	8.5	186	7	US-11-056-355B-3149	Sequence 3149, Ap
314	55.5	8.6	160	6	US-10-449-902-38324	Sequence 38324, A	387	54.5	8.5	205	7	US-11-056-355B-13844	Sequence 13844, A
315	55.5	8.6	178	7	US-11-330-403-7395	Sequence 7395, Ap	388	54.5	8.5	207	6	US-10-953-349-30895	Sequence 30895, A
316	55.5	8.6	193	6	US-10-449-902-53016	Sequence 53016, A	389	54.5	8.5	207	7	US-11-056-355B-60938	Sequence 60938, A
317	55.5	8.6	197	7	US-11-321-421-330	Sequence 330, App	390	54.5	8.5	216	7	US-11-056-355B-3148	Sequence 3148, Ap
318	55.5	8.6	243	6	US-10-953-349-4693	Sequence 4693, Ap	391	54.5	8.5	220	6	US-10-540-898-16	Sequence 16, Appli
319	55.5	8.6	255	6	US-10-449-902-55821	Sequence 55821, A	392	54.5	8.5	220	6	US-10-540-898-18	Sequence 18, Appli
320	55.5	8.6	256	6	US-10-449-902-49357	Sequence 49357, A	393	54.5	8.5	222	6	US-10-449-902-41871	Sequence 41871, A

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395	54.5	8.5	227	7	US-11-056-355B-3147	Sequence 3147, Ap	468	54	8.4	163	7	US-11-056-355B-28854	Sequence 28854, A
396	54.5	8.5	232	7	US-11-323-049-12	Sequence 12, Appl	469	54	8.4	163	7	US-11-056-355B-32444	Sequence 32444, A
397	54.5	8.5	232	7	US-11-323-964-21	Sequence 21, Appl	470	54	8.4	163	7	US-11-056-355B-102500	Sequence 102500, A
398	54.5	8.5	247	6	US-10-953-349-30894	Sequence 30894, A	471	54	8.4	163	7	US-11-056-355B-113739	Sequence 113739, A
399	54.5	8.5	247	6	US-11-056-355B-60937	Sequence 60937, A	472	54	8.4	174	6	US-10-953-349-2859	Sequence 2859, Ap
400	54.5	8.5	248	6	US-10-953-349-18703	Sequence 18703, A	473	54	8.4	174	6	US-10-374-780A-388	Sequence 388, App
401	54.5	8.5	259	6	US-10-953-349-18702	Sequence 18702, A	474	54	8.4	174	6	US-11-056-355B-28853	Sequence 28853, A
402	54.5	8.5	261	6	US-10-953-349-18701	Sequence 18701, A	475	54	8.4	174	7	US-11-056-355B-32443	Sequence 32443, A
403	54.5	8.5	267	6	US-10-953-349-36846	Sequence 36846, A	476	54	8.4	174	7	US-11-056-355B-102499	Sequence 102499, A
404	54.5	8.5	267	6	US-11-056-355B-1381	Sequence 1381, Ap	477	54	8.4	174	7	US-11-056-355B-113738	Sequence 113738, A
405	54.5	8.5	269	6	US-10-953-349-31264	Sequence 31264, A	478	54	8.4	176	7	US-11-056-355B-76576	Sequence 76576, A
406	54.5	8.5	269	6	US-11-056-355B-61381	Sequence 61381, A	479	54	8.4	177	7	US-11-056-355B-76575	Sequence 76575, A
407	54.5	8.5	279	6	US-10-953-349-36845	Sequence 36845, A	480	54	8.4	177	7	US-11-056-355B-61727	Sequence 61727, A
408	54.5	8.5	279	6	US-11-056-355B-1380	Sequence 1380, Ap	481	54	8.4	179	7	US-11-330-403-13709	Sequence 13709, A
409	54.5	8.5	333	7	US-11-056-355B-85739	Sequence 85739, A	482	54	8.4	183	7	US-11-174-307B-254	Sequence 254, App
410	54.5	8.5	342	7	US-11-056-355B-22140	Sequence 22140, A	483	54	8.4	183	7	US-11-056-355B-76574	Sequence 76574, A
411	54.5	8.5	342	7	US-11-056-355B-77107	Sequence 77107, A	484	54	8.4	201	6	US-10-553-436-159	Sequence 159, App
412	54.5	8.5	342	7	US-11-056-355B-85738	Sequence 85738, A	485	54	8.4	218	7	US-11-056-355B-53040	Sequence 53040, A
413	54.5	8.5	379	7	US-11-056-355B-22139	Sequence 22139, A	486	54	8.4	224	6	US-10-953-349-6356	Sequence 6356, Ap
414	54.5	8.5	379	7	US-11-056-355B-77106	Sequence 77106, A	487	54	8.4	234	6	US-10-953-349-6355	Sequence 6355, Ap
415	54.5	8.5	379	7	US-11-056-355B-85737	Sequence 85737, A	488	54	8.4	234	6	US-10-553-436-158	Sequence 158, App
416	54.5	8.5	387	7	US-11-056-355B-2998	Sequence 2998, Ap	489	54	8.4	257	7	US-11-056-355B-4176	Sequence 4176, Ap
417	54.5	8.5	394	7	US-11-293-697-3423	Sequence 3423, Ap	490	54	8.4	260	6	US-10-544-944-13	Sequence 13, Appl
418	54.5	8.5	399	7	US-11-056-355B-77105	Sequence 77105, A	491	54	8.4	260	7	US-11-319-952-83	Sequence 83, Appl
419	54.5	8.5	400	7	US-11-056-355B-22138	Sequence 22138, A	492	54	8.4	260	7	US-11-285-040-7	Sequence 7, Appl
420	54.5	8.5	404	7	US-11-251-465-23	Sequence 23, Appl	493	54	8.4	267	6	US-10-620-289-10	Sequence 10, Appl
421	54.5	8.5	404	7	US-11-283-329-90	Sequence 90, Appl	494	54	8.4	274	6	US-10-620-289-12	Sequence 12, Appl
422	54.5	8.5	411	6	US-10-449-902-51817	Sequence 51817, A	495	54	8.4	275	6	US-10-620-289-4	Sequence 4, Appl
423	54.5	8.5	455	7	US-11-283-329-130	Sequence 120, App	496	54	8.4	275	7	US-11-319-952-72	Sequence 72, Appl
424	54.5	8.5	526	7	US-11-293-697-3714	Sequence 3714, Ap	497	54	8.4	276	7	US-11-056-355B-40803	Sequence 40803, A
425	54.5	8.5	535	7	US-11-283-329-122	Sequence 122, App	498	54	8.4	291	6	US-10-620-289-6	Sequence 6, Appl
426	54.5	8.5	540	7	US-11-330-403-5650	Sequence 5650, Ap	499	54	8.4	296	6	US-10-620-289-8	Sequence 8, Appl
427	54.5	8.5	580	7	US-11-283-329-118	Sequence 118, App	500	54	8.4	297	6	US-10-620-289-2	Sequence 2, Appl
428	54.5	8.5	582	6	US-10-449-902-51959	Sequence 51959, A	501	54	8.4	297	6	US-10-504-973-25	Sequence 25, Appl
429	54.5	8.5	598	7	US-11-283-329-116	Sequence 116, App	502	54	8.4	301	6	US-10-449-902-37477	Sequence 37477, A
430	54.5	8.5	637	7	US-11-254-252-4	Sequence 4, Appl	503	54	8.4	304	7	US-11-056-355B-53039	Sequence 53039, A
431	54.5	8.5	845	7	US-11-254-252-16	Sequence 16, Appl	504	54	8.4	304	7	US-11-056-355B-53038	Sequence 53038, A
432	54.5	8.5	1545	7	US-11-051-725-64	Sequence 64, Appl	505	54	8.4	309	6	US-10-449-902-62679	Sequence 62679, A
433	54.5	8.5	1545	7	US-11-051-725-67	Sequence 67, Appl	506	54	8.4	317	7	US-11-056-355B-51486	Sequence 51486, A
434	54.5	8.5	1580	7	US-11-051-725-10	Sequence 10, Appl	507	54	8.4	336	6	US-10-374-780A-430	Sequence 430, Appl
435	54.5	8.5	1584	7	US-11-051-725-93	Sequence 93, Appl	508	54	8.4	359	6	US-10-620-289-14	Sequence 14, Appl
436	54.5	8.5	1584	7	US-11-051-725-97	Sequence 97, Appl	509	54	8.4	364	7	US-11-056-355B-53038	Sequence 53038, A
437	54.5	8.5	1644	7	US-11-051-725-15	Sequence 15, Appl	510	54	8.4	367	7	US-11-056-355B-18704	Sequence 18704, A
438	54.5	8.5	1737	7	US-11-051-725-55	Sequence 55, Appl	511	54	8.4	372	6	US-10-449-902-32853	Sequence 32853, A
439	54.5	8.5	1737	7	US-11-051-725-76	Sequence 76, Appl	512	54	8.4	380	6	US-10-449-902-31350	Sequence 31350, A
440	54.5	8.5	1943	7	US-11-051-725-68	Sequence 68, Appl	513	54	8.4	386	6	US-10-449-902-30831	Sequence 30831, A
441	54.5	8.5	1996	7	US-11-051-725-86	Sequence 86, Appl	514	54	8.4	405	6	US-10-953-349-3686	Sequence 3686, Ap
442	54.5	8.5	2205	7	US-11-051-725-62	Sequence 62, Appl	515	54	8.4	410	6	US-10-953-349-3686	Sequence 3686, Ap
443	54.5	8.5	2206	7	US-11-051-725-84	Sequence 84, Appl	516	54	8.4	412	6	US-10-449-902-53509	Sequence 53509, A
444	54.5	8.5	2206	7	US-11-051-725-91	Sequence 91, Appl	517	54	8.4	443	7	US-11-056-355B-40802	Sequence 40802, A
445	54.5	8.5	2261	6	US-10-829-000-10	Sequence 10, Appl	518	54	8.4	449	7	US-11-056-355B-40801	Sequence 40801, A
446	54.5	8.5	2312	7	US-11-051-725-74	Sequence 74, Appl	519	54	8.4	457	7	US-11-024-544A-115	Sequence 115, App
447	54.5	8.5	2505	6	US-10-829-000-9	Sequence 9, Appl	520	54	8.4	457	7	US-11-024-545-43	Sequence 43, Appl
448	54.5	8.5	2505	6	US-10-829-000-11	Sequence 11, Appl	521	54	8.4	457	7	US-11-185-301-31	Sequence 31, Appl
449	54.5	8.5	2511	7	US-11-051-725-12	Sequence 12, Appl	522	54	8.4	457	7	US-11-185-301-31	Sequence 31, Appl
450	54.5	8.5	2511	7	US-11-051-725-13	Sequence 13, Appl	523	54	8.4	457	7	US-11-251-466-17	Sequence 17, Appl
451	54.5	8.5	2523	7	US-11-051-725-11	Sequence 11, Appl	524	54	8.4	457	7	US-11-254-173-31	Sequence 31, Appl
452	54.5	8.5	2617	7	US-11-051-725-14	Sequence 14, Appl	525	54	8.4	457	7	US-11-264-784-2	Sequence 2, Appl
453	54.5	8.5	3011	6	US-10-520-153-14	Sequence 14, Appl	526	54	8.4	457	7	US-11-264-737-2	Sequence 2, Appl
454	54.5	8.5	3011	7	US-11-140-487A-771	Sequence 771, App	527	54	8.4	457	7	US-11-265-761-2	Sequence 2, Appl
455	54.5	8.5	3011	7	US-11-236-836-14	Sequence 14, Appl	528	54	8.4	458	7	US-11-024-544A-136	Sequence 136, App
456	54.5	8.5	3011	7	US-11-254-252-20	Sequence 20, Appl	529	54	8.4	458	7	US-11-190-750-119	Sequence 119, App
457	54.5	8.5	5738	6	US-10-505-928-150	Sequence 150, App	530	54	8.4	458	7	US-11-264-784-5	Sequence 5, Appl
458	54	8.4	79	7	US-11-056-355B-393	Sequence 393, App	531	54	8.4	458	7	US-11-264-737-5	Sequence 5, Appl
459	54	8.4	98	6	US-10-540-898-12	Sequence 12, Appl	532	54	8.4	458	7	US-11-265-761-5	Sequence 5, Appl
460	54	8.4	98	6	US-10-540-898-14	Sequence 14, Appl	533	54	8.4	461	7	US-11-056-355B-6754	Sequence 6754, Ap
461	54	8.4	129	6	US-10-953-349-6974	Sequence 6974, Ap	534	54	8.4	461	7	US-11-056-355B-55569	Sequence 55569, A
462	54	8.4	152	6	US-10-953-349-2861	Sequence 2861, Ap	535	54	8.4	493	6	US-10-449-902-55569	Sequence 45, Appl
463	54	8.4	152	7	US-11-056-355B-28855	Sequence 28855, A	536	54	8.4	524	6	US-10-828-564-11	Sequence 11, Appl
464	54	8.4	152	7	US-11-056-355B-32445	Sequence 32445, A	537	54	8.4	546	6	US-10-449-902-42635	Sequence 42635, A
465	54	8.4	152	7	US-11-056-355B-102501	Sequence 102501, A	538	54	8.4	606	7	US-11-330-403-4136	Sequence 4136, Ap
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541	54	8.4	720	6	US-10-449-902-53935	Sequence 53935, A	614	53	8.2	421	6	US-10-539-228-53	Sequence 53, Appl
542	54	8.4	720	6	US-10-449-902-54649	Sequence 54649, A	615	53	8.2	454	6	US-10-449-902-47778	Sequence 47778, A
543	54	8.4	751	7	US-11-226-554-121	Sequence 121, App	616	53	8.2	504	6	US-10-449-902-43689	Sequence 43689, A
544	54	8.4	751	7	US-11-248-718-121	Sequence 121, App	617	53	8.2	508	7	US-11-317-789A-407	Sequence 407, App
545	54	8.4	752	6	US-10-539-228-438	Sequence 438, App	618	53	8.2	515	7	US-11-056-355B-89867	Sequence 89867, A
546	54	8.4	779	7	US-11-226-554-123	Sequence 123, App	619	53	8.2	515	7	US-11-056-355B-93623	Sequence 93623, A
547	54	8.4	779	7	US-11-248-718-123	Sequence 123, App	620	53	8.2	532	7	US-11-330-403-18717	Sequence 18717, A
548	54	8.4	781	7	US-11-226-554-122	Sequence 122, App	621	53	8.2	537	6	US-10-539-228-322	Sequence 322, App
549	54	8.4	781	7	US-11-248-718-122	Sequence 122, App	622	53	8.2	546	6	US-10-449-902-46889	Sequence 46889, A
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551	54	8.4	809	7	US-11-248-718-120	Sequence 120, App	624	53	8.2	562	7	US-11-056-355B-93622	Sequence 93622, A
552	54	8.4	836	7	US-11-105-233-154	Sequence 154, App	625	53	8.2	622	7	US-11-056-355B-89865	Sequence 89865, A
553	54	8.4	836	7	US-11-226-554-119	Sequence 119, App	626	53	8.2	622	7	US-11-056-355B-93621	Sequence 93621, A
554	54	8.4	836	7	US-11-248-718-119	Sequence 119, App	627	53	8.2	653	6	US-10-449-902-41022	Sequence 41022, A
555	54	8.4	954	6	US-10-449-902-41286	Sequence 41286, A	628	53	8.2	727	7	US-11-293-697-3060	Sequence 3060, Ap
556	54	8.4	1014	6	US-10-953-349-16525	Sequence 16525, A	629	53	8.2	738	6	US-10-539-228-571	Sequence 571, App
557	53.5	8.3	133	6	US-10-449-902-37351	Sequence 37351, A	630	53	8.2	789	7	US-11-056-355B-79149	Sequence 79149, A
558	53.5	8.3	134	7	US-11-056-355B-61228	Sequence 61228, A	631	53	8.2	796	7	US-11-056-355B-79148	Sequence 79148, A
559	53.5	8.3	145	6	US-10-511-937-2430	Sequence 2430, Ap	632	53	8.2	799	7	US-11-056-355B-79147	Sequence 79147, A
560	53.5	8.3	192	6	US-10-449-902-39481	Sequence 39481, A	633	53	8.2	811	7	US-11-056-355B-20590	Sequence 20590, A
561	53.5	8.3	236	7	US-11-293-697-4829	Sequence 4829, Ap	634	53	8.2	832	6	US-10-449-902-45254	Sequence 45254, A
562	53.5	8.3	243	7	US-11-356-373-21	Sequence 21, Appl	635	53	8.2	853	7	US-11-056-355B-20589	Sequence 20589, A
563	53.5	8.3	263	7	US-11-356-373-18	Sequence 18, Appl	636	53	8.2	864	7	US-11-056-355B-20588	Sequence 20588, A
564	53.5	8.3	264	6	US-10-449-902-38887	Sequence 38887, A	637	53	8.2	904	6	US-10-449-902-41346	Sequence 41346, A
565	53.5	8.3	267	6	US-10-524-827-47	Sequence 47, Appl	638	53	8.2	905	6	US-10-839-442A-8	Sequence 8, Appl1
566	53.5	8.3	267	6	US-10-524-827-51	Sequence 51, Appl	639	53	8.2	1507	7	US-11-330-403-5475	Sequence 5475, Ap
567	53.5	8.3	268	7	US-11-238-035-29	Sequence 29, Appl	640	53	8.2	1538	7	US-11-330-403-11802	Sequence 11802, A
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569	53.5	8.3	270	7	US-11-056-355B-86362	Sequence 86362, A	642	53	8.2	2627	6	US-10-547-530-5	Sequence 5, Appl1
570	53.5	8.3	270	7	US-11-056-355B-99857	Sequence 99857, A	643	52.5	8.2	94	6	US-10-511-937-3011	Sequence 3011, Ap
571	53.5	8.3	270	7	US-11-056-355B-111096	Sequence 111096, A	644	52.5	8.2	102	6	US-10-449-903-53172	Sequence 53172, A
572	53.5	8.3	284	7	US-11-056-355B-80497	Sequence 80497, A	645	52.5	8.2	111	7	US-11-319-952-58	Sequence 58, Appl
573	53.5	8.3	300	7	US-11-056-355B-80496	Sequence 80496, A	646	52.5	8.2	146	6	US-10-953-349-33174	Sequence 33174, A
574	53.5	8.3	326	6	US-10-374-780A-2254	Sequence 2254, Ap	647	52.5	8.2	164	6	US-10-953-349-33379	Sequence 33379, A
575	53.5	8.3	326	7	US-11-056-355B-80495	Sequence 80495, A	648	52.5	8.2	164	6	US-11-056-355B-18282	Sequence 18282, A
576	53.5	8.3	376	7	US-11-056-355B-65698	Sequence 65698, A	649	52.5	8.2	172	7	US-11-293-697-3011	Sequence 3011, Ap
577	53.5	8.3	388	7	US-11-113-081A-10	Sequence 10, Appl	650	52.5	8.2	178	7	US-11-330-403-13302	Sequence 13302, A
578	53.5	8.3	398	7	US-11-056-355B-39668	Sequence 39668, A	651	52.5	8.2	190	6	US-10-953-349-29909	Sequence 29909, A
579	53.5	8.3	398	7	US-11-056-355B-104916	Sequence 104916, A	652	52.5	8.2	197	6	US-10-953-349-28555	Sequence 28555, A
580	53.5	8.3	398	7	US-11-056-355B-116155	Sequence 116155, A	653	52.5	8.2	224	7	US-11-056-355B-4521	Sequence 4521, Ap
581	53.5	8.3	413	6	US-10-449-902-51498	Sequence 51498, A	654	52.5	8.2	230	7	US-11-056-355B-63918	Sequence 63918, A
582	53.5	8.3	421	7	US-11-056-355B-39667	Sequence 39667, A	655	52.5	8.2	237	6	US-10-953-349-28670	Sequence 28670, A
583	53.5	8.3	421	7	US-11-056-355B-104915	Sequence 104915, A	656	52.5	8.2	237	6	US-10-953-349-39199	Sequence 39199, A
584	53.5	8.3	421	7	US-11-056-355B-116154	Sequence 116154, A	657	52.5	8.2	237	7	US-11-056-355B-1254	Sequence 1254, Ap
585	53.5	8.3	447	7	US-11-056-355B-1670	Sequence 1670, Ap	658	52.5	8.2	256	7	US-11-056-355B-14550	Sequence 14550, A
586	53.5	8.3	463	7	US-11-056-355B-1177	Sequence 1177, Ap	659	52.5	8.2	265	7	US-11-356-373-24	Sequence 24, Appl
587	53.5	8.3	487	7	US-11-056-355B-1176	Sequence 1176, Ap	660	52.5	8.2	275	6	US-10-540-898-639	Sequence 639, App
588	53.5	8.3	502	7	US-11-056-355B-1175	Sequence 1175, Ap	661	52.5	8.2	303	6	US-10-953-349-39198	Sequence 39198, A
589	53.5	8.3	534	6	US-10-449-902-48245	Sequence 48245, A	662	52.5	8.2	303	7	US-11-056-355B-1253	Sequence 1253, Ap
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591	53.5	8.3	672	6	US-10-449-902-43350	Sequence 43350, A	664	52.5	8.2	335	7	US-11-056-355B-55735	Sequence 55735, A
592	53.5	8.3	798	6	US-10-511-937-2445	Sequence 2445, Ap	665	52.5	8.2	339	7	US-11-056-355B-55734	Sequence 55734, A
593	53.5	8.3	811	7	US-11-330-403-12293	Sequence 12293, A	666	52.5	8.2	348	7	US-11-283-329-60	Sequence 60, Appl
594	53	8.2	103	7	US-11-056-355B-51134	Sequence 51134, A	667	52.5	8.2	364	7	US-11-056-355B-68938	Sequence 68938, A
595	53	8.2	113	7	US-11-056-355B-60882	Sequence 60882, A	668	52.5	8.2	393	7	US-11-056-355B-55733	Sequence 55733, A
596	53	8.2	139	7	US-10-449-902-35322	Sequence 35322, A	669	52.5	8.2	407	6	US-10-953-349-35758	Sequence 35758, A
597	53	8.2	148	7	US-11-295-040-2	Sequence 2, Appl1	670	52.5	8.2	417	6	US-10-449-902-36692	Sequence 36692, A
598	53	8.2	156	6	US-10-505-928-422	Sequence 422, App	671	52.5	8.2	419	6	US-10-953-349-1054	Sequence 1054, Ap
599	53	8.2	156	6	US-10-540-898-478	Sequence 478, App	672	52.5	8.2	419	7	US-11-056-355B-26877	Sequence 26877, A
600	53	8.2	156	6	US-10-540-898-482	Sequence 482, App	673	52.5	8.2	419	7	US-11-056-355B-79206	Sequence 79206, A
601	53	8.2	225	7	US-11-330-403-4628	Sequence 4628, Ap	674	52.5	8.2	426	7	US-11-174-307B-4268	Sequence 4268, Ap
602	53	8.2	233	6	US-10-449-902-40173	Sequence 40173, A	675	52.5	8.2	444	6	US-10-511-937-2962	Sequence 2962, Ap
603	53	8.2	237	7	US-11-293-697-4535	Sequence 4535, Ap	676	52.5	8.2	444	6	US-10-511-937-3014	Sequence 3014, Ap
604	53	8.2	241	6	US-10-953-349-27924	Sequence 27924, A	677	52.5	8.2	452	7	US-11-183-218-8	Sequence 8, Appl1
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611	53	8.2	350	7	US-11-056-355B-50521	Sequence 50521, A	684	52.5	8.2	515	7	US-11-330-403-14952	Sequence 14952, A
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688	52.5	8.2	598	6	US-10-540-898-465	Sequence 465, App	761	52	8.1	664	7	US-11-181-115-24	Sequence 24, Appl
689	52.5	8.2	644	7	US-11-330-403-6482	Sequence 6482, Ap	762	52	8.1	664	7	US-11-181-115-26	Sequence 26, Appl
690	52.5	8.2	644	7	US-11-330-403-15095	Sequence 15095, A	763	52	8.1	664	7	US-11-181-115-46	Sequence 46, Appl
691	52.5	8.2	676	7	US-11-181-115-28	Sequence 28, Appl	764	52	8.1	670	6	US-10-449-902-40607	Sequence 40607, A
692	52.5	8.2	676	7	US-11-181-115-29	Sequence 29, Appl	765	52	8.1	755	7	US-11-293-697-3722	Sequence 3722, Ap
693	52.5	8.2	676	7	US-11-181-115-48	Sequence 48, Appl	766	52	8.1	879	7	US-11-221-332-72	Sequence 72, Appl
694	52.5	8.2	769	7	US-11-246-999-67	Sequence 67, Appl	767	52	8.1	910	7	US-11-301-924-16	Sequence 16, Appl
695	52.5	8.2	804	6	US-10-449-902-53390	Sequence 53390, A	768	52	8.1	917	6	US-10-504-973-26	Sequence 26, Appl
696	52.5	8.2	950	7	US-11-330-403-6805	Sequence 6805, Ap	769	52	8.1	935	6	US-10-553-436-148	Sequence 148, App
697	52.5	8.2	1009	6	US-10-539-228-696	Sequence 696, App	771	52	8.1	1428	7	US-11-299-791-22	Sequence 22, Appl
698	52.5	8.2	1503	7	US-11-312-958-48	Sequence 48, Appl	772	52	8.1	1850	7	US-11-056-355B-40081	Sequence 40081, A
699	52	8.1	91	7	US-11-056-355B-383	Sequence 383, App	773	52	8.1	1850	7	US-11-056-355B-47197	Sequence 47197, A
700	52	8.1	102	7	US-11-056-355B-60290	Sequence 60290, A	774	52	8.1	1859	7	US-11-056-355B-40080	Sequence 40080, A
701	52	8.1	106	7	US-11-056-355B-6651	Sequence 6651, Ap	775	52	8.1	1859	7	US-11-056-355B-47196	Sequence 47196, A
702	52	8.1	108	7	US-11-056-355B-6650	Sequence 6650, Ap	776	52	8.1	1916	7	US-11-056-355B-40079	Sequence 40079, A
703	52	8.1	110	6	US-10-449-902-40848	Sequence 40848, A	777	52	8.1	1916	7	US-11-056-355B-47195	Sequence 47195, A
704	52	8.1	129	7	US-11-293-697-4223	Sequence 4223, Ap	778	51.5	8.0	67	6	US-10-525-126-245	Sequence 245, App
705	52	8.1	134	7	US-11-284-236-132	Sequence 192, App	779	51.5	8.0	72	6	US-10-449-902-44043	Sequence 44043, A
706	52	8.1	151	6	US-10-953-349-6993	Sequence 6993, Ap	780	51.5	8.0	72	6	US-10-449-902-51451	Sequence 51451, A
707	52	8.1	162	6	US-10-953-349-6392	Sequence 6992, Ap	781	51.5	8.0	89	6	US-10-953-349-7800	Sequence 7800, Ap
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711	52	8.1	173	7	US-11-056-355B-117507	Sequence 117507, A	785	51.5	8.0	122	6	US-10-953-349-9037	Sequence 9037, Ap
712	52	8.1	187	6	US-11-174-307B-2904	Sequence 2904, Ap	786	51.5	8.0	122	6	US-10-953-349-28599	Sequence 28599, A
713	52	8.1	187	6	US-10-953-349-33038	Sequence 33038, A	787	51.5	8.0	122	7	US-11-056-355B-37127	Sequence 37127, A
714	52	8.1	187	7	US-11-056-355B-7327	Sequence 7327, Ap	788	51.5	8.0	126	6	US-10-953-349-9036	Sequence 9036, Ap
715	52	8.1	187	7	US-11-056-355B-8417	Sequence 8417, Ap	789	51.5	8.0	126	7	US-11-056-355B-7126	Sequence 7126, A
716	52	8.1	203	7	US-11-056-355B-3644	Sequence 3644, Ap	790	51.5	8.0	126	7	US-11-056-355B-101940	Sequence 101940, A
717	52	8.1	220	7	US-11-056-355B-8325	Sequence 8325, Ap	791	51.5	8.0	126	7	US-11-056-355B-113179	Sequence 113179, A
718	52	8.1	233	6	US-10-953-349-3651	Sequence 3651, Ap	792	51.5	8.0	138	7	US-11-056-355B-95889	Sequence 95889, A
719	52	8.1	233	7	US-11-056-355B-27466	Sequence 27466, A	793	51.5	8.0	145	6	US-10-449-902-34135	Sequence 34135, A
720	52	8.1	233	7	US-11-056-355B-106267	Sequence 106267, A	794	51.5	8.0	171	6	US-10-953-349-28598	Sequence 28598, A
721	52	8.1	233	7	US-11-056-355B-117506	Sequence 117506, A	795	51.5	8.0	186	6	US-10-449-902-40629	Sequence 40629, A
722	52	8.1	249	6	US-10-449-902-46968	Sequence 46968, A	796	51.5	8.0	196	6	US-10-953-349-15978	Sequence 15978, A
723	52	8.1	265	7	US-11-284-236-124	Sequence 124, App	797	51.5	8.0	198	7	US-11-051-725-79	Sequence 79, Appl
724	52	8.1	271	6	US-10-991-309B-164	Sequence 16183, A	798	51.5	8.0	198	7	US-11-051-725-87	Sequence 87, Appl
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726	52	8.1	296	6	US-10-953-436-151	Sequence 151, App	800	51.5	8.0	210	7	US-11-056-355B-37125	Sequence 37125, A
727	52	8.1	305	7	US-10-953-349-35299	Sequence 35299, A	801	51.5	8.0	210	7	US-11-056-355B-101939	Sequence 101939, A
728	52	8.1	305	7	US-11-056-355B-8391	Sequence 8391, Ap	802	51.5	8.0	210	7	US-11-056-355B-113178	Sequence 113178, A
729	52	8.1	307	6	US-11-056-355B-6390	Sequence 6390, Ap	803	51.5	8.0	215	7	US-11-056-355B-16752	Sequence 16752, A
730	52	8.1	323	6	US-10-953-349-3650	Sequence 3650, Ap	804	51.5	8.0	226	7	US-11-056-355B-16751	Sequence 16751, A
731	52	8.1	323	7	US-11-056-355B-27465	Sequence 27465, A	805	51.5	8.0	232	7	US-11-056-355B-101938	Sequence 101938, A
732	52	8.1	323	7	US-11-056-355B-106266	Sequence 106266, A	806	51.5	8.0	232	7	US-11-056-355B-113177	Sequence 113177, A
733	52	8.1	323	7	US-11-056-355B-117505	Sequence 117505, A	807	51.5	8.0	235	7	US-11-056-355B-21384	Sequence 21384, A
734	52	8.1	329	7	US-11-140-450-69	Sequence 69, Appl	808	51.5	8.0	235	7	US-11-330-403-7047	Sequence 7047, Ap
735	52	8.1	330	7	US-11-056-355B-6389	Sequence 6389, Ap	809	51.5	8.0	245	7	US-11-056-355B-3881	Sequence 3881, Ap
736	52	8.1	331	6	US-10-449-902-46038	Sequence 46038, A	810	51.5	8.0	245	7	US-11-056-355B-3881	Sequence 3881, Ap
737	52	8.1	337	6	US-10-953-349-7389	Sequence 7389, Ap	811	51.5	8.0	267	6	US-10-953-349-23517	Sequence 23517, A
738	52	8.1	337	7	US-11-056-355B-25024	Sequence 25024, A	812	51.5	8.0	269	6	US-10-953-349-23516	Sequence 23516, A
739	52	8.1	337	7	US-11-056-355B-103005	Sequence 103005, A	813	51.5	8.0	279	6	US-10-449-902-29997	Sequence 29997, A
740	52	8.1	337	7	US-11-056-355B-114244	Sequence 114244, A	814	51.5	8.0	279	6	US-10-449-902-30297	Sequence 30297, A
741	52	8.1	345	6	US-10-449-902-54215	Sequence 54215, A	815	51.5	8.0	279	6	US-10-449-902-45407	Sequence 45407, A
742	52	8.1	349	6	US-10-449-902-49942	Sequence 49942, A	816	51.5	8.0	280	6	US-10-449-902-48848	Sequence 48848, A
743	52	8.1	349	6	US-10-449-902-50970	Sequence 50970, A	817	51.5	8.0	284	6	US-10-953-349-14864	Sequence 14864, A
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745	52	8.1	358	6	US-10-953-349-37125	Sequence 37125, A	819	51.5	8.0	301	6	US-10-953-349-14863	Sequence 14863, A
746	52	8.1	371	7	US-11-330-403-10198	Sequence 10198, A	820	51.5	8.0	301	7	US-11-056-355B-52108	Sequence 52108, A
747	52	8.1	401	6	US-10-953-349-3688	Sequence 3688, Ap	821	51.5	8.0	307	6	US-10-953-349-14862	Sequence 14862, A
748	52	8.1	438	7	US-11-174-307B-2968	Sequence 2968, Ap	822	51.5	8.0	307	6	US-11-056-355B-52107	Sequence 52107, A
749	52	8.1	439	7	US-11-342-731-4	Sequence 4, Appl	823	51.5	8.0	309	6	US-10-449-902-40558	Sequence 40558, A
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752	52	8.1	529	7	US-11-056-355B-69165	Sequence 69165, A	826	51.5	8.0	330	6	US-10-953-349-12685	Sequence 12685, A
753	52	8.1	550	6	US-10-449-902-48072	Sequence 48072, A	827	51.5	8.0	338	6	US-10-449-902-34689	Sequence 34689, A
754	52	8.1	578	7	US-11-330-403-13171	Sequence 13171, A	828	51.5	8.0	349	7	US-11-056-355B-807	Sequence 807, App
755	52	8.1	581	6	US-10-374-780A-2556	Sequence 2556, Ap	829	51.5	8.0	361	6	US-10-953-349-12684	Sequence 12684, A
756	52	8.1	603	6	US-10-449-902-53745	Sequence 53745, A	830	51.5	8.0	387	7	US-11-056-355B-72593	Sequence 72593, A
757	52	8.1	612	6	US-10-449-902-36368	Sequence 36368, A	831	51.5	8.0	390	7	US-11-056-355B-72592	Sequence 72592, A
758	52	8.1	612	6	US-10-449-902-55786	Sequence 55786, A	832	51.5	8.0	397	7	US-11-283-329-58	Sequence 58, Appl



833	51.5	8.0	407	7	US-11-056-355B-72597	Sequence 72597, A	908	51	7.9	291	7	US-11-292-215-11	Sequence 11, Appl
834	51.5	8.0	408	7	US-11-317-789A-593	Sequence 593, App	909	51	7.9	324	6	US-10-449-902-36620	Sequence 36620, A
835	51.5	8.0	422	7	US-11-056-355B-72591	Sequence 72591, A	910	51	7.9	325	6	US-10-449-902-34685	Sequence 34685, A
836	51.5	8.0	427	7	US-11-056-355B-72596	Sequence 72596, A	911	51	7.9	328	6	US-10-953-349-28707	Sequence 28707, A
837	51.5	8.0	433	7	US-11-056-355B-52655	Sequence 52655, A	912	51	7.9	328	6	US-11-056-355B-68554	Sequence 68554, A
838	51.5	8.0	434	7	US-11-283-329-54	Sequence 54, Appl	913	51	7.9	329	6	US-10-953-349-28706	Sequence 28706, A
839	51.5	8.0	437	7	US-11-051-725-57	Sequence 57, Appl	914	51	7.9	329	6	US-11-056-355B-68553	Sequence 68553, A
840	51.5	8.0	437	7	US-11-051-725-69	Sequence 69, Appl	915	51	7.9	345	6	US-10-953-349-38193	Sequence 38193, A
841	51.5	8.0	448	7	US-11-056-355B-52654	Sequence 52654, A	916	51	7.9	351	6	US-11-056-355B-65495	Sequence 65495, A
842	51.5	8.0	450	6	US-10-539-228-553	Sequence 553, App	917	51	7.9	378	6	US-10-953-349-7748	Sequence 7748, Ap
843	51.5	8.0	466	7	US-11-355-324-2	Sequence 2, Appl	918	51	7.9	385	6	US-10-953-349-7747	Sequence 7747, Ap
844	51.5	8.0	473	7	US-11-283-329-56	Sequence 56, Appl	919	51	7.9	388	7	US-11-056-355B-99650	Sequence 99650, A
845	51.5	8.0	473	7	US-11-355-324-18	Sequence 18, Appl	920	51	7.9	388	7	US-11-056-355B-110889	Sequence 110889, A
846	51.5	8.0	496	7	US-11-056-355B-72595	Sequence 72595, A	921	51	7.9	408	6	US-10-713-648A-60	Sequence 60, Appl
847	51.5	8.0	502	7	US-11-317-789A-595	Sequence 595, App	922	51	7.9	420	7	US-11-056-355B-7713	Sequence 7713, Ap
848	51.5	8.0	504	6	US-10-449-902-51798	Sequence 51798, A	923	51	7.9	420	7	US-11-317-789A-794	Sequence 794, App
849	51.5	8.0	556	7	US-11-330-403-6684	Sequence 6684, Ap	924	51	7.9	438	7	US-11-330-403-1788	Sequence 1788, Ap
850	51.5	8.0	556	7	US-11-330-403-16027	Sequence 16027, A	925	51	7.9	442	7	US-11-234-173-56	Sequence 56, Appl
851	51.5	8.0	557	7	US-11-293-697-3317	Sequence 3317, Ap	926	51	7.9	442	7	US-11-264-784-9	Sequence 9, Appl
852	51.5	8.0	588	6	US-10-449-902-37712	Sequence 37712, A	927	51	7.9	442	7	US-11-264-737-9	Sequence 9, Appl
853	51.5	8.0	591	6	US-10-449-902-46347	Sequence 46347, A	928	51	7.9	442	7	US-11-265-761-9	Sequence 9, Appl
854	51.5	8.0	594	6	US-10-449-902-54008	Sequence 54008, A	929	51	7.9	467	6	US-10-953-349-28705	Sequence 28705, A
855	51.5	8.0	663	7	US-11-293-697-3986	Sequence 3986, Ap	930	51	7.9	467	7	US-11-056-355B-68552	Sequence 68552, A
856	51.5	8.0	717	7	US-11-175-714-9	Sequence 9, Appl	931	51	7.9	468	6	US-10-953-349-7746	Sequence 7746, Ap
857	51.5	8.0	727	6	US-10-449-902-53529	Sequence 53529, A	932	51	7.9	472	6	US-11-056-355B-46575	Sequence 46575, A
858	51.5	8.0	756	7	US-11-289-102-324	Sequence 324, App	933	51	7.9	476	7	US-11-056-355B-99649	Sequence 99649, A
859	51.5	8.0	756	7	US-11-223-738-6	Sequence 6, Appl	934	51	7.9	476	7	US-11-056-355B-110888	Sequence 110888, A
860	51.5	8.0	764	7	US-11-056-355B-42000	Sequence 42000, A	935	51	7.9	489	7	US-11-330-403-15924	Sequence 15924, A
861	51.5	8.0	811	7	US-11-056-355B-74245	Sequence 74245, A	936	51	7.9	496	7	US-11-056-355B-99648	Sequence 99648, A
862	51.5	8.0	842	7	US-11-293-697-4134	Sequence 4134, Ap	937	51	7.9	496	7	US-11-056-355B-110887	Sequence 110887, A
863	51.5	8.0	853	6	US-10-449-902-55541	Sequence 55541, A	938	51	7.9	513	6	US-10-374-780A-1130	Sequence 1130, Ap
864	51.5	8.0	916	7	US-11-056-355B-49199	Sequence 49199, A	939	51	7.9	523	6	US-10-449-902-45098	Sequence 45098, A
865	51.5	8.0	924	6	US-10-520-470-70	Sequence 70, Appl	940	51	7.9	527	6	US-10-449-902-50925	Sequence 50925, A
866	51.5	8.0	938	7	US-11-056-355B-49198	Sequence 49198, A	941	51	7.9	529	7	US-11-106-014-44	Sequence 44, Appl
867	51.5	8.0	949	7	US-11-056-355B-74244	Sequence 74244, A	942	51	7.9	535	7	US-11-293-697-3884	Sequence 3884, Ap
868	51.5	8.0	949	7	US-11-293-697-3033	Sequence 3033, Ap	943	51	7.9	555	6	US-10-449-902-36526	Sequence 36526, A
869	51.5	8.0	971	6	US-11-056-355B-74243	Sequence 74243, A	944	51	7.9	584	6	US-11-330-403-5825	Sequence 5825, Ap
870	51.5	8.0	971	6	US-11-056-355B-74243	Sequence 74243, A	945	51	7.9	595	7	US-11-258-767-26	Sequence 26, Appl
871	51.5	8.0	115	6	US-10-953-349-18159	Sequence 18159, A	946	51	7.9	695	7	US-11-056-355B-46118	Sequence 46118, A
872	51	7.9	115	7	US-11-056-355B-52366	Sequence 52366, A	947	51	7.9	735	7	US-11-056-355B-75493	Sequence 75493, A
873	51	7.9	117	7	US-11-330-403-6268	Sequence 6268, Ap	948	51	7.9	735	7	US-11-056-355B-45530	Sequence 45530, A
874	51	7.9	133	7	US-11-056-355B-15139	Sequence 15139, A	949	51	7.9	757	7	US-11-056-355B-45529	Sequence 45529, A
875	51	7.9	153	7	US-11-293-697-3623	Sequence 3623, Ap	950	51	7.9	774	7	US-11-056-355B-48657	Sequence 48657, A
876	51	7.9	156	6	US-10-449-902-40285	Sequence 40285, A	951	51	7.9	778	7	US-11-056-355B-48656	Sequence 48656, A
877	51	7.9	157	6	US-10-540-898-473	Sequence 473, App	952	51	7.9	782	7	US-11-056-355B-48655	Sequence 48655, A
878	51	7.9	157	6	US-11-056-355B-57064	Sequence 57064, A	953	51	7.9	878	6	US-10-449-902-54103	Sequence 54103, A
879	51	7.9	167	6	US-10-449-902-36906	Sequence 36906, A	954	51	7.9	910	7	US-11-056-355B-46117	Sequence 46117, A
880	51	7.9	167	6	US-10-449-902-41961	Sequence 41961, A	955	51	7.9	910	7	US-11-056-355B-75492	Sequence 75492, A
881	51	7.9	172	6	US-10-449-902-54022	Sequence 54022, A	956	51	7.9	925	6	US-10-449-902-42277	Sequence 42277, A
882	51	7.9	172	6	US-11-056-355B-4679	Sequence 4679, Ap	957	51	7.9	933	7	US-11-056-355B-45528	Sequence 45528, A
883	51	7.9	184	7	US-11-056-355B-4717	Sequence 4717, Ap	958	51	7.9	933	7	US-10-449-902-51776	Sequence 51776, A
884	51	7.9	185	6	US-10-953-349-25301	Sequence 25301, A	959	51	7.9	950	6	US-11-056-355B-46116	Sequence 46116, A
885	51	7.9	195	7	US-11-056-355B-84565	Sequence 84565, A	960	51	7.9	961	7	US-11-056-355B-73491	Sequence 73491, A
886	51	7.9	201	6	US-10-449-902-28923	Sequence 28923, A	961	51	7.9	962	7	US-10-449-902-50509	Sequence 50509, A
887	51	7.9	201	6	US-11-330-403-6275	Sequence 6275, Ap	962	51	7.9	1206	6	US-10-449-902-47190	Sequence 47190, A
888	51	7.9	203	7	US-11-056-355B-20880	Sequence 20880, A	963	51	7.9	1426	6	US-10-505-928-831	Sequence 831, App
889	51	7.9	204	7	US-11-056-355B-20879	Sequence 20879, A	964	51	7.9	2027	6	US-11-063-439-278	Sequence 278, App
890	51	7.9	207	7	US-11-056-355B-67864	Sequence 67864, A	965	50.5	7.8	96	6	US-10-449-902-37750	Sequence 37750, A
891	51	7.9	213	7	US-11-056-355B-2528	Sequence 2528, Ap	966	50.5	7.8	96	6	US-10-953-349-28693	Sequence 28693, A
892	51	7.9	220	6	US-10-953-349-12454	Sequence 12454, A	967	50.5	7.8	112	6	US-11-056-355B-68365	Sequence 68365, A
893	51	7.9	226	7	US-11-056-355B-9248	Sequence 9248, Ap	968	50.5	7.8	112	6	US-10-953-349-35200	Sequence 35200, A
894	51	7.9	226	7	US-10-449-902-55034	Sequence 55034, A	969	50.5	7.8	114	6	US-10-953-349-35200	Sequence 35200, A
895	51	7.9	229	6	US-10-449-902-55034	Sequence 55034, A	970	50.5	7.8	126	7	US-11-293-697-4734	Sequence 4734, Ap
896	51	7.9	231	7	US-11-056-355B-9247	Sequence 9247, Ap	971	50.5	7.8	130	7	US-11-056-355B-580	Sequence 580, App
897	51	7.9	235	7	US-11-056-355B-4715	Sequence 4715, Ap	972	50.5	7.8	133	6	US-10-449-902-35994	Sequence 35994, A
898	51	7.9	244	7	US-11-056-355B-57063	Sequence 57063, A	973	50.5	7.8	134	7	US-11-056-355B-579	Sequence 579, App
899	51	7.9	246	7	US-11-056-355B-57062	Sequence 57062, A	974	50.5	7.8	147	7	US-11-056-355B-9499	Sequence 9499, Ap
900	51	7.9	246	7	US-11-056-355B-67863	Sequence 67863, A	975	50.5	7.8	148	7	US-11-056-355B-60989	Sequence 60989, A
901	51	7.9	248	7	US-11-330-403-379	Sequence 379, App	976	50.5	7.8	157	7	US-11-056-355B-74469	Sequence 74469, A
902	51	7.9	262	6	US-11-056-355B-9087	Sequence 9087, Ap	977	50.5	7.8	157	7	US-11-056-355B-948	Sequence 948, Ap
903	51	7.9	263	6	US-10-449-902-37027	Sequence 37027, A	978	50.5	7.8	163	7	US-11-056-355B-948	Sequence 948, Ap
904	51	7.9	263	6	US-10-449-902-37323	Sequence 37323, A	979	50.5	7.8	168	6	US-10-953-349-35399	Sequence 35399, A
905	51	7.9	268	7	US-11-056-355B-9086	Sequence 9086, Ap	980	50.5	7.8	169	6	US-10-953-349-29043	Sequence 29043, A
906	51	7.9	268	7	US-11-056-355B-46567	Sequence 46567, A	981	50.5	7.8	174	7	US-11-056-355B-51604	Sequence 51604, A
907	51	7.9	282	6	US-10-471-571A-2348	Sequence 2348, Ap	982	50.5	7.8	175	7	US-11-056-355B-66858	Sequence 66858, A

981	50.5	7.8	181	7	US-11-056-355B-9498	Sequence 9498, Ap	1057	50.5	7.8	1181	7	US-11-241-596-355	Sequence 255, App
982	50.5	7.8	201	7	US-11-056-355B-21385	Sequence 21385, A	1058	50.5	7.8	1181	7	US-11-241-596-356	Sequence 256, App
983	50.5	7.8	204	6	US-10-953-349-37463	Sequence 37463, A	1059	50.5	7.8	1181	7	US-11-241-596-357	Sequence 257, App
984	50.5	7.8	216	6	US-10-449-902-35401	Sequence 35401, A	1060	50.5	7.8	1181	7	US-11-241-596-258	Sequence 258, App
985	50.5	7.8	216	6	US-10-449-902-51074	Sequence 51074, A	1061	50.5	7.8	1384	6	US-10-529-931-18	Sequence 18, Appl
986	50.5	7.8	251	6	US-10-953-349-38140	Sequence 38140, A	1062	50.5	7.8	1384	6	US-10-529-931-20	Sequence 20, Appl
987	50.5	7.8	260	7	US-11-056-355B-8517	Sequence 8517, Ap	1063	50.5	7.8	1384	6	US-10-529-931-22	Sequence 22, Appl
988	50.5	7.8	264	7	US-11-056-355B-10540	Sequence 10540, A	1064	50.5	7.8	2440	6	US-11-283-329-196	Sequence 196, App
989	50.5	7.8	268	7	US-11-056-355B-51603	Sequence 51603, A	1065	50.5	7.8	3010	6	US-10-534-774-24	Sequence 24, Appl
990	50.5	7.8	280	6	US-10-953-349-38139	Sequence 38139, A	1066	50.5	7.8	3010	7	US-11-140-487A-769	Sequence 769, App
991	50.5	7.8	289	7	US-11-056-355B-8516	Sequence 8516, Ap	1067	50.5	7.8	3010	7	US-11-140-487A-770	Sequence 770, App
992	50.5	7.8	295	6	US-10-504-973-34	Sequence 34, Appl	1068	50.5	7.8	3697	6	US-11-063-439-288	Sequence 288, App
993	50.5	7.8	304	7	US-11-056-355B-8515	Sequence 8515, Ap	1069	50	7.8	88	6	US-10-449-902-40412	Sequence 40412, A
994	50.5	7.8	327	7	US-11-056-355B-78632	Sequence 78632, A	1070	50	7.8	107	7	US-11-056-355B-56113	Sequence 56113, A
995	50.5	7.8	327	7	US-11-056-355B-84860	Sequence 84860, A	1071	50	7.8	109	7	US-11-330-403-2710	Sequence 2710, Ap
996	50.5	7.8	331	7	US-11-293-697-2499	Sequence 2499, Ap	1072	50	7.8	112	6	US-10-449-902-33801	Sequence 33801, A
997	50.5	7.8	332	6	US-10-953-349-27867	Sequence 27867, A	1073	50	7.8	132	7	US-11-056-355B-55088	Sequence 55088, A
998	50.5	7.8	332	7	US-11-056-355B-65336	Sequence 65336, A	1074	50	7.8	145	6	US-10-449-902-42184	Sequence 42184, A
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1001	50.5	7.8	336	7	US-11-056-355B-111197	Sequence 111197, A	1077	50	7.8	150	6	US-10-953-349-28732	Sequence 28732, A
1002	50.5	7.8	342	7	US-11-056-355B-99957	Sequence 99957, A	1078	50	7.8	185	7	US-11-056-355B-55087	Sequence 55087, A
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1005	50.5	7.8	343	7	US-11-056-355B-111195	Sequence 111195, A	1081	50	7.8	215	7	US-11-056-355B-70364	Sequence 70364, A
1006	50.5	7.8	358	7	US-11-293-697-3662	Sequence 3662, Ap	1082	50	7.8	229	6	US-10-449-902-30195	Sequence 30195, A
1007	50.5	7.8	360	7	US-11-242-111-19	Sequence 19, Appl	1083	50	7.8	266	6	US-10-449-902-48321	Sequence 48321, A
1008	50.5	7.8	361	6	US-10-953-349-27866	Sequence 27866, A	1084	50	7.8	267	6	US-10-953-349-31474	Sequence 31474, A
1009	50.5	7.8	361	7	US-11-056-355B-10726	Sequence 10726, A	1085	50	7.8	278	7	US-11-056-355B-67750	Sequence 67750, A
1010	50.5	7.8	361	7	US-11-056-355B-65335	Sequence 65335, A	1086	50	7.8	278	7	US-11-056-355B-70363	Sequence 70363, A
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1013	50.5	7.8	376	7	US-11-056-355B-30978	Sequence 30978, A	1089	50	7.8	303	6	US-10-953-349-3570	Sequence 3570, Ap
1014	50.5	7.8	376	7	US-11-056-355B-34568	Sequence 34568, A	1090	50	7.8	303	7	US-11-056-355B-23699	Sequence 23699, A
1015	50.5	7.8	382	7	US-11-056-355B-30977	Sequence 30977, A	1091	50	7.8	303	7	US-11-056-355B-35347	Sequence 35347, A
1016	50.5	7.8	382	7	US-11-056-355B-34567	Sequence 34567, A	1092	50	7.8	303	7	US-11-056-355B-77906	Sequence 77906, A
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1018	50.5	7.8	383	7	US-11-056-355B-34566	Sequence 34566, A	1094	50	7.8	303	7	US-11-056-355B-77461	Sequence 77461, A
1019	50.5	7.8	384	7	US-11-056-355B-69080	Sequence 69080, A	1095	50	7.8	303	7	US-11-056-355B-84737	Sequence 84737, A
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1021	50.5	7.8	457	7	US-11-101-316-12	Sequence 12, Appl	1097	50	7.8	303	7	US-11-056-355B-95028	Sequence 95028, A
1022	50.5	7.8	457	7	US-11-376-673-12	Sequence 12, Appl	1098	50	7.8	303	7	US-11-056-355B-101694	Sequence 101694, A
1023	50.5	7.8	474	7	US-11-241-596-46	Sequence 46, Appl	1099	50	7.8	303	7	US-11-056-355B-112933	Sequence 112933, A
1024	50.5	7.8	474	7	US-11-241-596-46	Sequence 46, Appl	1100	50	7.8	313	6	US-10-953-349-33024	Sequence 33024, A
1025	50.5	7.8	474	7	US-11-056-355B-41124	Sequence 41124, A	1101	50	7.8	318	7	US-11-056-355B-75936	Sequence 75936, A
1026	50.5	7.8	474	7	US-11-056-355B-47702	Sequence 47702, A	1102	50	7.8	319	7	US-11-369-089-7	Sequence 7, Appl
1027	50.5	7.8	488	7	US-11-330-403-2937	Sequence 2937, Ap	1103	50	7.8	322	7	US-11-056-355B-77460	Sequence 77460, A
1028	50.5	7.8	526	7	US-11-174-307B-4392	Sequence 4392, Ap	1104	50	7.8	325	7	US-11-056-355B-6688	Sequence 6688, Ap
1029	50.5	7.8	541	7	US-11-241-596-45	Sequence 45, Appl	1105	50	7.8	325	7	US-11-056-355B-6688	Sequence 1982, Ap
1030	50.5	7.8	541	7	US-11-056-355B-41123	Sequence 41123, A	1106	50	7.8	326	7	US-11-056-355B-3928	Sequence 3928, Ap
1031	50.5	7.8	541	7	US-11-056-355B-47701	Sequence 47701, A	1107	50	7.8	326	7	US-11-056-355B-3928	Sequence 3928, Ap
1032	50.5	7.8	552	7	US-11-330-403-1522	Sequence 1522, Ap	1108	50	7.8	337	7	US-10-449-902-39501	Sequence 39501, A
1033	50.5	7.8	583	7	US-11-241-596-44	Sequence 44, Appl	1109	50	7.8	337	7	US-11-056-355B-76203	Sequence 76203, A
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1035	50.5	7.8	583	7	US-11-056-355B-47700	Sequence 47700, A	1111	50	7.8	353	6	US-10-449-902-44136	Sequence 44136, A
1036	50.5	7.8	607	6	US-10-449-902-37969	Sequence 37969, A	1112	50	7.8	377	7	US-11-056-355B-69081	Sequence 69081, A
1037	50.5	7.8	615	7	US-11-283-329-78	Sequence 78, Appl	1113	50	7.8	378	7	US-11-330-403-15891	Sequence 15891, A
1038	50.5	7.8	625	7	US-11-056-355B-95905	Sequence 95905, A	1114	50	7.8	392	6	US-10-449-902-35428	Sequence 35428, A
1039	50.5	7.8	628	7	US-11-056-355B-95904	Sequence 95904, A	1115	50	7.8	392	6	US-10-449-902-35428	Sequence 44, Appl
1040	50.5	7.8	632	6	US-10-534-774-10	Sequence 10, Appl	1116	50	7.8	419	7	US-11-056-355B-1981	Sequence 1981, Ap
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1042	50.5	7.8	648	7	US-11-056-355B-95903	Sequence 95903, A	1118	50	7.8	440	7	US-11-056-355B-3927	Sequence 3926, Ap
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1053	50.5	7.8	978	7	US-11-293-697-4153	Sequence 4153, Ap	1129	50	7.8	533	6	US-10-449-902-31287	Sequence 8726, Ap
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1141	50	7.8	1182	7	US-11-191-644-5	Sequence 5, Appl	1214	49.5	7.7	409	6	US-10-953-349-12949	Sequence 12949, A
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1176	49.5	7.7	236	7	US-11-056-355B-74298	Sequence 74298, A	1249	49.5	7.7	580	6	US-10-449-902-31501	Sequence 31501, A
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1287	49	7.6	239	7	US-11-056-355B-27425	Sequence 27425, A	1361	49	7.6	505	6	US-10-374-780A-1710	Sequence 1710, Ap
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1289	49	7.6	245	7	US-11-056-355B-65967	Sequence 65967, A	1364	49	7.6	518	6	US-10-374-780A-2692	Sequence 2692, Ap
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Job time : 34 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)

10287.399 Million cell updates/sec

Title: US-10-015-967-1

Perfect score: 870

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Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

GenEmbl.\*

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5: gb pr.\*

6: gb ro.\*

7: gb sts.\*

8: gb sy.\*

9: gb un.\*

10: gb vi.\*

11: gb ov.\*

12: gb htg.\*

13: gb in.\*

14: gb om.\*

15: gb ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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 AC092641 Homo sapi  
 DQ369265 Anopheles  
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 AB179302 Macaca fa  
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 BV059932 S212P6027  
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 AC095909 Rattus no  
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 AC024913 Homo sapi  
 AC009318 Arabidops  
 AC181901 Strongylo  
 AC149804 Medicago  
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 CR376853 Danio rer  
 CQ523955 Sequence  
 CQ519528 Sequence



238	39.4	4.5	541	6	BC046339	BC046339 Mus muscu	311	4.5	167159	12	AC073481	AC073481 Homo sapi
239	39.4	4.5	733	11	BC020319	BC020319 Mus muscu	312	4.5	168154	5	AC012174	AC012174 Homo sapi
240	39.4	4.5	1022	6	BC0711345	BC0711345 Danio rer	313	4.5	169310	11	BX323461	BX323461 Zebrafish
241	39.4	4.5	1637	6	BC085715	BC085715 Rattus no	314	4.5	169942	12	AC124793	AC124793 Homo sapi
242	39.4	4.5	101076	12	AC178032	AC178032 Strongylo	315	4.5	171239	12	AC010652	AC010652 Homo sapi
243	39.4	4.5	103610	5	HS024088	AL049544 Human DNA	C 316	4.5	173043	12	AC124792	AC124792 Homo sapi
244	39.4	4.5	110000	13	AC116305_1	Continuation (2 of	C 317	4.5	174287	5	AC010840	AC010840 Homo sapi
245	39.4	4.5	141681	12	CR513785	AC102722 Mus muscu	318	4.5	175258	12	AC017098	AC017098 Homo sapi
246	39.4	4.5	162364	12	CR513785	CR513785 Danio rer	319	4.5	178344	6	AC067846	AC067846 Homo sapi
247	39.4	4.5	163519	11	CR388067	CR388067 Zebrafish	320	4.5	178609	6	AC155298	AC155298 Mus muscu
248	39.4	4.5	165454	5	AL138880	AL138880 Human DNA	321	4.5	178611	12	AC024631	AC024631 Homo sapi
249	39.4	4.5	174126	12	AC135552	AC135552 Canis fam	322	4.5	178810	6	AC099621	AC099621 Mus muscu
250	39.4	4.5	176042	11	CR589876	CR589876 Zebrafish	323	4.5	184697	6	AL627403	AL627403 Mouse DNA
251	39.4	4.5	176392	12	AC135954	AC135954 Papio anu	C 324	4.5	190333	5	AC092129	AC092129 Homo sapi
252	39.4	4.5	207504	6	AC157986	AC157986 Mus muscu	325	4.5	193604	12	AC174144	AC174144 Medicago
253	39.4	4.5	230186	6	AL731678	AL731678 Mouse DNA	326	4.5	194023	5	AC021541	AC021541 Homo sapi
254	39.4	4.5	231146	12	AC172467	AC172467 Bos tauru	327	4.5	196416	5	AC006483	AC006483 Homo sapi
255	39.4	4.5	249136	12	AC106242	AC106242 Rattus no	328	4.5	198019	6	AC116856	AC116856 Mus muscu
256	39.4	4.5	253001	13	AE014834	AE014834 Plasmodiu	329	4.5	201911	12	AC118294	AC118294 Rattus no
257	39.4	4.5	262388	6	AL670959	AL670959 Mouse DNA	330	4.5	210184	11	BX537272	BX537272 Zebrafish
258	39.4	4.5	270983	12	AC172936	AC172936 Bos tauru	331	4.5	220857	12	AC178319	AC178319 Strongylo
259	39.4	4.5	276477	12	AC158009	AC158009 Bos tauru	332	4.5	225611	12	AC111446	AC111446 Rattus no
260	39.2	4.5	309	2	CQ513146	CQ513146 Sequence	C 333	4.5	239891	12	AC096274	AC096274 Rattus no
261	39.2	4.5	337	7	AB134616	AB134616 Homo sapi	334	4.5	254733	13	AC117075	AC117075 Dictyoste
262	39.2	4.5	424	7	BV237881	BV237881 S234P6478	335	4.5	310779	12	AC005140	AC005140 Plasmodiu
263	39.2	4.5	436	7	BV257903	BV257903 S235P6125	336	4.5	333321	13	AC116986	AC116986 Dictyoste
264	39.2	4.5	546	14	BC108236	BC108236 Bos tauru	C 337	4.5	524	7	BV412862	BV412862 S229P6516
265	39.2	4.5	818	6	BC100523	BC100523 Mus muscu	C 338	4.5	633	7	BV288848	BV288848 S232P6214
266	39.2	4.5	913	13	AY542994	AY542994 Bigelowie	C 339	4.5	667	7	BV221313	BV221313 S233P6118
267	39.2	4.5	1805	13	DDIDPP5A	L05617 Dictyosteli	340	4.5	1447	5	AC020589	AC020589 Homo sapi
268	39.2	4.5	1858	5	AB168514	AB168514 Macaca fa	341	4.5	1497	6	BC087038	BC087038 Rattus no
269	39.2	4.5	1974	6	BC023938	BC023938 Mus muscu	342	4.5	1724	6	BC096761	BC096761 Mus muscu
270	39.2	4.5	2158	6	BC031195	BC031195 Mus muscu	343	4.5	1743	11	BC061441	BC061441 Xenopus t
271	39.2	4.5	2433	5	BC041141	BC041141 Homo sapi	344	4.5	1913	6	BC012362	BC012362 Homo sapi
272	39.2	4.5	2702	5	BC004119	BC004119 Homo sapi	345	4.5	2170	6	BC101874	BC101874 Rattus no
273	39.2	4.5	3016	13	DDU31631	U31631 Dictyosteli	346	4.5	2363	6	BC083812	BC083812 Rattus no
274	39.2	4.5	3764	6	BC054483	BC054483 Mus muscu	347	4.5	3863	6	BC088732	BC088732 Mus muscu
275	39.2	4.5	5321	2	AX348330	AX348330 Sequence	C 348	4.5	166333	2	AX344576	AX344576 Sequence
276	39.2	4.5	5321	2	AX356369	AX356369 Sequence	C 349	4.5	95655	12	AC110069	AC110069 Homo sapi
277	39.2	4.5	2568	13	AC116955	AC116955 Dictyoste	C 350	4.5	131633	6	AL713982	AL713982 Mouse DNA
278	39.2	4.5	35102	5	AL591932	AL591932 Human DNA	351	4.5	162726	12	AC179001	AC179001 Strongylo
279	39.2	4.5	110000	12	PFMALBP1_00	AL844507 Plasmodiu	352	4.5	182151	5	AC011835	AC011835 Homo sapi
280	39.2	4.5	110000	12	PFMALBP1_01	Continuation (2 of	353	4.5	185463	5	AC016065	AC016065 Homo sapi
281	39.2	4.5	110000	13	AC116984_2	Continuation (3 of	354	4.5	190623	6	AC121790	AC121790 Mus muscu
282	39.2	4.5	124464	6	AC123927_2	AC123927 Mus muscu	355	4.5	191377	5	AC018398	AC018398 Homo sapi
283	39.2	4.5	164611	6	AC156268	AC156268 Mus muscu	C 356	4.5	201274	6	AC129335	AC129335 Mus muscu
284	39.2	4.5	167792	12	AC113226	AC113226 Papio anu	357	4.5	204114	12	AC153019	AC153019 Mus muscu
285	39.2	4.5	171612	5	AC099742	AC099742 Papio anu	358	4.5	226069	12	AC095365	AC095365 Rattus no
286	39.2	4.5	172335	12	AC181638	AC181638 Strongylo	359	4.5	236105	12	AC165587	AC165587 Bos tauru
287	39.2	4.5	182141	11	AL954645	AL954645 Zebrafish	C 360	4.5	250195	13	AE014831	AE014831 Plasmodiu
288	39.2	4.5	187926	6	AC122801	AC122801 Mus muscu	C 361	4.5	343050	13	PFA929353	AL929353 Plasmodiu
289	39.2	4.5	194207	6	AC163218	AC163218 Mus muscu	362	4.4	582	5	AB168303	AB168303 Macaca fa
290	39.2	4.5	197397	6	AC113115	AC113115 Mus muscu	C 363	4.4	631	7	BV221702	BV221702 S233P645R
291	39.2	4.5	200417	12	AC134192	AC134192 Rattus no	364	4.4	2115	4	AY739287	AY739287 Zea mays
292	39.2	4.5	205150	5	AC005274	AC005274 Homo sapi	365	4.4	2125	2	AX409766	AX409766 Sequence
293	39.2	4.5	217156	6	AC116393	AC116393 Mus muscu	C 366	4.4	2125	5	HUMIGPACID	M86826 Human IGF b
294	39.2	4.5	232208	12	AC097430	AC097430 Rattus no	367	4.4	2480	6	BC107938	BC107938 Rattus no
295	39	4.5	2599	6	BC093588	BC093588 Mus muscu	C 368	4.4	6609	2	AX344839	AX344839 Sequence
296	39	4.5	1575	13	AY069691	AY069691 Drosophil	C 369	4.4	6609	2	AX346785	AX346785 Sequence
297	39	4.5	1790	5	AF136630	AF136630 Homo sapi	C 370	4.4	7218	2	I66494	I66494 Human DNA
298	39	4.5	1999	13	BT004867	BT004867 Drosophil	371	4.4	17598	5	HSJ839811	AL121778 Human DNA
299	39	4.5	2219	5	BC008719	BC008719 Homo sapi	C 372	4.4	30849	13	AC117082	AC117082 Dictyoste
300	39	4.5	2221	5	BC018665	BC018665 Homo sapi	C 373	4.4	33270	13	AC116921	AC116921 Dictyoste
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303	39	4.5	120809	5	AC007026	AC007026 Homo sapi	376	4.4	134768	11	BX537293	BX537293 Zebrafish
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306	39	4.5	164118	12	AC020804	AC020804 Mus muscu	379	4.4	152252	5	AP003039	AP003039 Homo sapi
307	39	4.5	164496	12	AC147881	AC147881 Xenopus t	380	4.4	152719	12	AC012545	AC012545 Homo sapi
308	39	4.5	165641	6	AC135469	AC135469 Mus muscu	C 381	4.4	155949	5	AC091022	AC091022 Homo sapi
309	39	4.5	166236	5	AC022832	AC022832 Homo sapi	C 382	4.4	156863	12	AC069249	AC069249 Homo sapi
310	39	4.5	166411	12	AC178635	AC178635 Strongylo	383	4.4	159036	12	AC180339	AC180339 Strongylo

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384 38.6 4.4 159336 5 AC020584 Homo sapi
385 38.6 AC171167 Strongylo
386 38.6 AC131782 Homo sapi
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BD276277 Serine pr
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BC072923 Xenopus l
AC115608 Dictyoste
AC115594 Dictyoste
AC116987 Dictyoste
AC113330 Homo sapi
AL138643 Arabidops
BX004762 Mus muscu
AL844509 Plasmodiu
AC152492 Rhinoph
AC113331 Homo sapi
AC018375 Homo sapi
AL161633 Bos tauru
AL590419 Homo sapi
CR855265 Danio rer
AC159965 Mus muscu
AC020597 Homo sapi
AC104102 Mus muscu
AC090893 Homo sapi
AL049180 Plasmodiu
AP000752 Homo sapi
AC167784 Glycine m
AC124502 Mus muscu
AC108641 Rattus no
AC134131 Rattus no
BX088646 Zebrafish
CT573229 Danio rer
CR388143 Zebrafish
AC096251 Rattus no
AC105807 Rattus no
AC087226 Mus muscu
AX300942 Sequence
G90722 S08P5777RD
BC058843 Homo sapi
BC058435 Mus muscu
AY069237 Drosophil
BD270518 Novel mai
AX049486 Sequence
AX046601 Sequence
BC102072 Bos tauru
BT010124 Drosophil
BC092417 Homo sapi
AB168314 Macaca fa
BC054868 Xenopus t
BC051810 Homo sapi
BC043451 Mus muscu
BC068304 Mus muscu
AF465310 Dictyoste
AF228873 Strongylo
AX458606 Sequence
AX346544 Sequence
AF465309 Dictyoste
AC115588 Dictyoste
Continuation (4 of
238877 Caenorhabdi
AC095760 Rattus no
BX890561 Danio rer
Continuation (6 of
AC119412 Medicago
AC112499 Homo sapi
AC149953 Strongylo
AC180462 Strongylo
AC067940 Homo sapi
AC180507 Strongylo
AL772321 Mouse chr
AL358332 Human chr
AC124814 Mus muscu
AC011587 Homo sapi
AC180313 Strongylo
BX005481 Zebrafish
AC025298 Homo sapi

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C 530	38	4.4	181351	12	AC021471	AC021471 Homo sapi	603	37.6	4.3	1807	14	BC109511
C 531	38	4.4	182321	5	AL356866	AL356866 Human DNA	604	37.6	4.3	1817	5	BC038370
C 532	38	4.4	183670	12	AC109485	AC109485 Homo sapi	605	37.6	4.3	2018	11	CR761244
C 533	38	4.4	184528	12	AC167463	AC167463 Mus muscu	606	37.6	4.3	2103	6	BC063757
C 534	38	4.4	185255	6	AC127359	AC127359 Mus muscu	607	37.6	4.3	2731	13	AY058318
C 535	38	4.4	190598	6	AC135017	AC135017 Mus muscu	608	37.6	4.3	3133	6	BC058693
C 536	38	4.4	196842	12	AC178756	AC178756 Strongylo	609	37.6	4.3	3151	2	CS150684
C 537	38	4.4	204400	6	AC159812	AC159812 Mus muscu	610	37.6	4.3	3258	4	AB030491
C 538	38	4.4	209529	6	AC154172	AC154172 Mus muscu	611	37.6	4.3	8649	2	AX251083
C 539	38	4.4	213090	6	AL691427	AL691427 Mouse DNA	612	37.6	4.3	8649	2	AX251856
C 540	38	4.4	215559	12	AC141086	AC141086 Mus muscu	613	37.6	4.3	8649	2	AX344242
C 541	38	4.4	238427	12	CR774193	CR774193 Danio rer	C 614	37.6	4.3	8649	2	AX348633
C 542	38	4.4	239995	12	AC073154	AC073154 Mus muscu	C 615	37.6	4.3	35080	13	U29382
C 543	38	4.4	245210	12	AC137771	AC137771 Homo sapi	616	37.6	4.3	36731	13	AC110142
C 544	38	4.4	246196	12	AC105641	AC105641 Rattus no	617	37.6	4.3	37203	13	AC115581
C 545	38	4.4	250029	13	AE014830	AE014830 Plasmodiu	618	37.6	4.3	37538	13	AC115682
C 546	38	4.4	259691	12	AC166835	AC166835 Mus muscu	619	37.6	4.3	79904	6	AL589767
C 547	38	4.4	260085	12	AC164859	AC164859 Mus muscu	C 620	37.6	4.3	89306	12	AL581498
C 548	38	4.4	282899	12	AC095879	AC095879 Rattus no	C 621	37.6	4.3	98204	11	AL645800
C 549	38	4.4	289192	12	AC139506	AC139506 Homo sapi	622	37.6	4.3	106568	12	AC139803
C 550	38	4.4	304391	12	AC158106	AC158106 Bos tauru	623	37.6	4.3	110000	12	AC139803
C 551	38	4.4	329599	12	AC162572	AC162572 Bos tauru	624	37.6	4.3	110000	12	AC140020
C 552	38	4.4	337265	12	AC175878	AC175878 Strongylo	625	37.6	4.3	116280	12	AC179096
C 553	37.8	4.3	664	11	CT025311	CT025311 Xenopus t	C 626	37.6	4.3	124498	12	AC141194
C 554	37.8	4.3	817	14	BC102542	BC102542 Bos tauru	C 627	37.6	4.3	125587	12	AC179714
C 555	37.8	4.3	818	14	CT025519	CT025519 Xenopus t	C 628	37.6	4.3	127449	12	AC180443
C 556	37.8	4.3	851	6	BC024348	BC024348 Mus muscu	C 629	37.6	4.3	136695	12	AC168810
C 557	37.8	4.3	1006	14	BC111143	BC111143 Bos tauru	C 630	37.6	4.3	143124	12	AC176835
C 558	37.8	4.3	1065	6	BC049634	BC049634 Mus muscu	C 631	37.6	4.3	144072	6	CT030862
C 559	37.8	4.3	1443	6	BC061219	BC061219 Mus muscu	C 632	37.6	4.3	147954	12	AC177640
C 560	37.8	4.3	1500	5	BC036796	BC036796 Homo sapi	C 633	37.6	4.3	149129	12	CT027791
C 561	37.8	4.3	1571	14	BC102904	BC102904 Bos tauru	C 634	37.6	4.3	151555	12	AC139276
C 562	37.8	4.3	1910	5	BC043519	BC043519 Homo sapi	C 635	37.6	4.3	157780	12	AC179634
C 563	37.8	4.3	2170	11	BC067704	BC067704 Danio rer	C 636	37.6	4.3	163349	12	AC168256
C 564	37.8	4.3	2446	5	BC046497	BC046497 Homo sapi	C 637	37.6	4.3	166824	11	BX470265
C 565	37.8	4.3	2627	11	XLA440222	AJ440222 Xenopus l	C 638	37.6	4.3	169056	12	AC145104
C 566	37.8	4.3	68805	12	AC101557	AC101557 Mus muscu	C 639	37.6	4.3	171745	12	AC138935
C 567	37.8	4.3	94454	12	AC178937	AC178937 Strongylo	640	37.6	4.3	174329	6	AC140981
C 568	37.8	4.3	110000	12	PMAL8P1	Continuation (12 o	641	37.6	4.3	177492	12	AC168350
C 569	37.8	4.3	125081	12	CR854824	CR854824 Danio rer	642	37.6	4.3	180261	12	AC180779
C 570	37.8	4.3	138038	5	AL591435	AL591435 Human DNA	C 643	37.6	4.3	180480	12	AC140174
C 571	37.8	4.3	140466	5	AL355529	AL355529 Human DNA	644	37.6	4.3	180958	12	AC025779
C 572	37.8	4.3	143057	12	AC176229	AC176229 Strongylo	645	37.6	4.3	183309	11	BX572641
C 573	37.8	4.3	144500	12	AC010231	AC010231 Homo sapi	C 646	37.6	4.3	185162	5	AC140132
C 574	37.8	4.3	149529	12	AC177084	AC177084 Strongylo	647	37.6	4.3	185370	12	CR513788
C 575	37.8	4.3	162564	6	AC127575	AC127575 Mus muscu	648	37.6	4.3	185336	12	AC139837
C 576	37.8	4.3	165490	14	CR925799	CR925799 Wallaby D	649	37.6	4.3	191038	6	AC124719
C 577	37.8	4.3	171722	12	AC162117	AC162117 Ovis arie	C 650	37.6	4.3	193305	12	AC177326
C 578	37.8	4.3	172477	12	CR936378	CR936378 Danio rer	C 651	37.6	4.3	194268	6	AC107863
C 579	37.8	4.3	174019	12	AC025734	AC025734 Homo sapi	C 652	37.6	4.3	196432	11	BX936462
C 580	37.8	4.3	174627	5	AC022138	AC022138 Homo sapi	C 653	37.6	4.3	197523	12	AC018883
C 581	37.8	4.3	176451	12	AC147930	AC147930 Ovis arie	C 654	37.6	4.3	198615	6	AC123678
C 582	37.8	4.3	177308	5	AC009560	AC009560 Homo sapi	C 655	37.6	4.3	199128	5	AC091946
C 583	37.8	4.3	178233	12	AC182141	AC182141 Bos tauru	656	37.6	4.3	200362	6	AC115865
C 584	37.8	4.3	183412	12	AP001899	AP001899 Homo sapi	657	37.6	4.3	205782	6	AC124402
C 585	37.8	4.3	185203	12	AL161649	AL161649 Homo sapi	658	37.6	4.3	210297	12	AC168246
C 586	37.8	4.3	206254	5	AC093283	AC093283 Homo sapi	659	37.6	4.3	212827	6	AC137970
C 587	37.8	4.3	211576	6	AC110564	AC110564 Mus muscu	660	37.6	4.3	217621	12	BX901924
C 588	37.8	4.3	215018	12	AC139113	AC139113 Pongo pyg	661	37.6	4.3	220025	12	AC155769
C 589	37.8	4.3	224076	12	AC119090	AC119090 Rattus no	C 662	37.6	4.3	220171	12	AC113111
C 590	37.8	4.3	228004	12	AC094278	AC094278 Rattus no	663	37.6	4.3	223342	12	AC094125
C 591	37.8	4.3	228925	12	AC158278	AC158278 Canis fam	C 664	37.6	4.3	225302	6	AC109205
C 592	37.8	4.3	240344	12	AC127886	AC127886 Rattus no	C 665	37.6	4.3	229305	12	AC165535
C 593	37.8	4.3	256172	12	AC005139	AC005139 Plasmodiu	666	37.6	4.3	230536	12	AC176874
C 594	37.8	4.3	257109	13	AC116963	AC116963 Dictyoste	C 667	37.6	4.3	232159	12	AC182457
C 595	37.8	4.3	266837	12	AC171870	AC171870 Bos tauru	C 668	37.6	4.3	233321	6	AL732546
C 596	37.8	4.3	279836	12	AC117954	AC117954 Rattus no	C 669	37.6	4.3	236376	12	AC170244
C 597	37.8	4.3	346939	15	BX842643	BX842643 Mycoplasma	C 670	37.6	4.3	238123	12	AC136571
C 598	37.6	4.3	332	2	CQ524615	CQ524615 Sequence	671	37.6	4.3	238598	6	AC117570
C 599	37.6	4.3	650	4	AY731584	AY731584 Arachnis h	C 672	37.6	4.3	244471	12	AC106677
C 600	37.6	4.3	983	5	HSW802179	AL137463 Homo sapi	C 673	37.6	4.3	257109	13	AC116963
C 601	37.6	4.3	999	5	BC073929	BC073929 Homo sapi	C 674	37.6	4.3	257757	13	AE014837
C 602	37.6	4.3	1240	5	BC055418	BC055418 Homo sapi	C 675	37.6	4.3	288857	12	AC128817

676	37.4	4.3	158	2	AX203305	AX203305 Sequence	c 749	37.4	4.3	210010	12	AC146135	AC146135 Pan trogl
677	37.4	4.3	774	7	BV638413	BV638413 S215P060	c 750	37.4	4.3	212717	6	AL929228	AL929228 Mouse DNA
678	37.4	4.3	911	6	BC061126	BC061126 Mus muscu	c 751	37.4	4.3	214189	5	BS000022	BS000022 Pan trogl
679	37.4	4.3	913	6	BC100331	BC100331 Mus muscu	c 752	37.4	4.3	223232	6	AC164312	AC164312 Mus muscu
680	37.4	4.3	989	11	BC083533	BC083533 Danio rer	c 753	37.4	4.3	225196	6	AL672067	AL672067 Mouse DNA
681	37.4	4.3	1113	6	BC100322	BC100322 Mus muscu	c 754	37.4	4.3	228709	12	AC020620	AC020620 Mus muscu
682	37.4	4.3	1138	11	BC046570	BC046570 Xenopus l	c 755	37.4	4.3	229410	12	AC172241	AC172241 Bos tauru
683	37.4	4.3	1367	5	AB179271	AB179271 Macaca fa	c 756	37.4	4.3	230204	12	CR933860	CR933860 Danio rer
684	37.4	4.3	1431	13	AK116801	AK116801 Ciona int	c 757	37.4	4.3	231530	6	AL671975	AL671975 Mouse DNA
685	37.4	4.3	1458	5	BC063635	BC063635 Homo sapi	c 758	37.4	4.3	239450	12	AC106212	AC106212 Rattus no
686	37.4	4.3	1570	5	BC036920	BC036920 Homo sapi	c 759	37.4	4.3	240562	12	AC166667	AC166667 Bos tauru
687	37.4	4.3	1641	5	AK024802	AK024802 Homo sapi	c 760	37.4	4.3	246070	12	AC135737	AC135737 Mus muscu
688	37.4	4.3	1641	5	AK223414	AK223414 Homo sapi	c 761	37.4	4.3	246348	6	AC138611	AC138611 Mus muscu
689	37.4	4.3	1767	4	AF062467	AF062467 Cucumis m	c 762	37.4	4.3	256298	6	AC153651	AC153651 Mus muscu
690	37.4	4.3	1793	4	AY598342	AY598342 Solanum t	c 763	37.4	4.3	277028	12	AC161977	AC161977 Bos tauru
691	37.4	4.3	1973	13	AK116690	AK116690 Ciona int	c 764	37.4	4.3	283992	12	AC096048	AC096048 Rattus no
692	37.4	4.3	2150	13	BT010126	BT010126 Drosophil	c 765	37.4	4.3	307657	13	AE003468	AE003468 Drosophil
693	37.4	4.3	2219	5	BC091490	BC091490 Homo sapi	c 766	37.2	4.3	307657	13	AE003468	AE003468 Drosophil
694	37.4	4.3	2398	2	CS135310	CS135310 Sequence	c 767	37.2	4.3	993	6	BC085939	BC085939 Rattus no
695	37.4	4.3	2398	5	AK000197	AK000197 Homo sapi	c 768	37.2	4.3	1204	5	BC014356	BC014356 Homo sapi
696	37.4	4.3	2601	14	RABTRB2	Me1124 Rabbit germ	c 769	37.2	4.3	1212	13	AF019112	AF019112 Dictyoste
697	37.4	4.3	2601	14	S60737	S60737 T-cell rece	c 770	37.2	4.3	1303	13	BT024358	BT024358 Drosophil
698	37.4	4.3	2633	5	HSM804701	AL833388 Homo sapi	c 771	37.2	4.3	1340	11	BC054234	BC054234 Xenopus l
699	37.4	4.3	2641	6	BC044860	BC044860 Mus muscu	c 772	37.2	4.3	1609	11	BC057515	BC057515 Danio rer
700	37.4	4.3	3084	11	CR942351	CR942351 Xenopus t	c 773	37.2	4.3	1864	11	BC084240	BC084240 Xenopus l
701	37.4	4.3	5054	13	AF298204	AF298204 Dictyoste	c 774	37.2	4.3	1980	5	BC015791	BC015791 Homo sapi
702	37.4	4.3	6013	13	BT015250	BT015250 Drosophil	c 775	37.2	4.3	2085	5	AB168378	AB168378 Macaca fa
703	37.4	4.3	8047	2	AX344916	AX344916 Sequence	c 776	37.2	4.3	2477	14	BC112800	BC112800 Bos tauru
704	37.4	4.3	8111	2	AX347438	AX347438 Sequence	c 777	37.2	4.3	2811	5	BC018650	BC018650 Homo sapi
705	37.4	4.3	8111	2	AX349159	AX349159 Sequence	c 778	37.2	4.3	2986	11	BC084243	BC084243 Xenopus l
706	37.4	4.3	8111	2	AX657810	AX657810 Sequence	c 779	37.2	4.3	3075	13	AF118151	AF118151 Dictyoste
707	37.4	4.3	8111	2	AX659084	AX659084 Sequence	c 780	37.2	4.3	3363	11	CR942633	CR942633 Xenopus t
708	37.4	4.3	14950	2	AX346159	AX346159 Sequence	c 781	37.2	4.3	3890	5	AB097511	AB097511 Macaca fa
709	37.4	4.3	35444	13	U43375	U43375 Caenorhabdi	c 782	37.2	4.3	3993	6	BC060090	BC060090 Mus muscu
710	37.4	4.3	46739	4	AP002052	AP002052 Arabidops	c 783	37.2	4.3	6577	2	AX251920	AX251920 Sequence
711	37.4	4.3	80226	2	CQ597458	CQ597458 Sequence	c 784	37.2	4.3	6577	2	AX346258	AX346258 Sequence
712	37.4	4.3	82139	13	AC115684	AC115684 Dictyoste	c 785	37.2	4.3	6577	2	AX348993	AX348993 Sequence
713	37.4	4.3	109331	12	AC117866	AC117866 Strongylo	c 786	37.2	4.3	9323	6	AJ616838	AJ616838 Mus muscu
714	37.4	4.3	110000	12	AC117108	AC117108 Rattus no	c 787	37.2	4.3	38194	11	BX571725	BX571725 Carp DNA
715	37.4	4.3	110000	12	BX322642_0	BX322642_0 Mus muscu	c 788	37.2	4.3	44851	6	AC004404	AC004404 Mus muscu
716	37.4	4.3	110000	12	BX322642_1	BX322642_1 Mus muscu	c 789	37.2	4.3	46463	12	AC102078	AC102078 Mus muscu
717	37.4	4.3	110000	12	BX322642_3	Continuation (2 of	c 790	37.2	4.3	46463	12	AC102078	AC102078 Mus muscu
718	37.4	4.3	110000	12	AC007125	Continuation (4 of	c 791	37.2	4.3	88549	13	AC116924	AC116924 Dictyoste
719	37.4	4.3	115022	5	AC099743	AC099743 Arabidops	c 792	37.2	4.3	95359	5	AC078903	AC078903 Homo sapi
720	37.4	4.3	127508	5	AP002864	AP002864 Homo sapi	c 793	37.2	4.3	103275	12	AC136252	AC136252 Rattus no
721	37.4	4.3	130435	5	HS71807	AL035541 Human DNA	c 794	37.2	4.3	110000	6	AE008686_3	Continuation (4 of
722	37.4	4.3	136119	5	HS1028D15	AL121886 Human DNA	c 795	37.2	4.3	110000	12	AC112368_3	Continuation (4 of
723	37.4	4.3	147934	6	AC164113	AC164113 Mus muscu	c 796	37.2	4.3	120448	6	AC174651	AC174651 Mus muscu
724	37.4	4.3	149264	6	AC140283	AC140283 Mus muscu	c 797	37.2	4.3	126804	12	AC179202	AC179202 Strongylo
725	37.4	4.3	149291	6	AC116328	AC116328 Mus muscu	c 798	37.2	4.3	137911	6	AC115015	AC115015 Mus muscu
726	37.4	4.3	151643	6	AC127227	AC127227 Mus muscu	c 799	37.2	4.3	142781	12	AC141934	AC141934 Rattus no
727	37.4	4.3	159426	12	AC178902	AC178902 Strongylo	c 800	37.2	4.3	148361	12	AC179290	AC179290 Strongylo
728	37.4	4.3	159980	12	AC149021	AC149021 Daelypus n	c 801	37.2	4.3	150385	11	BX511147	BX511147 Zebrafish
729	37.4	4.3	162921	12	AC013528	AC013528 Homo sapi	c 802	37.2	4.3	153083	6	CR936849	CR936849 Mouse DNA
730	37.4	4.3	164399	13	PPMAL3P6	Z98551 Plasmodium	c 803	37.2	4.3	155132	12	AC080148	AC080148 Homo sapi
731	37.4	4.3	170575	12	AC019758	AC019758 Drosophil	c 804	37.2	4.3	160295	6	AC140358	AC140358 Mus muscu
732	37.4	4.3	170705	12	AC178099	AC178099 Strongylo	c 805	37.2	4.3	168698	5	AC068138	AC068138 Homo sapi
733	37.4	4.3	170788	12	AC139387	AC139387 Rattus no	c 806	37.2	4.3	169599	12	AC180326	AC180326 Strongylo
734	37.4	4.3	172472	5	AC095058	AC095058 Homo sapi	c 807	37.2	4.3	171785	12	AC176265	AC176265 Strongylo
735	37.4	4.3	176086	6	AC124729	AC124729 Mus muscu	c 808	37.2	4.3	172465	12	BX324192	BX324192 Mus muscu
736	37.4	4.3	176455	12	AC178313	AC178313 Strongylo	c 809	37.2	4.3	173134	11	AL935282	AL935282 Zebrafish
737	37.4	4.3	179776	13	AC010026	AC010026 Drosophil	c 810	37.2	4.3	176533	12	AC179122	AC179122 Strongylo
738	37.4	4.3	181076	6	AC110803	AC110803 Mus muscu	c 811	37.2	4.3	176793	12	AC167130	AC167130 Mus muscu
739	37.4	4.3	181179	6	AC102031	AC102031 Mus muscu	c 812	37.2	4.3	177363	5	AC073856	AC073856 Homo sapi
740	37.4	4.3	181308	12	BT030718	BT030718 Danio rer	c 813	37.2	4.3	177745	6	AC144923	AC144923 Mus muscu
741	37.4	4.3	183533	5	BS000021	BS000021 Pan trogl	c 814	37.2	4.3	185146	6	AC102573	AC102573 Mus muscu
742	37.4	4.3	186197	12	AL627384	AL627384 Homo sapi	c 815	37.2	4.3	185517	6	AC140231	AC140231 Mus muscu
743	37.4	4.3	195837	4	ATCHR1V21	AL161509 Arabidops	c 816	37.2	4.3	186218	6	AC129592	AC129592 Mus muscu
744	37.4	4.3	201073	6	AC158903	AC158903 Mus muscu	c 817	37.2	4.3	189063	6	AC123736	AC123736 Mus muscu
745	37.4	4.3	202001	6	AL772303	AL772303 Mouse DNA	c 818	37.2	4.3	195662	12	AC173888	AC173888 Bos tauru
746	37.4	4.3	205310	12	AC134491	AC134491 Rattus no	c 819	37.2	4.3	196377	14	AC105306	AC105306 Bos tauru
747	37.4	4.3	208914	12	BX927237	BX927237 Danio rer	c 820	37.2	4.3	196902	6	AC153381	AC153381 Mus muscu
748	37.4	4.3	209251	5	AC100848	AC100848 Homo sapi	c 821	37.2	4.3	197913	6	AC163657	AC163657 Mus muscu

822	37.2	4.3	200477	12	AC158221	AC158221 Mus muscu	895	37	4.3	140288	12	CR631128	CR631128 Danio rer
823	37.2	4.3	203296	12	AC152839	AC152839 Bos tauru	c 896	37	4.3	140288	12	CR631128	CR631128 Danio rer
824	37.2	4.3	203628	6	AC160633	AC160633 Mus muscu	897	37	4.3	140288	12	CR954190	CR954190 Medicago
c 825	37.2	4.3	204465	6	AC117232	AC117232 Mus muscu	898	37	4.3	143996	12	AC068859	AC068859 Homo sapi
c 826	37.2	4.3	205870	11	AX088895	AX088895 Zebrafish	899	37	4.3	154402	12	AC139634	AC139634 Gallus ga
c 827	37.2	4.3	207354	6	AL671857	AL671857 Mouse DNA	900	37	4.3	154847	5	AL357894	AL357894 Human DNA
c 828	37.2	4.3	208625	12	AC164605	AC164605 Mus muscu	901	37	4.3	155023	11	CR354440	CR354440 Zebrafish
c 829	37.2	4.3	214911	12	CT009578	CT009578 Mus muscu	902	37	4.3	161881	12	CT033841	CT033841 Danio rer
c 830	37.2	4.3	215095	12	AC126729	AC126729 Rattus no	903	37	4.3	162826	11	AX248393	AX248393 Zebrafish
c 831	37.2	4.3	215566	6	AC119805	AC119805 Mus muscu	904	37	4.3	168027	12	AC177170	AC177170 Strongylo
c 832	37.2	4.3	217361	12	AC159695	AC159695 Bos tauru	905	37	4.3	169330	6	AC162869	AC162869 Mus muscu
c 833	37.2	4.3	226664	12	AC157175	AC157175 Bos tauru	c 906	37	4.3	175003	6	AC115900	AC115900 Mus muscu
c 834	37.2	4.3	231934	12	AC169709	AC169709 Bos tauru	c 907	37	4.3	176702	12	AC011206	AC011206 Homo sapi
c 835	37.2	4.3	233274	12	AC106465	AC106465 Rattus no	c 908	37	4.3	182043	6	AC102166	AC102166 Mus muscu
c 836	37.2	4.3	236692	12	AC119690	AC119690 Rattus no	c 909	37	4.3	182303	11	AX470267	AX470267 Zebrafish
c 837	37.2	4.3	239426	12	AC111207	AC111207 Rattus no	910	37	4.3	183648	13	AC117081	AC117081 Dictyoste
c 838	37.2	4.3	240825	2	AX087869	AX087869 Sequence	911	37	4.3	186842	6	AC154553	AC154553 Mus muscu
c 839	37.2	4.3	240825	2	AX523960	AX523960 Sequence	912	37	4.3	187725	5	AC146205	AC146205 Pan trogl
c 840	37.2	4.3	245802	12	AC006279	AC006279 Plasmodiu	c 913	37	4.3	190210	12	AC022318	AC022318 Homo sapi
c 841	37.2	4.3	250707	13	AE014848	AE014848 Plasmodiu	c 914	37	4.3	192915	12	AC181115	AC181115 Strongylo
c 842	37.2	4.3	253540	12	AC095829	AC095829 Rattus no	915	37	4.3	193531	12	AC181266	AC181266 Strongylo
c 843	37.2	4.3	254175	12	AC122615	AC122615 Rattus no	c 916	37	4.3	193623	12	AC117843	AC117843 Rattus no
c 844	37.2	4.3	260929	13	AE014852	AE014852 Plasmodiu	c 917	37	4.3	193882	6	AC161231	AC161231 Mus muscu
c 845	37.2	4.3	262212	12	AC103198	AC103198 Rattus no	918	37	4.3	197147	12	AC172910	AC172910 Bos tauru
c 846	37.2	4.3	279278	12	AC158093	AC158093 Bos tauru	c 919	37	4.3	199549	5	AC100773	AC100773 Homo sapi
c 847	37.2	4.3	281723	13	PFA929359	AL929359 Plasmodiu	c 920	37	4.3	199782	6	AC134985	AC134985 Mus muscu
c 848	37.2	4.3	301168	12	AC172631	AC172631 Bos tauru	c 921	37	4.3	199914	5	BS000009	BS000009 Pan trogl
c 849	37.2	4.3	319485	12	AC078979	AC078979 Homo sapi	922	37	4.3	200205	12	CR388366	CR388366 Danio rer
c 850	37	4.3	127	2	CQ777636	CQ777636 Sequence	923	37	4.3	200631	6	AC134867	AC134867 Mus muscu
c 851	37	4.3	518	4	QSAJ692	AJ000692 Quercus s	924	37	4.3	201739	6	AC134698	AC134698 Mus muscu
c 852	37	4.3	602	7	BV252778	BV252778 S234P653R	925	37	4.3	202336	6	AC087727	AC087727 Mus muscu
c 853	37	4.3	810	7	BV479961	BV479961 qhg30g10.	c 926	37	4.3	204569	6	AC169384	AC169384 Mus muscu
c 854	37	4.3	1040	13	AY069658	AY069658 Drosophil	927	37	4.3	211183	6	AL731771	AL731771 Mouse DNA
c 855	37	4.3	1085	11	CT025478	CT025478 Xenopus t	928	37	4.3	241400	6	AL646093	AL646093 Mouse DNA
c 856	37	4.3	1172	11	BC088827	BC088827 Xenopus t	c 929	37	4.3	243036	12	AC112103	AC112103 Rattus no
c 857	37	4.3	1291	5	BC093090	BC093090 Homo sapi	c 930	37	4.3	245812	12	AC131444	AC131444 Rattus no
c 858	37	4.3	1315	11	BC084499	BC084499 Xenopus t	c 931	37	4.3	250022	13	AE014824	AE014824 Plasmodiu
c 859	37	4.3	1356	6	BC034886	BC034886 Mus muscu	932	37	4.3	250823	13	AE014821	AE014821 Plasmodiu
c 860	37	4.3	1555	11	BC064241	BC064241 Xenopus t	933	37	4.3	257581	12	AC157013	AC157013 Bos tauru
c 861	37	4.3	2171	2	CS113396	CS113396 Sequence	c 934	37	4.3	271629	12	AC143316	AC143316 Macaca mu
c 862	37	4.3	2171	2	CS113514	CS113514 Sequence	935	36.8	4.2	282	2	CQ515927	CQ515927 Sequence
c 863	37	4.3	2249	5	BC092410	BC092410 Homo sapi	936	36.8	4.2	360	2	CQ527206	CQ527206 Sequence
c 864	37	4.3	2274	6	BC096371	BC096371 Mus muscu	c 937	37	4.2	370	2	CQ476082	CQ476082 Sequence
c 865	37	4.3	2307	13	AY095053	AY095053 Drosophil	938	36.8	4.2	400	5	AF041005	AF041005 Homo sapi
c 866	37	4.3	2587	11	CR926175	CR926175 Xenopus t	939	36.8	4.2	441	2	AR506593	AR506593 Sequence
c 867	37	4.3	2820	13	BT010288	BT010288 Drosophil	c 940	36.8	4.2	445	2	CQ410337	CQ410337 Sequence
c 868	37	4.3	2723	5	BC042178	BC042178 Homo sapi	941	36.8	4.2	533	6	BC090389	BC090389 Mus muscu
c 869	37	4.3	2783	11	BC081012	BC081012 Xenopus l	942	36.8	4.2	565	14	BC105433	BC105433 Bos tauru
c 870	37	4.3	3238	6	BC069041	BC069041 Mus muscu	c 943	36.8	4.2	672	7	BV426135	BV426135 S237P6520
c 871	37	4.3	3348	11	BC066759	BC066759 Danio rer	944	36.8	4.2	1046	5	AB168908	AB168908 Macaca fa
c 872	37	4.3	3973	2	AX345073	AX345073 Sequence	945	36.8	4.2	1166	11	BC097178	BC097178 Danio rer
c 873	37	4.3	5597	2	AX347107	AX347107 Sequence	946	36.8	4.2	1182	6	BC049567	BC049567 Mus muscu
c 874	37	4.3	6136	2	AX348428	AX348428 Sequence	947	36.8	4.2	1257	13	BT001395	BT001395 Drosophil
c 875	37	4.3	6232	11	BC084088	BC084088 Xenopus l	948	36.8	4.2	1290	2	CQ981351	CQ981351 Sequence
c 876	37	4.3	7686	5	HSM808085	BS467939 Homo sapi	949	36.8	4.2	1290	5	BC007024	BC007024 Homo sapi
c 877	37	4.3	8234	2	AX346551	AX346551 Sequence	950	36.8	4.2	1316	5	HSM801735	AL136767 Homo sapi
c 878	37	4.3	10039	5	AX346944	AX346944 Sequence	951	36.8	4.2	1508	2	AR264367	AR264367 Sequence
c 879	37	4.3	34516	5	BSX01885	BSX01885 Human DNA	952	36.8	4.2	1607	5	BC068273	BC068273 Homo sapi
c 880	37	4.3	34969	12	AC180530	AC180530 Strongylo	953	36.8	4.2	1633	11	BC084760	BC084760 Xenopus l
c 881	37	4.3	79976	4	AB008264	AB008264 Arabidops	954	36.8	4.2	1697	2	AR310263	AR310263 Sequence
c 882	37	4.3	84821	6	AB0076123	AB0076123 Mouse DNA	955	36.8	4.2	1697	2	AR640306	AR640306 Sequence
c 883	37	4.3	89995	5	AC133794	AC133794 Homo sapi	956	36.8	4.2	1725	2	AR451632	AR451632 Sequence
c 884	37	4.3	91319	12	AC172456	AC172456 Bos tauru	957	36.8	4.2	1841	4	AF387639	AF387639 Arabidops
c 885	37	4.3	92815	5	AC067990	AC067990 Homo sapi	958	36.8	4.2	1877	5	BC062584	BC062584 Homo sapi
c 886	37	4.3	94153	12	AC139443	AC139443 Rattus no	959	36.8	4.2	1898	2	I46765	I46765 Sequence 1
c 887	37	4.3	97428	11	BS323028	BS323028 Zebrafish	960	36.8	4.2	1933	5	HSM806724	BS406667 Homo sapi
c 888	37	4.3	105682	6	AL929160	Continuation (4 of	961	36.8	4.2	2141	5	BC053352	BC053352 Homo sapi
c 889	37	4.3	107366	3	AL929160	Continuation (4 of	962	36.8	4.2	2196	5	HSM801403	AL133557 Homo sapi
c 890	37	4.3	110000	12	AC115497	AC115497 Rattus no	963	36.8	4.2	2219	13	AY061258	AY061258 Drosophil
c 891	37	4.3	110000	15	BSX08798	Continuation (19 o	964	36.8	4.2	2245	6	BC005686	BC005686 Mus muscu
c 892	37	4.3	113880	13	PFNAL3P4	AL008970 Plasmodiu	965	36.8	4.2	2262	5	BC041668	BC041668 Homo sapi
c 893	37	4.3	117343	12	AC177694	AC177694 Strongylo	966	36.8	4.2	2294	11	BC045728	BC045728 Xenopus l
c 894	37	4.3	129256	12	BSX27183	BSX27183 Danio rer	967	36.8	4.2	2291	5	BC045767	BC045767 Homo sapi

968	36.8	4.2	3000	11	BC068787	1041	36.8	4.2	170233	5	AC147091
969	36.8	4.2	3066	11	BC074642	1042	36.8	4.2	170998	5	AL390071
970	36.8	4.2	4346	13	BT016106	1043	36.8	4.2	171430	12	AC110599
c 971	36.8	4.2	5511	2	AC346773	c1044	36.8	4.2	173547	12	AC073637
972	36.8	4.2	5774	6	BC060122	1045	36.8	4.2	173614	6	AC125122
c 973	36.8	4.2	7742	2	AC348912	c1046	36.8	4.2	175166	12	AC128626
c 974	36.8	4.2	9742	2	AC348912	c1047	36.8	4.2	175166	5	AC021049
c 975	36.8	4.2	1135	5	AL589808	c1048	36.8	4.2	175315	5	AC021049
c 976	36.8	4.2	13670	13	AY380531	c1049	36.8	4.2	176045	6	AC122370
c 977	36.8	4.2	13670	13	AY380567	c1050	36.8	4.2	176045	6	AC122370
c 978	36.8	4.2	14112	2	AC251232	1051	36.8	4.2	178129	12	AC179763
c 979	36.8	4.2	14112	2	AC344329	1052	36.8	4.2	178273	12	AC005308
c 980	36.8	4.2	14112	2	AC346345	1053	36.8	4.2	180465	6	AC163390
c 981	36.8	4.2	14112	2	AX458464	1054	36.8	4.2	180854	5	AC107960
c 982	36.8	4.2	29571	13	AF077541	1055	36.8	4.2	181313	6	AC124332
c 983	36.8	4.2	36454	13	AC006670	1056	36.8	4.2	181519	6	AC112968
c 984	36.8	4.2	57705	12	AC104245	1057	36.8	4.2	181796	12	AC178482
c 985	36.8	4.2	57817	12	AC173970	1058	36.8	4.2	182871	13	AC111716
c 986	36.8	4.2	64491	5	AL365188	1059	36.8	4.2	185938	6	AC122802
c 987	36.8	4.2	68190	12	AC090604	1060	36.8	4.2	186717	12	AC147894
c 988	36.8	4.2	73572	12	AC170406	1061	36.8	4.2	188449	12	CR381660
c 989	36.8	4.2	78579	12	AC177634	1062	36.8	4.2	189038	12	AC120323
c 990	36.8	4.2	85916	13	AC117080	1063	36.8	4.2	197092	12	AC036155
c 991	36.8	4.2	87485	11	AL627170	c1064	36.8	4.2	201389	12	CT485674
c 992	36.8	4.2	90578	5	AC128686	c1065	36.8	4.2	202967	12	AC175374
c 993	36.8	4.2	93831	11	AL627163	1066	36.8	4.2	202967	12	CR753862
c 994	36.8	4.2	99216	12	AC179582	1067	36.8	4.2	204840	12	Danio rer
c 995	36.8	4.2	105240	5	AC002124	1068	36.8	4.2	205273	6	AL845364
c 996	36.8	4.2	105488	11	BX537356	1069	36.8	4.2	205429	12	AC005506
c 997	36.8	4.2	108780	5	AC021945	1070	36.8	4.2	205508	6	AC079243
c 998	36.8	4.2	108994	5	HS124K22	1071	36.8	4.2	206489	12	CR956401
c 999	36.8	4.2	109973	12	AC007555	1072	36.8	4.2	207400	6	AL155261
1000	36.8	4.2	110000	13	AC105546 <sup>2</sup>	1073	36.8	4.2	212973	6	AL683847
1001	36.8	4.2	110000	15	AB017243 <sup>5</sup>	1074	36.8	4.2	214419	6	AC101932
c1002	36.8	4.2	110035	5	AC022405	1075	36.8	4.2	216008	12	AC178129
c1003	36.8	4.2	114664	4	AC130809	c1076	36.8	4.2	221584	12	AC177229
c1004	36.8	4.2	119944	5	AC111162	c1077	36.8	4.2	221990	12	AC161923
1005	36.8	4.2	125855	4	AC151823	c1078	36.8	4.2	222981	6	AL669981
1006	36.8	4.2	127831	12	AC177469	c1079	36.8	4.2	224108	12	AC182012
c1007	36.8	4.2	133263	12	AC126235	1080	36.8	4.2	225457	12	AC110659
1008	36.8	4.2	134640	13	AC181778	1081	36.8	4.2	225545	12	AC110659
1009	36.8	4.2	136240	13	AC117070	1082	36.8	4.2	225873	12	AC111240
c1010	36.8	4.2	136285	12	AC160608	1083	36.8	4.2	227450	12	AC103214
1011	36.8	4.2	139640	11	BX511108	c1084	36.8	4.2	232225	6	AL662876
1012	36.8	4.2	139852	5	AC156620	1085	36.8	4.2	232225	6	AL662876
1013	36.8	4.2	141672	4	AC146567	1086	36.8	4.2	236652	12	AC109202
1014	36.8	4.2	143137	12	AC180304	1087	36.8	4.2	236652	12	AC095395
c1015	36.8	4.2	143585	12	AC013349	c1088	36.8	4.2	245030	12	AC106061
c1016	36.8	4.2	145271	12	AC169089	c1089	36.8	4.2	245472	12	AC137473
c1017	36.8	4.2	147160	12	AC181723	c1090	36.8	4.2	247979	13	AC092261
1018	36.8	4.2	148782	12	CT573397	1091	36.8	4.2	250421	13	AE014849
1019	36.8	4.2	148890	12	AC022614	1092	36.8	4.2	250531	13	AE014845
1020	36.8	4.2	150963	12	AC006727	1093	36.8	4.2	250713	13	AE014850
c1021	36.8	4.2	151763	12	AC001715	1094	36.6	4.2	251814	6	AL591882
c1022	36.8	4.2	153439	5	AL138914	c1095	36.6	4.2	252394	13	AE014833
c1023	36.8	4.2	154071	13	AC115598	1096	36.6	4.2	265	2	CQ516973
c1024	36.8	4.2	154883	5	AC154914	1097	36.6	4.2	265	2	CQ516973
c1025	36.8	4.2	155270	5	AL391384	1098	36.6	4.2	265	2	CQ516973
1026	36.8	4.2	156328	12	AC148280	1099	36.6	4.2	265	2	CQ516973
1027	36.8	4.2	156466	12	AL139181	1100	36.6	4.2	265	2	CQ516973
c1028	36.8	4.2	157054	12	AC021782	1101	36.6	4.2	265	2	CQ516973
1029	36.8	4.2	157402	12	AC034161	1102	36.6	4.2	265	2	CQ516973
c1030	36.8	4.2	159723	12	AC021862	1103	36.6	4.2	265	2	CQ516973
c1031	36.8	4.2	160748	5	AC001234	1104	36.6	4.2	265	2	CQ516973
1032	36.8	4.2	165254	6	AC117189	1105	36.6	4.2	265	2	CQ516973
1033	36.8	4.2	165287	5	AC090599	1106	36.6	4.2	265	2	CQ516973
c1034	36.8	4.2	167196	12	CT025585	1107	36.6	4.2	265	2	CQ516973
1035	36.8	4.2	168492	5	AC092989	1108	36.6	4.2	265	2	CQ516973
c1036	36.8	4.2	169054	12	AC068444	1109	36.6	4.2	265	2	CQ516973
c1037	36.8	4.2	169135	11	BX649325	1110	36.6	4.2	265	2	CQ516973
1038	36.8	4.2	169150	12	AC026141	1111	36.6	4.2	265	2	CQ516973
1039	36.8	4.2	169418	5	AC104163	1112	36.6	4.2	265	2	CQ516973
1040	36.8	4.2	169546	12	AC004157	1113	36.6	4.2	265	2	CQ516973

AC147091	Pan trogl
AL390071	Human DNA
AC110599	Homo sapi
AC073637	Homo sapi
AC125122	Mus muscu
AC128626	Rattus no
AC021049	Homo sapi
AC122370	Mus muscu
AC179763	Strongylo
AC005308	Plasmodiu
AC163390	Mus muscu
AC107960	Homo sapi
AC124332	Mus muscu
AC112968	Mus muscu
AC178482	Strongylo
AC111716	Dictyoste
AC122802	Mus muscu
AC147894	Xenopus t
CR381660	Danio rer
AC120323	Rattus no
AC036155	Homo sapi
CT485674	Danio rer
AC175374	Colobus g
CR753862	Danio rer
AL845364	Mouse DNA
AC005506	Plasmodiu
AC079243	Mus muscu
CR956401	Danio rer
AC155261	Mus muscu
AL683847	Mouse DNA
AC101932	Mus muscu
AC178129	Strongylo
AC177229	Strongylo
AL669981	Mouse DNA
AC182012	Otolemur
AC110659	Rattus no
AC11240	Rattus no
AC103214	Rattus no
AL662876	Mouse DNA
AC181741	Strongylo
AC129111	Rattus no
AC109202	Mus muscu
AC095395	Rattus no
AC106061	Rattus no
AC137473	Rattus no
AC092261	Mus muscu
AE014849	Plasmodiu
AE014845	Plasmodiu
AE014850	Plasmodiu
AL591882	Mouse DNA
AE014833	Plasmodiu
CQ516973	Sequence
AX185705	Sequence
BC034898	Mus muscu
BC091177	Rattus no
CR848247	Xenopus t
BC027418	Mus muscu
BC013496	Mus muscu
AR110206	Sequence
AR169965	Sequence
AR171774	Sequence
BD009002	Promoter
BD189471	PROMOTER
AR264114	Sequence
BC095695	Danio rer
CQ981633	Sequence
BC016808	Homo sapi
AK113486	Ciona int
BC103477	Rattus no
BC052355	Mus muscu
BC102907	Bos tauru

1114	36.6	4.2	1880	14	BC1111249	BC111249 Bos tauru	1187	36.6	4.2	200476	5	AL845433	AL845433 Human DNA
1115	36.6	4.2	1976	6	BC086985	BC086985 Rattus no	1188	36.6	4.2	200787	12	AL154588	AL154588 Mus muscu
1116	36.6	4.2	2096	5	BC050272	BC050272 Homo sapi	1189	36.6	4.2	200900	6	CT573810	CT573810 Danio rer
1117	36.6	4.2	2171	5	BC054515	BC054515 Homo sapi	1190	36.6	4.2	203380	12	AC178118	AC178118 Strongylo
1118	36.6	4.2	2210	5	AB066547	AB066547 Macaca fa	1191	36.6	4.2	205762	12	AC156303	AC156303 Bos tauru
1119	36.6	4.2	2411	5	AF262962	AF262962 Homo sapi	1192	36.6	4.2	206494	12	AC098183	AC098183 Rattus no
1120	36.6	4.2	2421	14	BC112771	BC112771 Bos tauru	1193	36.6	4.2	206687	12	AC167986	AC167986 Bos tauru
1121	36.6	4.2	2597	5	BC041693	BC041693 Homo sapi	1194	36.6	4.2	209782	6	AL603905	AL603905 Mouse DNA
1122	36.6	4.2	2821	6	BC031460	BC031460 Mus muscu	1195	36.6	4.2	210086	6	AL105256	AL105256 Mus muscu
1123	36.6	4.2	3000	14	SSPA11	Y11347 S. scrofa mR	1196	36.6	4.2	212224	12	AC176556	AC176556 Strongylo
1124	36.6	4.2	7781	2	AX346071	AX346071 Sequence	1197	36.6	4.2	214204	12	AC167255	AC167255 Bos tauru
1125	36.6	4.2	15367	2	AX059499	AX059499 Sequence	1198	36.6	4.2	216397	12	AC115199	AC115199 Rattus no
1126	36.6	4.2	16439	2	AX345789	AX345789 Sequence	1199	36.6	4.2	216405	12	AC173414	AC173414 Bos tauru
1127	36.6	4.2	16633	12	AC169896	AC169896 Macaca mu	1200	36.6	4.2	217542	12	AC1112847	AC112847 Rattus no
1128	36.6	4.2	58483	12	AC100352	AC100352 Mus muscu	1201	36.6	4.2	218081	6	AC068607	AC068607 Mus muscu
1129	36.6	4.2	83745	12	AC169858	AC169858 Macaca mu	1202	36.6	4.2	219382	11	BX247881	BX247881 Zebrafish
1130	36.6	4.2	90506	12	AC1808954	AC1808954 Strongylo	1203	36.6	4.2	220520	12	CT554371	CT554371 Danio rer
1131	36.6	4.2	93301	12	AC074165	AC074165 Mus muscu	1204	36.6	4.2	222308	11	BX530069	BX530069 Zebrafish
1132	36.6	4.2	94191	12	AC178461	AC178461 Strongylo	1205	36.6	4.2	224470	12	AC160358	AC160358 Bos tauru
1133	36.6	4.2	96583	2	AR777048	AR777048 Sequence	1206	36.6	4.2	225125	12	AC179910	AC179910 Strongylo
1134	36.6	4.2	96583	4	ATAC009992	ATAC009992 Arabidops	1207	36.6	4.2	228276	12	AC120908	AC120908 Rattus no
1135	36.6	4.2	97505	6	BX293544	BX293544 Mouse DNA	1208	36.6	4.2	239170	12	AC153414	AC153414 Bos tauru
1136	36.6	4.2	99670	6	AC123709	AC123709 Mus muscu	1209	36.6	4.2	248203	12	AC155036	AC155036 Bos tauru
1137	36.6	4.2	106742	5	AC008904	AC008904 Homo sapi	1210	36.6	4.2	251527	12	AC170673	AC170673 Bos tauru
1138	36.6	4.2	111995	4	AP006663	AP006663 Lotus cor	1211	36.6	4.2	266544	13	AC116956	AC116956 Dictyoste
1139	36.6	4.2	113884	5	AL512442	AL512442 Human DNA	1212	36.6	4.2	266884	12	CT033803	CT033803 Danio rer
1140	36.6	4.2	114820	12	AC157796	AC157796 Mus muscu	1213	36.6	4.2	286149	12	CT033805	CT033805 Danio rer
1141	36.6	4.2	121190	12	AC151659	AC151659 Dasypus n	1214	36.6	4.2	288211	12	AC181676	AC181676 Strongylo
1142	36.6	4.2	122923	5	AC092289	AC092289 Homo sapi	1215	36.6	4.2	298960	12	AC006896	AC006896 Caenorhab
1143	36.6	4.2	132910	12	AC016342	AC016342 Homo sapi	1216	36.6	4.2	302156	13	AC116977	AC116977 Dictyoste
1144	36.6	4.2	134430	12	AC151130	AC151130 Xenopus t	1217	36.6	4.2	313050	13	PFAM23352	AL929352 Plasmodiu
1145	36.6	4.2	135552	12	AC019251	AC019251 Homo sapi	1218	36.6	4.2	349751	13	PFAM14P3	AL035476 Plasmodiu
1146	36.6	4.2	136450	5	AC111194	AC111194 Homo sapi	1219	36.6	4.2	349980	2	AX344567	AX344567 Sequence
1147	36.6	4.2	142178	13	AC024859	AC024859 Caenorhab	1220	36.6	4.2	361535	2	CQ415635	CQ415635 Sequence
1148	36.6	4.2	143843	12	AC103633	AC103633 Mus muscu	1221	36.6	4.2	361535	2	CQ663870	CQ663870 Sequence
1149	36.6	4.2	144018	12	AC115856	AC115856 Mus muscu	1222	36.6	4.2	313	2	CQ433394	CQ433394 Sequence
1150	36.6	4.2	145459	5	AC010748	AC010748 Homo sapi	1223	36.6	4.2	424	2	CQ395140	CQ395140 Sequence
1151	36.6	4.2	146123	12	AC147458	AC147458 Felis cat	1224	36.6	4.2	424	2	AF266182	AF266182 Gillichth
1152	36.6	4.2	149505	12	AC126927	AC126927 Felis cat	1225	36.6	4.2	440	11	CQ401480	CQ401480 Sequence
1153	36.6	4.2	149718	12	AC016633	AC016633 Homo sapi	1226	36.6	4.2	449	6	AF329091	AF329091 Rattus no
1154	36.6	4.2	151340	6	AC132463	AC132463 Mus muscu	1227	36.6	4.2	472	2	CQ426555	CQ426555 Sequence
1155	36.6	4.2	151986	12	AC180730	AC180730 Strongylo	1228	36.6	4.2	578	2	AX282981	AX282981 Sequence
1156	36.6	4.2	154419	5	AC073054	AC073054 Homo sapi	1229	36.6	4.2	578	2	AX429956	AX429956 Sequence
1157	36.6	4.2	154590	5	AC016634	AC016634 Homo sapi	1230	36.6	4.2	585	6	BC021916	BC021916 Mus muscu
1158	36.6	4.2	157452	12	AC020841	AC020841 Mus muscu	1231	36.6	4.2	650	7	BV313173	BV313173 S236P664R
1159	36.6	4.2	158335	12	AC025393	AC025393 Homo sapi	1232	36.6	4.2	716	5	BC044235	BC044235 Homo sapi
1160	36.6	4.2	159689	12	AC176566	AC176566 Strongylo	1233	36.6	4.2	732	14	BC111655	BC111655 Bos tauru
1161	36.6	4.2	160586	12	AC180596	AC180596 Strongylo	1234	36.6	4.2	774	6	BC006824	BC006824 Mus muscu
1162	36.6	4.2	161304	12	AC016174	AC016174 Homo sapi	1235	36.6	4.2	803	14	BC111167	BC111167 Bos tauru
1163	36.6	4.2	161689	12	AC015623	AC015623 Homo sapi	1236	36.6	4.2	867	7	CNS06K94	AL403274 T7 end of
1164	36.6	4.2	164375	11	AL840627	AL840627 Zebrafish	1237	36.6	4.2	896	6	BC100430	BC100430 Mus muscu
1165	36.6	4.2	164396	5	AC108034	AC108034 Homo sapi	1238	36.6	4.2	955	5	BC039522	BC039522 Homo sapi
1166	36.6	4.2	168186	12	AC146425	AC146425 Pan trogl	1239	36.6	4.2	1135	6	BC039769	BC039769 Mus muscu
1167	36.6	4.2	168300	6	AC154277	AC154277 Mus muscu	1240	36.6	4.2	1152	6	BC030375	BC030375 Mus muscu
1168	36.6	4.2	168837	5	AL583804	AL583804 Human DNA	1241	36.6	4.2	1243	5	BC034369	BC034369 Homo sapi
1169	36.6	4.2	171533	6	AC140454	AC140454 Mus muscu	1242	36.6	4.2	1265	5	BC033301	BC033301 Homo sapi
1170	36.6	4.2	171942	6	AC120541	AC120541 Mus muscu	1243	36.6	4.2	1366	6	BC097331	BC097331 Rattus no
1171	36.6	4.2	173929	6	AL732487	AL732487 Mouse DNA	1244	36.6	4.2	1513	6	BC097387	BC097387 Rattus no
1172	36.6	4.2	177664	6	AC141869	AC141869 Mus muscu	1245	36.6	4.2	1640	5	BC033803	BC033803 Homo sapi
1173	36.6	4.2	179538	12	AC180295	AC180295 Strongylo	1246	36.6	4.2	1709	5	BC039890	BC039890 Homo sapi
1174	36.6	4.2	180368	12	AC024276	AC024276 Homo sapi	1247	36.6	4.2	1741	11	BC047856	BC047856 Danio rer
1175	36.6	4.2	181343	6	AL671882	AL671882 Mouse DNA	1248	36.6	4.2	1849	11	BC061396	BC061396 Xenopus t
1176	36.6	4.2	182673	12	AC159028	AC159028 Pan trogl	1249	36.6	4.2	1873	14	BC102874	BC102874 Bos tauru
1177	36.6	4.2	184012	6	AC116523	AC116523 Mus muscu	1250	36.6	4.2	1880	5	BC063457	BC063457 Homo sapi
1178	36.6	4.2	185931	6	AC155257	AC155257 Mus muscu	1251	36.6	4.2	2152	6	BC008638	BC008638 Mus muscu
1179	36.6	4.2	187770	12	AC181113	AC181113 Strongylo	1252	36.6	4.2	2197	6	BC087036	BC087036 Rattus no
1180	36.6	4.2	188121	12	AC156322	AC156322 Bos tauru	1253	36.6	4.2	2239	6	BC056224	BC056224 Mus muscu
1181	36.6	4.2	188864	12	AC135951	AC135951 Macaca mu	1254	36.6	4.2	2455	6	BC097368	BC097368 Rattus no
1182	36.6	4.2	190489	12	AC172490	AC172490 Bos tauru	1255	36.6	4.2	2479	2	CS239222	CS239222 Sequence
1183	36.6	4.2	191582	11	AL954687	AL954687 Zebrafish	1256	36.6	4.2	2479	5	BC050450	BC050450 Homo sapi
1184	36.6	4.2	192927	6	AL805928	AL805928 Mouse DNA	1257	36.6	4.2	2510	11	BC061960	BC061960 Danio rer
1185	36.6	4.2	198116	6	AC130217	AC130217 Mus muscu	1258	36.6	4.2	2547	5	AB169258	AB169258 Macaca fa
1186	36.6	4.2	198579	6	AC149277	AC149277 Mus muscu	1259	36.6	4.2	2598	6	BC031474	BC031474 Mus muscu



c1260	36.4	4.2	2865	2	AX251074	Sequence	1333	36.4	4.2	171510	6	AC154102	AC154102 Mus muscu
c1261	36.4	4.2	2865	2	AX344643	Sequence	1334	36.4	4.2	171551	4	OSJN00177	AL662976 Oryza sat
1262	36.4	4.2	3000	5	BC036812	Homo sapi	1335	36.4	4.2	175037	12	AC180563	AC180563 Strongylo
c1263	36.4	4.2	3416	11	BC076684	Xenopus t	1336	36.4	4.2	175372	5	AC009659	AC009659 Homo sapi
c1264	36.4	4.2	3531	13	AF447572	Plasmodiu	1337	36.4	4.2	176223	5	AC034192	AC034192 Homo sapi
c1265	36.4	4.2	3700	13	DGP80G	X66483 D.discoidu	1338	36.4	4.2	178860	11	BX001036	BX001036 Zebrafish
1266	36.4	4.2	4424	6	BC050125	Mus muscu	1339	36.4	4.2	179058	6	AC122420	AC122420 Mus muscu
1267	36.4	4.2	4815	5	HSN803690	AL832382 Homo sapi	1340	36.4	4.2	180629	6	AL670939	AL670939 Mouse DNA
1268	36.4	4.2	4930	5	HSN805943	BS37846 Homo sapi	1341	36.4	4.2	182870	13	AC116960	AC116960 Dictyoste
c1269	36.4	4.2	6636	2	AX344614	Sequence	1342	36.4	4.2	184483	12	AC182175	AC093865 Homo sapi
c1270	36.4	4.2	8305	2	AX346470	Sequence	1343	36.4	4.2	186218	5	AC093865	AC133876 Mus muscu
1271	36.4	4.2	12940	13	AE001386	AB001386 Plasmodiu	1344	36.4	4.2	187088	6	AC133876	AL292031 Zebrafish
1272	36.4	4.2	36148	13	AC116100	Dictyoste	1345	36.4	4.2	187548	11	AL929031	AC068262 Homo sapi
c1273	36.4	4.2	41070	12	AC171812	AL171812 Spermophi	1346	36.4	4.2	189148	12	AC088262	AC17766 Mus muscu
c1274	36.4	4.2	64707	13	AC115607	AP005842 Dictyoste	1347	36.4	4.2	190180	6	AC117766	AC176755 Strongylo
1275	36.4	4.2	68256	4	AP005842	AP005842 Oryza sat	1348	36.4	4.2	190426	14	AC149571	AC149571 Rhinolph
1276	36.4	4.2	80339	11	BX663495	BS663495 Zebrafish	1349	36.4	4.2	191921	12	AC175656	AC175656 Microcebu
c1277	36.4	4.2	84506	5	AL591867	AL591867 Human DNA	1350	36.4	4.2	192187	13	AC117072	AC117072 Dictyoste
c1278	36.4	4.2	85781	5	AL663074	AL663074 Human DNA	1351	36.4	4.2	193117	5	AC163767	AC163767 Pan trogl
c1279	36.4	4.2	99228	5	AL133376	AL133376 Human DNA	1352	36.4	4.2	195151	6	AC154357	AC154357 Mus muscu
c1280	36.4	4.2	101080	12	BX004860	BX004860 Danio rer	1353	36.4	4.2	196024	6	AC114602	AC114602 Mus muscu
c1281	36.4	4.2	101241	11	AL8445510	AL8445510 Zebrafish	1354	36.4	4.2	198089	12	AC176755	AC176755 Strongylo
c1282	36.4	4.2	103888	12	AC149916	AC149916 Strongylo	1355	36.4	4.2	201418	12	AC144493	AC144493 Bos tauru
1283	36.4	4.2	110000	4	AP008208	Continuation (190	1356	36.4	4.2	203351	12	AC171851	AC171851 Bos tauru
1284	36.4	4.2	110000	4	AP008210	Continuation (265	1357	36.4	4.2	210405	12	AC172537	AC172537 Bos tauru
1285	36.4	4.2	110000	12	AC098456	AC098456 Rattus no	1358	36.4	4.2	211803	12	AC117813	AC117813 Mus muscu
1286	36.4	4.2	110000	12	PPMAU13_22	Continuation (23 o	1359	36.4	4.2	213482	6	AC164971	AC164971 Mus muscu
c1287	36.4	4.2	110000	13	AC116984_0	AC116984 Dictyoste	1360	36.4	4.2	214285	12	AC125812	AC125812 Rattus no
1288	36.4	4.2	110000	13	AC116984_1	Continuation (2 of	1361	36.4	4.2	220203	6	AC116584	AC116584 Mus muscu
1289	36.4	4.2	111167	12	AC171545	AC171545 Bos tauru	1362	36.4	4.2	220671	11	BX276106	BX276106 Zebrafish
c1290	36.4	4.2	113547	12	AC152350	AC152350 Medicago	1363	36.4	4.2	221053	12	AC166447	AC166447 Bos tauru
1291	36.4	4.2	114870	12	AC010755	AC010755 Homo sapi	1364	36.4	4.2	223402	12	AC175067	AC175067 Bos tauru
c1292	36.4	4.2	117886	12	AC178818	AC178818 Strongylo	1365	36.4	4.2	223545	12	AC100545	AC100545 Mus muscu
1293	36.4	4.2	123282	12	OSJN01004	AL607096 Oryza sat	1366	36.4	4.2	224141	6	AC110576	AC110576 Mus muscu
1294	36.4	4.2	124231	12	AC016466	AC016466 Homo sapi	1367	36.4	4.2	228633	11	BX649600	BX649600 Zebrafish
c1295	36.4	4.2	126004	11	BX914219	BX914219 Zebrafish	1368	36.4	4.2	228869	6	BX470109	BX470109 Mouse DNA
1296	36.4	4.2	132131	5	AB045357	AB045357 Homo sapi	1369	36.4	4.2	229685	12	BX927087	BX927087 Danio rer
c1297	36.4	4.2	134328	12	AC181359	AC181359 Strongylo	1370	36.4	4.2	230215	12	AC152328	AC152328 Bos tauru
c1298	36.4	4.2	135124	5	AC177676	AC177676 Strongylo	1371	36.4	4.2	230283	12	AC160055	AC160055 Pan trogl
c1299	36.4	4.2	135955	5	HS135814	AJ010598 Homo sapi	1372	36.4	4.2	230853	12	AC161842	AC161842 Bos tauru
1300	36.4	4.2	140454	4	OSJN00183	AL662984 Oryza sat	1373	36.4	4.2	231435	12	AC130519	AC130519 Rattus no
1301	36.4	4.2	140484	11	CR854834	CR854834 Zebrafish	1374	36.4	4.2	231797	6	AC121848	AC121848 Mus muscu
c1302	36.4	4.2	140523	12	AC173432	AC173432 Muntiacus	1375	36.4	4.2	232491	11	BX908747	BX908747 Zebrafish
c1303	36.4	4.2	141646	12	AC179856	AC179856 Strongylo	1376	36.4	4.2	232594	11	BX005006	BX005006 Zebrafish
1304	36.4	4.2	142704	6	AC157558	AC157558 Mus muscu	1377	36.4	4.2	234483	12	AC098407	AC098407 Rattus no
1305	36.4	4.2	143573	12	CF7573424	CF7573424 Danio rer	1378	36.4	4.2	235237	6	AC160995	AC160995 Mus muscu
c1306	36.4	4.2	149596	12	CR391909	CR391909 Danio rer	1379	36.4	4.2	241428	12	BX649537	BX649537 Danio rer
1307	36.4	4.2	150313	5	AC179580	AC179580 Strongylo	1380	36.4	4.2	243770	12	AC123492	AC123492 Rattus no
c1308	36.4	4.2	150434	5	AL138784	AL138784 Human DNA	1381	36.4	4.2	245403	12	AC133063	AC133063 Rattus no
c1309	36.4	4.2	151349	12	AL353647	AL353647 Homo sapi	1382	36.4	4.2	246577	12	AC136124	AC136124 Rattus no
1310	36.4	4.2	151923	6	AL845499	AL845499 Mouse DNA	1383	36.4	4.2	247073	12	AC160164	AC160164 Bos tauru
1311	36.4	4.2	152742	12	AC022381	AC022381 Homo sapi	1384	36.4	4.2	249982	12	AC108661	AC108661 Rattus no
1312	36.4	4.2	153258	12	AC062606	AC062606 Homo sapi	1385	36.4	4.2	251551	13	AE014844	AE014844 Plasmodiu
1313	36.4	4.2	153477	12	AC006278	AC006278 Plasmodiu	1386	36.4	4.2	252236	12	AC131533	AC131533 Rattus no
1314	36.4	4.2	153704	5	AC145897	AC145897 Pan trogl	1387	36.4	4.2	259800	12	AC113162	AC113162 Rattus no
1315	36.4	4.2	153751	13	AC118551	AC118551 Dictyoste	1388	36.4	4.2	267584	12	AC094973	AC094973 Rattus no
c1316	36.4	4.2	155332	12	AL365439	AL365439 Homo sapi	1389	36.4	4.2	270075	12	AC114451	AC114451 Rattus no
1317	36.4	4.2	156379	12	AC139583	AC139583 Rattus no	1390	36.4	4.2	281723	13	PFA929359	PFA929359 Plasmodiu
1318	36.4	4.2	156693	12	AC144997	AC144997 Bos tauru	1391	36.4	4.2	295760	12	AC125718	AC125718 Rattus no
c1319	36.4	4.2	157140	5	AC018514	AC018514 Homo sapi	1392	36.4	4.2	300000	5	AP002532	AP002532 Homo sapi
1320	36.4	4.2	157530	5	AC146247	AC146247 Pan trogl	1393	36.4	4.2	313050	13	PFA929352	PFA929352 Plasmodiu
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c1327	36.4	4.2	166125	5	AC023332	AC023332 Homo sapi	1400	36.2	4.2	771	7	BV591840	BV591840 G591P5036
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Db 841 TTTTAAATGTCAAAAAA 870

RESULT 2  
LOCUS CS257510 870 bp DNA linear PAT 10-FEB-2006  
DEFINITION Sequence 25 from Patent EP1623991.  
ACCESSION CS257510  
VERSION CS257510.1 GI:87159018  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Eaton, D.L.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same  
JOURNAL Patent: EP 1623991-A 25 08-FEB-2006;  
GENENTECH, INC. (US)  
FEATURES  
source Location/Qualifiers  
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ORIGIN  
Query Match 100.0%; Score 870; DB 2; Length 870;  
Best Local Similarity 100.0%; Pred. No. 9.9e-268;  
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3  
LOCUS CS257680 870 bp DNA linear PAT 10-FEB-2006  
DEFINITION Sequence 25 from Patent EP1623993.  
ACCESSION CS257680  
VERSION CS257680.1 GI:87159104  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Baton, D.L.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same  
JOURNAL Patent: EP 1623993-A 25 08-FEB-2006;  
Genetech, Inc. (US)  
FEATURES Location/Qualifiers  
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ORIGIN  
Query Match 100.0%; Score 870; DB 2; Length 870;  
Best Local Similarity 100.0%; Pred. No. 9.9e-268;  
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4  
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LOCUS CS257850  
DEFINITION Sequence 25 from Patent EP1623992.  
ACCESSION CS257850  
VERSION CS257850.1 GI:87159190  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Baton, D.L.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same  
JOURNAL Patent: EP 1623992-A 25 08-FEB-2006;  
GENENTECH, INC. (US)  
FEATURES Location/Qualifiers  
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Query Match 100.0%; Score 870; DB 2; Length 870;  
Best Local Similarity 100.0%; Pred. No. 9.9e-268;  
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 841 TTTTAAATGTCAAAAAAATAAAAAA 870

RESULT 5
AR252494
LOCUS AR252494 870 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 164 from patent US 6478825.
ACCESSION AR252494
VERSION AR252494.1 GI:27300402
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 870)
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE Implant, method of making same and use of the implant for the
treatment of bone defects
JOURNAL Patent: US 6478825-A 164 12-NOV-2002;
Osteotech, Inc.; Eatontown, NJ
FEATURES
source Location/Qualifiers
1..870
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ORIGIN
Query Match 100.0%; Score 870; DB 2; Length 870;
Best Local Similarity 100.0%; Pred. No. 9.9e-268;
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AR693384 870 bp DNA linear PAT 14-SEP-2005
DEFINITION Sequence 164 from patent US 6913919.
ACCESSION AR693384
VERSION AR693384.1 GI:75183789
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 870)
AUTHORS Botstein,D., Goddard,A., Godowski,P.J., Gurney,A.L., Roy,M.A. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: US 6913919-A 164 05-JUL-2005;
Genetech, Inc.; South San Francisco, CA
FEATURES
source Location/Qualifiers
1..870
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ORIGIN
Query Match 100.0%; Score 870; DB 2; Length 870;
Best Local Similarity 100.0%; Pred. No. 9.9e-268;
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCGCCCTCAAAATGGGAACGCTGGCTGGACTAAAGCATAGACCACGAGCTGAGTATC 60
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RESULT 7
AR705936
LOCUS
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AUTHORS
TITLE
JOURNAL
FEATURES
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RESULT 10  
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DEFINITION Sequence 164 from patent US 6972185.  
ACCESSION AR776123  
VERSION AR776123.1 GI:83353462  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 870)  
AUTHORS Desnoyers, L., Goddard, A., Godowski, P.J., Gurney, A.L. and Wood, W.I.  
TITLE Nucleic acids encoding PRO844 polypeptides  
JOURNAL Patent: US 6972185-A 164 06-DEC-2005;  
Genentech, Inc.; South San Francisco, CA

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source Location/Qualifiers  
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RESULT 11  
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LOCUS AX092294 870 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 25 from Patent WO0116318.  
ACCESSION AX092294  
VERSION AX092294.1 GI:13444461  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Eaton, D.L., Filvaroff, E., Gerritsen, M.E., Goddard, A., and Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Watanabe, C.K. and Wood, W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same  
JOURNAL Patent: WO 0116318-A 25 08-MAR-2001;  
Genentech, Inc. (US)  
FEATURES  
source Location/Qualifiers  
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LOCUS AX376072 870 bp DNA linear PAT 01-MAR-2002  
DEFINITION Sequence 139 from Patent WO0168848.  
ACCESSION AX376072  
VERSION AX376072.1 GI:19170428  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,  
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and  
Zhang, Z.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0168848-A 139 20-SEP-2001;  
Genentech, Inc. (US)  
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source 1..870

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RESULT 13  
AX403277  
LOCUS AX403277

AX403277 870 bp DNA linear PAT 14-JUN-2002



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ACCESSION	GI:21436848	
VERSION	1	
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SOURCE	Homo sapiens	
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REFERENCE	Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnovers,L., Eaton,D., Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P., Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J., Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K., Williams,P., Wood,W.I. and Zhang,Z.	
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same	
JOURNAL	Patent: WO 0073454-A 164 07-DEC-2000;	
Genentech Inc.(US)		
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RESULT 15
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DEFINITION Homo sapiens clone DNA56855 DMC (UNQ473) mRNA, complete cds.
ACCESSION AY358433
VERSION AY358433.1 GI:37181990
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ORGANISM Homo sapiens
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Hominidae; Homo.
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Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Haas,P.E.,
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Stinson,J., Vagts,A., Vandlen,K., Watanabe,C., Wiedan,D., Woods,K.,
Xie,M.H., Yaneura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
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Clark,H.F.
Direct Submission
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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JOURNAL
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Best Local Similarity 100.0%; Pred. No. 9.9e-268;
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ID ABS74390 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO842.
PN US2002119130-A1.
PD 29-AUG-2002.
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PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 6; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 6
ID ABV73914 standard; cDNA; 870 BP.
DE Human cytokine PRO842 (CK27) cDNA.
PN WO200270706-A2.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 6; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 7
ID ACA89444 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003036141-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 8; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 8
ID ACA73454 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 8; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 9
ID ACA05769 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 8; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 10
ID ACA66603 standard; cDNA; 870 BP.
DE cDNA encoding human PRO protein #70.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 8; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 11
ID ACA64277 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 8; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 12
ID ACA91176 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 8; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 13
ID ACD81553 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO842.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 8; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 14
ID ACF20178 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003040063-A1.
PD 27-FEB-2003.
  Query Match 100.0%; Score 870; DB 8; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
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RESULT 15  
ID ACF19564 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 16  
ID ACD21852 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 17  
ID ACF13017 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 18  
ID ACD25120 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 19  
ID ACF00169 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 20  
ID ACA60375 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 21  
ID ACA72226 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 22  
ID ACD04750 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 23  
ID ACD18211 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 24  
ID ACD08218 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 25

ID ACA88652 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 26  
ID ACA70094 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 27  
ID ACD12316 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 28  
ID ACC74231 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 29  
ID ACD15859 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 30  
ID ACD25427 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 31  
ID ACD17904 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 32  
ID ACC88191 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 33  
ID ACD21545 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 34  
ID ACD18612 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 35  
ID ACA58822 standard; cDNA; 870 BP.  
DE cDNA encoding human secreted polypeptide PRO842.

PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 36  
ID ABX98222 standard; cDNA; 870 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 139.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 37  
ID ACD13973 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 38  
ID ACD09753 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 39  
ID ACC88498 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 40  
ID ACD21238 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 41  
ID ABX75610 standard; cDNA; 870 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO842.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 42  
ID ACA63998 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #13.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 43  
ID ABX97813 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #70.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 44  
ID ACA97289 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 45  
ID ACA57752 standard; cDNA; 870 BP.  
DE Human PRO842 cDNA.

PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 46  
ID ACD14280 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #70.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 47  
ID ACC91063 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 48  
ID ACC88805 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 49  
ID ACD07002 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #70.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 50  
ID ACA67453 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #70.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 51  
ID ACC81508 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 52  
ID ACA91262 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #13.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 53  
ID ACC89112 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 54  
ID ACC86468 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 55  
ID ACC89726 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.

PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 56  
ID ACC92905 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 57  
ID ABX80736 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein cDNA, #61.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 58  
ID ACAY7533 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #70.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 59  
ID ACRA89051 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 60  
ID ACA69787 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 61  
ID ACA96930 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 62  
ID ACA50926 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 63  
ID ACA70708 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 64  
ID ACA95218 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 65  
ID ACD44245 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO842 polypeptide.  
PN US2002127576-A1.

PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 66  
ID ACC86161 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 67  
ID ACD45161 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane polypeptide PRO842 cDNA.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 68  
ID ACC90033 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 69  
ID ACD12641 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 70  
ID ACP19871 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 71  
ID ABX76815 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #70.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 72  
ID ACA73147 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 73  
ID ACA68690 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 74  
ID ACA74534 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 75  
ID ACA70401 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003032109-A1.  
PD 13-FEB-2003.



Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 76  
ID ACD14587 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #70.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 77  
ID ACA93709 standard; cDNA; 870 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO842.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 78  
ID ACA68259 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 79  
ID ABX98724 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 80  
ID ACA67283 standard; cDNA; 870 BP.  
DE cDNA encoding human secreted polypeptide PRO842.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 81  
ID ACC81201 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 82  
ID ACA95525 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 83  
ID ACD04443 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 84  
ID ACC87884 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 85  
ID ACF12546 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003040058-A1.  
PD 27-FEB-2003.

Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 86  
ID ACH66256 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 87  
ID ABX79416 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein cDNA, #61.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 88  
ID ACA96261 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #70.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 89  
ID ACA65035 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #70.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 90  
ID ACA73761 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 91  
ID ACA74173 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 92  
ID ACA96568 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #70.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 93  
ID ACD10674 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 94  
ID ACC91370 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 95  
ID ACA93437 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;

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Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 96
ID AC020705 standard; cDNA; 870 BP.
DE CDNA encoding human PRO polypeptide #70.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 97
ID ACC87270 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003036165-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
RESULT 98
ID ACC85854 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
RESULT 99
ID ABX81119 standard; DNA; 870 BP.
DE Novel human secreted or transmembrane protein PRO839 DNA.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
RESULT 100
ID ACA85342 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
RESULT 101
ID ACA94159 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
RESULT 102
ID ACA97903 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
RESULT 103
ID ACA91405 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
RESULT 104
ID ACA90619 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
RESULT 105
ID ACD16166 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
RESULT 106
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
ID ACD17327 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
RESULT 107
ID ACC91984 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
RESULT 108
ID ACD02310 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
RESULT 109
ID ACA74841 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
RESULT 110
ID ACA91712 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
RESULT 111
ID ACA89301 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
RESULT 112
ID ACA71356 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
RESULT 113
ID ACC90756 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
RESULT 114
ID ACA65766 standard; cDNA; 870 BP.
DE cDNA encoding human PRO protein #70.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
RESULT 115
ID ACA68938 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 8; Length 870;
RESULT 116
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ID ACA92935 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 117  
ID ACA94911 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 118  
ID ACD16473 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 119  
ID ACD15552 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 120  
ID ACA98460 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #13.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 121  
ID ABX17019 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #38.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 122  
ID ABX16655 standard; cDNA; 870 BP.  
DE Human cDNA encoding secreted/transmembrane protein #70.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 8; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 123  
ID ACA67874 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 124  
ID ACA63385 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #13.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 125  
ID ACA97596 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #70.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;

Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 126  
ID ACA95045 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 127  
ID ACC91677 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 128  
ID ACD11088 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 129  
ID ACD14938 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 130  
ID ACA98323 standard; cDNA; 870 BP.  
DE Human secreted and transmembrane polypeptide PRO842 cDNA.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 131  
ID ACD81830 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO842 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 132  
ID ACD11702 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 133  
ID ACC95831 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 134  
ID ACF16394 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 135  
ID ACF02512 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003049741-A1.  
PD 13-MAR-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 136
ID ACF02819 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 137
ID ACF21406 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 138
ID ACF10090 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 139
ID ACF77983 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 140
ID ACD4688 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 141
ID ACD49451 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 142
ID ACF28218 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 143
ID ACD88908 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 144
ID ACD84303 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 145
ID ACD99077 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 146
ID ADA77891 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 147
ID ACF48819 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 148
ID ACD09139 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 149
ID ACF11932 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 150
ID ACF41166 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 151
ID ACF15780 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 152
ID ACF16087 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 153
ID ADB17082 standard; cDNA; 870 BP.
DE Human cDNA clone (SeqID 25) encoding the transmembrane PRO protein.
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 154
ID ACD31914 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
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PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 9; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 154
ID ACF13631 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 9; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 164
ID ACF13631 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 9; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 165
ID ACD41557 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 9; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 166
ID ADA37675 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO842.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 9; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 167
ID ACF31970 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 9; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 168
ID ACF23248 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 9; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 169
ID ACF39938 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 9; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 170
ID ACD45460 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 9; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 171
ID ACF53117 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 9; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 172
ID ACF27297 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 9; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 173
ID ACH07825 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 9; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 174
ID ACF09169 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 9; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 175
ID ACF09169 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 9; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 176
ID ACF78290 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 9; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 177
ID ACF51889 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 9; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 178
ID ACF26376 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 9; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 179
ID ACF24169 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 9; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 180
ID ACF50354 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 9; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 181
ID ACF63480 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 9; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 182
ID ACF50354 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 870; DB 9; Length 870;
  Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 183
ID ACH07825 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
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Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 173
ID ACF45135 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 174
ID ACF29753 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 175
ID ACB9829 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 176
ID ACD84610 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 177
ID ACD98770 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 178
ID ACF77062 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 179
ID ACF76755 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 180
ID ACF49740 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 181
ID ACF50047 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 182
ID ADA21361 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO842.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 183
ID ACD09446 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 184
ID ACD08525 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 185
ID ACH03588 standard; cDNA; 870 BP.
DE Human secreted/transmembrane polypeptide PRO 842 cDNA.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 186
ID ACF12239 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 187
ID ACC94747 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 188
ID ACD22466 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 189
ID ACF15166 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 190
ID ACC97261 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 191
ID ACC92291 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 192
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ID ACF13938 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 193  
ID ACF14245 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 194  
ID ADA10148 standard; cDNA; 870 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO842.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 195  
ID ACF09476 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 196  
ID ACD45767 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 197  
ID ACD47916 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 198  
ID ACD67647 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 199  
ID ACF25455 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 200  
ID ACF29139 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 201  
ID ACD84917 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.

PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 202  
ID ACD81996 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #70.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 203  
ID ACD87987 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 204  
ID ACF30674 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 205  
ID ACF32277 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 206  
ID ACH11937 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 207  
ID ACH12244 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 208  
ID ADA19887 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 209  
ID ACD40636 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 210  
ID ADB17270 standard; cDNA; 870 BP.  
DE Human cDNA clone (SeqID 25) encoding the transmembrane PRO protein.  
PN US2003050465-A1.  
PD 13-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 211  
ID ADA17692 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO842 polypeptide.  
PN US2003054387-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 212  
ID ACF18108 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 213  
ID ACF08555 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 214  
ID ACF31356 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 215  
ID ACF52196 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 216  
ID ACD50065 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 217  
ID ACF38768 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 218  
ID ACF26683 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 219  
ID ACF24783 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;

Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 220  
ID ACF46363 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 221  
ID ACF27911 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 222  
ID ACD89215 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 223  
ID ACF63787 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 224  
ID ACF60427 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 225  
ID ACH12551 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 226  
ID ACH09974 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 227  
ID ACD03829 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 228  
ID ACD10367 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 229  
ID ACD12009 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.



PN US2003040074-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
Pred. No. 4.3e-229;  
RESULT 230  
ID ACF42394 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
Pred. No. 4.3e-229;  
RESULT 231  
ID ADA27800 standard; cDNA; 870 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO842.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
Pred. No. 4.3e-229;  
RESULT 232  
ID ACF18415 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
Pred. No. 4.3e-229;  
RESULT 233  
ID ACF02205 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
Pred. No. 4.3e-229;  
RESULT 234  
ID ACF21713 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
Pred. No. 4.3e-229;  
RESULT 235  
ID ACF10397 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
Pred. No. 4.3e-229;  
RESULT 236  
ID ACF33849 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
Pred. No. 4.3e-229;  
RESULT 237  
ID ACF44811 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
Pred. No. 4.3e-229;  
RESULT 238  
ID ACD90443 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
Pred. No. 4.3e-229;

Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 239  
ID ACD91056 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
Pred. No. 4.3e-229;  
RESULT 240  
ID ACF10367 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
Pred. No. 4.3e-229;  
RESULT 241  
ID ACD87066 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
Pred. No. 4.3e-229;  
RESULT 242  
ID ACF60120 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
Pred. No. 4.3e-229;  
RESULT 243  
ID ACF46670 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
Pred. No. 4.3e-229;  
RESULT 244  
ID ACF75527 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
Pred. No. 4.3e-229;  
RESULT 245  
ID ADA79683 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003073173-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
Pred. No. 4.3e-229;  
RESULT 246  
ID ACF17187 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
Pred. No. 4.3e-229;  
RESULT 247  
ID ACF22941 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
Pred. No. 4.3e-229;  
RESULT 248  
ID ACF07941 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003049758-A1.

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PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 258
ID ACF52810 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 259
ID ACF64803 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 260
ID ACF76448 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 261
ID ACF61348 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 262
ID ACF61655 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 263
ID ACD30686 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 264
ID ACD31607 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 265
ID ACD32528 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 266
ID ADA20059 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 267
ID ACD82102 standard; cDNA; 870 BP.
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PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 249
ID ACF08248 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 250
ID ACF40552 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 251
ID ACF53731 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 252
ID ACD46995 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 253
ID ACF47898 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 254
ID ACF47284 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 255
ID ACF46056 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 256
ID ACD86145 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 257
ID ACF52503 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003082715-A1.
PD 01-MAY-2003.
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DE Human secreted/transmembrane polypeptide PRO 842 cDNA, SEQ ID NO:139.  
PN US200306061-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 268  
ID ACF17494 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 269  
ID ADA94380 standard; cDNA; 870 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO842.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 270  
ID ACF07327 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 271  
ID ACF20485 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 272  
ID ACF21099 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 273  
ID ACF20792 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 274  
ID ACD47609 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 275  
ID ACF47591 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 276  
ID ACF53424 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 277  
ID ACD86759 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 278  
ID ACH05007 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 279  
ID ACF44504 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 280  
ID ADA81410 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 281  
ID ACD22159 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 282  
ID ACD24506 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 283  
ID ACD39709 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003027285-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 284  
ID ACD40016 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 285  
ID ACF13324 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 286  
ID ACF03126 standard; cDNA; 870 BP.

DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
RESULT 287  
ID ACP78597 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
RESULT 288  
ID ACF11318 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003073171-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
RESULT 289  
ID ACF50661 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
RESULT 290  
ID ACF34156 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
RESULT 291  
ID ACD46381 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
RESULT 292  
ID ACD48223 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
RESULT 293  
ID ACF27604 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
RESULT 294  
ID ACF24476 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
RESULT 295  
ID ACD85531 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003068719-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
RESULT 296  
ID ACD90136 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
RESULT 297  
ID ACD83689 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #70.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
RESULT 298  
ID ACF49126 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
RESULT 299  
ID ACH07211 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
RESULT 300  
ID ACH07518 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
RESULT 301  
ID ACH08132 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
RESULT 302  
ID ACH11323 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
RESULT 303  
ID ACH11630 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
RESULT 304  
ID ACH10281 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;  
RESULT 305  
ID ACH10281 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;

Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 305  
ID ACF01284 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 306  
ID ACF40859 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 307  
ID ACD24199 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 308  
ID ACD31300 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 309  
ID ACF17801 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 310  
ID ADA38605 standard; cDNA; 870 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO842.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 311  
ID ACF32584 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 312  
ID ACF40245 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 313  
ID ACF48205 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 314  
ID ACF38154 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068696-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 315  
ID ACF25090 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 316  
ID ACF26990 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 317  
ID ACF29446 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 318  
ID ACD87680 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 319  
ID ACF76141 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 320  
ID ACF49433 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 321  
ID ACF43890 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 322  
ID ACH06235 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 323  
ID ACH06542 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 324  
ID ACH06542 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;

RESULT 324  
ID ADA83208 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 325  
ID ACC92598 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 326  
ID ACC93212 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 327  
ID ACF19257 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 328  
ID ACD12948 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 329  
ID ACF06406 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 330  
ID ACC94440 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 331  
ID ACC97868 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 332  
ID ACC94133 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 333  
ID ACF42087 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;

RESULT 334  
ID ACD30993 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 335  
ID ACD43022 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 336  
ID ACD43329 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 337  
ID ACF14859 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 338  
ID ADA92726 standard; cDNA; 870 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO842.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 339  
ID ACF01591 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 340  
ID ACF31663 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 341  
ID ACD67340 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 342  
ID ACD48530 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 343  
ID ACD48837 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003064468-A1.

PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 344  
ID ACF51275 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 345  
ID ACF54038 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 346  
ID ACF25762 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 347  
ID ACF39075 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 348  
ID ACF28832 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 349  
ID ACD90749 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 350  
ID ACD86452 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 351  
ID ACH05314 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 352  
ID ACF65110 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068688-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 353  
ID ADB20251 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 354  
ID ACF43583 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 355  
ID ACH09053 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 356  
ID ACH09360 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 357  
ID ADA78503 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 358  
ID ACF09783 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 359  
ID ADA00356 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane polypeptide PRO 842 cDNA.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 360  
ID ACF50968 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 361  
ID ACF23862 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;

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Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 362
ID ACD88294 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 363
ID ACH09667 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 364
ID ACH10588 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 365
ID ACD11395 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 366
ID ACC96445 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 367
ID ACC98475 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 368
ID ACF41780 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 369
ID ACF16701 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 370
ID ACD32221 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 371
ID ACD30379 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 372
ID ACD41250 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 373
ID ACF07634 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 374
ID ACF31049 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 375
ID ACF77369 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 376
ID ACF11011 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 377
ID ACF32891 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 378
ID ACF26069 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 379
ID ACD83382 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 380
ID ACF23555 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 9; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
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RESULT 381  
ID ACF42969 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 382  
ID ACF43276 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 383  
ID ACH05928 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 384  
ID ACH08746 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 385  
ID ACC90340 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 386  
ID ACF10704 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 387  
ID ACC93519 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 388  
ID ACC96138 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 389  
ID ACD24813 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 390  
ID ACF01898 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003049739-A1.  
PD 13-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 391  
ID ACF22020 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003059892-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 392  
ID ACF22634 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003059894-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 393  
ID ACF08862 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 394  
ID ACF33198 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 395  
ID ACF54652 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 396  
ID ACF48512 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 397  
ID ACD47302 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 398  
ID ACD49144 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 399  
ID ACF37847 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 400  
ID ACF30060 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 401  
ID AC087373 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 402  
ID ACF61962 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 403  
ID ACH10895 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 404  
ID ACD10060 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 405  
ID ACD16785 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 406  
ID ACH65391 standard; cDNA; 870 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO842.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 407  
ID ACC99082 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 408  
ID ACF00476 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 409  
ID ACD40943 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003054482-A1.  
PD 20-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 410  
ID ACF14552 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 411  
ID ACF22327 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 412  
ID ACF78904 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 413  
ID ACF11625 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 414  
ID ADA22287 standard; cDNA; 870 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO842.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 415  
ID ACF51582 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 416  
ID ACF33505 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 417  
ID ACD49758 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 418  
ID ACF37540 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068683-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;

PD 27-FEB-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 429  
ID ACD20624 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
FN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 430  
ID ACD22773 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
FN US2003040077-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 431  
ID ACF41473 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
FN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 432  
ID ADA06453 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #38.  
FN US2003049638-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 433  
ID ADA39146 standard; cDNA; 870 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO842.  
FN US2003059782-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 434  
ID ACF07020 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
FN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 435  
ID ACF77676 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
FN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 436  
ID ACD46074 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
FN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 437  
ID ACF46977 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
FN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 438  
ID ACF54345 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.

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PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 439
ID ACF45749 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 440
ID ACF45442 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 441
ID ACF38461 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 442
ID ACD89522 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 443
ID ACD85224 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 444
ID ACD85838 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 445
ID ACF75834 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 446
ID ACF60734 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 447
ID ACH05621 standard; cDNA; 870 BP.
DE cDNA encoding human PRO polypeptide #70.
PN US2003049760-A1.

PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 448
ID ADA82574 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 449
ID ADB85598 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 450
ID ADB96172 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #38.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 451
ID ACF55880 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 9; Length 870;
RESULT 452
ID ACF55266 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 453
ID ADB85882 standard; cDNA; 870 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #70.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 454
ID ACF56187 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 455
ID ACF56494 standard; cDNA; 870 BP.
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 456
ID ADB88277 standard; cDNA; 870 BP.
DE Human PRO842 cDNA.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
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Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 457  
ID ADB68084 standard; cDNA; 870 BP.  
DE Human PRO842 cDNA.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 458  
ID ACF55573 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 459  
ID ACF54959 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 460  
ID ADB90901 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003083473-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 461  
ID ADC57644 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #38.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 462  
ID ADC55008 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #38.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 463  
ID ADC11875 standard; cDNA; 870 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO842.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 464  
ID ADC06981 standard; cDNA; 870 BP.  
DE Human PRO842 cDNA.  
PN US2003060602-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 465  
ID ADC56297 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #38.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 466  
ID ADC17160 standard; cDNA; 870 BP.  
DE cDNA sequence encoding a PRO polypeptide (seqID 25).  
PN US2003065143-A1.

PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 467  
ID ADC07352 standard; cDNA; 870 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO842.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 468  
ID ADC11342 standard; cDNA; 870 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO842.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 469  
ID ADC14858 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003073208-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 470  
ID ADC52353 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003138882-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 471  
ID ADC14464 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 472  
ID ADD07996 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003068623-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 473  
ID ADC81821 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #38.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 474  
ID ADD07463 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 475  
ID ADC82354 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #38.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 476  
ID ADD05612 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.

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PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 477
ID AD008534 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 478
ID AD006783 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 479
ID ADC83030 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #38.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 480
ID ADD55137 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #38.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 481
ID ADD36029 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 482
ID ADD56095 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #38.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 483
ID ADD54533 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #38.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 484
ID ADE26687 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 485
ID ADE26154 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 486
ID ADF67091 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 487
ID ADG01030 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 488
ID ADG08583 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 489
ID ADG02607 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 490
ID ADG01314 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 491
ID ADF95489 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 492
ID ADF95204 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 493
ID ADG12304 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 494
ID ADH24057 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
RESULT 495
ID ADH34083 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180858-A1.
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PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
  RESULT 496
  ID ADH29916 standard; cDNA; 870 BP.
  DE Novel human secreted and transmembrane protein PRO842 cDNA.
  PN US2003180859-A1.
  PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
  RESULT 497
  ID ADH33887 standard; cDNA; 870 BP.
  DE Novel human secreted and transmembrane protein PRO842 cDNA.
  PN US2003180919-A1.
  PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
  RESULT 498
  ID ADH08964 standard; cDNA; 870 BP.
  DE Human PRO polynucleotide #70.
  PN US2003207395-A1.
  PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
  RESULT 499
  ID ADH85291 standard; cDNA; 870 BP.
  DE Novel human secreted and transmembrane protein PRO842 cDNA.
  PN US2003180904-A1.
  PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
  RESULT 500
  ID ADH24567 standard; cDNA; 870 BP.
  DE Novel human secreted and transmembrane protein PRO842 cDNA.
  PN US2003180907-A1.
  PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
  RESULT 501
  ID ADH37423 standard; cDNA; 870 BP.
  DE Human secreted and transmembrane protein PRO842 cDNA.
  PN US2003181646-A1.
  PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
  RESULT 502
  ID ADH02012 standard; cDNA; 870 BP.
  DE Human PRO polynucleotide #13.
  PN US2003180837-A1.
  PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
  RESULT 503
  ID ADH37593 standard; cDNA; 870 BP.
  DE Human secreted and transmembrane protein PRO842 cDNA.
  PN US2003181648-A1.
  PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
  RESULT 504
  ID ADH85631 standard; cDNA; 870 BP.
  DE Novel human secreted and transmembrane protein PRO842 cDNA.
  PN US2003180905-A1.
  PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
  RESULT 505
  ID ADH24227 standard; cDNA; 870 BP.
  DE Novel human secreted and transmembrane protein PRO842 cDNA.
  PN US2003180914-A1.
  PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
  RESULT 506
  ID ADH38521 standard; cDNA; 870 BP.
  DE Novel human secreted and transmembrane protein PRO842 cDNA.
  PN US2003181643-A1.
  PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
  RESULT 507
  ID ADG83642 standard; cDNA; 870 BP.
  DE Human PRO polynucleotide #13.
  PN US2003180794-A1.
  PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
  RESULT 508
  ID ADH29450 standard; cDNA; 870 BP.
  DE Novel human secreted and transmembrane protein PRO842 cDNA.
  PN US2003180860-A1.
  PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
  RESULT 509
  ID ADH27566 standard; cDNA; 870 BP.
  DE Novel human secreted and transmembrane protein PRO842 cDNA.
  PN US2003180906-A1.
  PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
  RESULT 510
  ID ADH37663 standard; cDNA; 870 BP.
  DE Human secreted and transmembrane protein PRO842 cDNA.
  PN US2003181647-A1.
  PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
  RESULT 511
  ID ADH37940 standard; cDNA; 870 BP.
  DE Human secreted and transmembrane protein PRO842 cDNA.
  PN US2003181649-A1.
  PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
  RESULT 512
  ID ADH57360 standard; cDNA; 870 BP.
  DE Novel human secreted and transmembrane protein PRO842 cDNA.
  PN US2003180920-A1.
  PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 870; DB 10; Length 870;
  RESULT 513
  ID ADH53502 standard; cDNA; 870 BP.
  DE Novel human secreted and transmembrane protein PRO842 cDNA.
  PN US2003181636-A1.
  PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
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Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 514  
ID ADH53672 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 515  
ID ADH52008 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 516  
ID ADH49863 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 517  
ID ADI25373 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 518  
ID ADH90166 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 519  
ID ADI25543 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 520  
ID ADH9717 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 521  
ID ADI35345 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #38.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 522  
ID ADI03565 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 523  
ID ADH78597 standard; cDNA; 870 BP.

RESULT 523  
ID ADI11922 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #13.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 524  
ID ADH89996 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 525  
ID ADH9837 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 526  
ID ADH98397 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 527  
ID ADI11072 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #13.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 528  
ID ADI11582 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #13.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 529  
ID ADH98227 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 530  
ID ADH98567 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003181708-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 531  
ID ADH98057 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003181673-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 532  
ID ABX78597 standard; cDNA; 870 BP.



DE Human PRO polynucleotide #70.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 533  
ID ACA75569 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 534  
ID ACA71049 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 535  
ID ACC87577 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003027278-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 536  
ID ACC86963 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 537  
ID ACD04136 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 538  
ID ABX77820 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #38.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 539  
ID ABX80232 standard; DNA; 870 BP.  
DE Novel human secreted or transmembrane protein PRO839 DNA.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 540  
ID ACA69138 standard; cDNA; 870 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO842.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 541  
ID ACA69467 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO polypeptide #70.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 542  
ID ACA90312 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003036147-A1.

PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 543  
ID ACC89419 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 544  
ID ABX90209 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein cDNA, #61.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 545  
ID ACA98210 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 546  
ID ACA93852 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 547  
ID ACD15245 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 548  
ID ACD08832 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #70.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 549  
ID ACC96752 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 550  
ID ACF15473 standard; cDNA; 870 BP.  
DE Human secreted polypeptide PRO842-encoding cDNA, SEQ ID NO:139.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 551  
ID ABX64055 standard; cDNA; 870 BP.  
DE cDNA encoding human PRO842 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match  
Best Local Similarity 100.0%; Score 870; DB 10; Length 870;  
RESULT 552  
ID ACA72840 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #70.  
PN US2003036140-A1.  
PD 20-FEB-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 553
ID AC03012 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 554
ID AC01827 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 555
ID ACA92019 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 556
ID ADI05045 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 557
ID ADI03395 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 558
ID ADI04790 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 559
ID ADH78244 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003181658-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 560
ID ADI19588 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 561
ID ADH90336 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 562
ID ADI05389 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 563
ID ADI03055 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 564
ID ADH77904 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 565
ID ADH97887 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 566
ID ADI01272 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 567
ID ADI01967 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 568
ID ADI11412 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 569
ID ADI02314 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 570
ID ADI11752 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 571
ID ADI05389 standard; cDNA; 870 BP.
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DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 572  
ID ADH79461 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 573  
ID ADI19418 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 574  
ID ADI05219 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 575  
ID ADH79631 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 576  
ID ADI01457 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 577  
ID ADI01627 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 578  
ID ADI01797 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 579  
ID ADH79801 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 580  
ID ADI04619 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.

PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 581  
ID ADI02755 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 582  
ID ADH78074 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #13.  
PN US2003181687-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 583  
ID ADI25713 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 584  
ID ADI25883 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 585  
ID ADK65395 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 586  
ID ADH98737 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 587  
ID ADH79978 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 588  
ID ADL32745 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 589  
ID ADL32745 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003073813-A1.



DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 12; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 609  
ID ADH39177 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 12; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 610  
ID ADH26069 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 12; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 611  
ID ADG83917 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #13.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 12; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 612  
ID ADH19410 standard; cDNA; 870 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO842.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 12; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 613  
ID ADG85461 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 12; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 614  
ID ADH06255 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 12; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 615  
ID ADH30085 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 12; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 616  
ID ADH24397 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 12; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 617  
ID ADH33038 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #70.

PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 12; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 618  
ID ADG69526 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 12; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 619  
ID ADH07789 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 12; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 620  
ID ADG85801 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 12; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 621  
ID ADH39347 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 12; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 622  
ID ADH33539 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #13.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 12; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 623  
ID ADH33879 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #13.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 12; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 624  
ID ADH01089 standard; cDNA; 870 BP.  
DE Human PRO polynucleotide #13.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 12; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 625  
ID ADG49696 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 12; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 626  
ID ADH20903 standard; cDNA; 870 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO842.  
PN US2003224358-A1.

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PD 04-DEC-2003.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 627
ID ADH02182 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 628
ID ADG69186 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 629
ID ADG85971 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 630
ID ADH24907 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 631
ID ADH39524 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 632
ID ADH19943 standard; cDNA; 870 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO842.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 633
ID ADH02523 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 634
ID ADG69016 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 635
ID ADH07619 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 636
ID ADG86141 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 637
ID ADH24737 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 638
ID ADH25785 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 639
ID ADH38351 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 640
ID ADH57190 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 641
ID ADH52178 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 642
ID ADH49544 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 643
ID ADH90506 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 644
ID ADI11242 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
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Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 645
ID ADJ98907 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 646
ID ADJ02137 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 647
ID ADJ90676 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 648
ID ADJ54777 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 649
ID ADJ98551 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 650
ID ADJ98721 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 651
ID ADJ78880 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 652
ID ADJ99114 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 653
ID ADJ93284 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 654
ID ADJ98902 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 655
ID ADH79050 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 656
ID ADK00910 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 657
ID ADK14431 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 658
ID ADJ64548 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #70.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 659
ID ADM31444 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 660
ID ADM36491 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 661
ID ADM40296 standard; cDNA; 870 BP.
DE Novel human secreted and transmembrane protein PRO842 cDNA.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 662
ID ADM80880 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
RESULT 663
ID ADM80880 standard; cDNA; 870 BP.
DE Human PRO polynucleotide #13.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 870; DB 12; Length 870;
Best Local Similarity 100.0%; Pred. No. 4.3e-229;
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ID ADN37904 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 12; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 664  
ID ADY77720 standard; cDNA; 870 BP.  
DE Neoplastic disease detection cDNA PRO842.  
PN US2005059102-A1.  
PD 17-MAR-2005.  
PA (EATO/) EATON D L.  
PA (FILV/) FILVAROFF E.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 870; DB 14; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 665  
ID AD245056 standard; cDNA; 870 BP.  
DE Human PRO842 encoding cDNA SEQ ID NO:1.  
PN US2005100544-A1.  
PD 12-MAY-2005.  
PA (EATO/) EATON D L.  
PA (PLSA/) PISABARRO M T.  
PA (SCHM/) SCHMIDT K N.  
PA (VAND/) VANDLEN R.  
PA (CHIA/) CHIANG N.  
PA (DIEH/) DIEHL L.  
Query Match 100.0%; Score 870; DB 14; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 666  
ID AEA38433 standard; cDNA; 870 BP.  
DE Human secreted/transmembrane protein cDNA, #107.  
PN US2005112725-A1.  
PD 26-MAY-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 14; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 667  
ID AED50134 standard; cDNA; 870 BP.  
DE Novel human secreted and transmembrane protein PRO842 cDNA.  
PN US2005163766-A1.  
PD 28-JUL-2005.  
Query Match 100.0%; Score 870; DB 14; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 668  
ID AEF12551 standard; cDNA; 870 BP.  
DE Human PRO842 cDNA SEQ ID NO:25.  
PN US2006008901-A1.  
PD 12-JAN-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 870; DB 15; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 669  
ID AEF74240 standard; cDNA; 870 BP.  
DE Human PRO842 encoding cDNA SEQ ID NO:25.  
PN US2005260647-A1.  
PD 24-NOV-2005.  
PA (FILV/) FILVAROFF E.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W L.

Query Match 100.0%; Score 870; DB 15; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
RESULT 670  
ID ACD27900 standard; cDNA; 868 BP.  
DE cDNA encoding human PRO842 polypeptide.  
PN US2003065154-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 99.8%; Score 868; DB 9; Length 868;  
Best Local Similarity 100.0%; Pred. No. 1.5e-228;  
RESULT 671  
ID AAZ98202 standard; cDNA; 870 BP.  
DE Human signal peptide containing protein HSPP-94 cDNA SEQ ID NO:228.  
PN WO200000610-A2.  
PD 06-JAN-2000.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 99.1%; Score 862.4; DB 3; Length 870;  
Best Local Similarity 99.9%; Pred. No. 5.3e-227;  
RESULT 672  
ID ADQ86898 standard; cDNA; 1118 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3773.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 98.5%; Score 856.6; DB 12; Length 1118;  
Best Local Similarity 99.5%; Pred. No. 2.4e-225;  
RESULT 673  
ID AAH7951 standard; DNA; 1171 BP.  
DE Nucleotide sequence of a human Lng104 polypeptide.  
PN WO200161055-A2.  
PD 23-AUG-2001.  
PA (DIAD-) DIADEXUS INC.  
Query Match 98.5%; Score 856.6; DB 4; Length 1171;  
Best Local Similarity 99.5%; Pred. No. 2.4e-225;  
RESULT 674  
ID ADE39934 standard; cDNA; 1171 BP.  
DE Human lung disorder-related cDNA - SEQ ID 4.  
PN US2003124580-A1.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 98.5%; Score 856.6; DB 10; Length 1171;  
Best Local Similarity 99.5%; Pred. No. 2.4e-225;  
RESULT 675  
ID ACF58050 standard; cDNA; 1172 BP.  
DE Human VCC-1 polypeptide encoding cDNA.  
PN WO2003087157-A2.  
PD 23-OCT-2003.  
PA (PHAA ) PHARMACIA CORP.  
Query Match 98.5%; Score 856.6; DB 10; Length 1172;  
Best Local Similarity 99.5%; Pred. No. 2.4e-225;  
RESULT 676  
ID ADL01574 standard; DNA; 1172 BP.  
DE Human VEGF co-regulated chemokine-1 (VCC-1) DNA.  
PN WO2004016224-A2.  
PD 26-FEB-2004.  
PA (PHAA ) PHARMACIA CORP.  
Query Match 98.5%; Score 856.6; DB 12; Length 1172;  
Best Local Similarity 99.5%; Pred. No. 2.4e-225;  
RESULT 677  
ID ADP07625 standard; DNA; 1214 BP.  
DE Human secreted protein encoding DNA, seq id 108.  
PN WO2004042000-A2.  
PD 21-MAY-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 98.5%; Score 856.6; DB 12; Length 1214;  
Best Local Similarity 99.5%; Pred. No. 2.4e-225;  
RESULT 678  
ID ABA09257 standard; cDNA; 1148 BP.  
DE Human TGC-440 homologue-encoding cDNA, SEQ ID NO:1033.  
PN WO200157188-A2.  
PD 09-AUG-2001.



PA (HYSE-) HYSEQ INC.  
 Query Match 98.3%; Score 855; DB 4; Length 1148;  
 Best Local Similarity 99.4%; Pred. No. 6.6e-225;  
 RESULT 679  
 ID AAZ29726 standard; DNA; 895 BP.  
 DE Human lung specific gene-3.  
 PN WO9960160-A1.  
 PD 25-NOV-1999.  
 PA (DIAD-) DIADEXUS LLC.  
 Query Match 97.9%; Score 852; DB 3; Length 895;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-224;  
 RESULT 680  
 ID AAH77949 standard; DNA; 895 BP.  
 DE Nucleotide sequence of a human Lng104 polypeptide.  
 PN WO200161055-A2.  
 PD 23-AUG-2001.  
 PA (DIAD-) DIADEXUS INC.  
 Query Match 97.9%; Score 852; DB 4; Length 895;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-224;  
 RESULT 681  
 ID ADK70291 standard; cDNA; 856 BP.  
 DE Respiratory disease differentially expressed cDNA #27.  
 PN WO2003101283-A2.  
 PD 11-DEC-2003.  
 PA (INCY-) INCYTE CORP.  
 Query Match 97.7%; Score 850; DB 12; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-223;  
 RESULT 682  
 ID ADY30447 standard; DNA; 1131 BP.  
 DE Human splice variant DNA expressed in ovary cells DEX0487\_006.nt.1.  
 PN WO2005017102-A2.  
 PD 24-FEB-2005.  
 PA (DIAD-) DIADEXUS INC.  
 Query Match 92.2%; Score 802.2; DB 14; Length 1131;  
 Best Local Similarity 97.8%; Pred. No. 2.3e-210;  
 RESULT 683  
 ID ADY30448 standard; DNA; 1111 BP.  
 DE Human splice variant DNA expressed in ovary cells DEX0487\_006.nt.2.  
 PN WO2005017102-A2.  
 PD 24-FEB-2005.  
 PA (DIAD-) DIADEXUS INC.  
 Query Match 89.3%; Score 777; DB 14; Length 1111;  
 Best Local Similarity 99.4%; Pred. No. 2e-203;  
 RESULT 684  
 ID ADP07697 standard; DNA; 750 BP.  
 DE Human secreted protein encoding DNA, seq id 180.  
 PN WO2004042000-A2.  
 PD 21-MAY-2004.  
 PA (HUNA-) HUMAN GENOME SCI INC.  
 Query Match 81.4%; Score 708.6; DB 12; Length 750;  
 Best Local Similarity 99.4%; Pred. No. 1.2e-184;  
 RESULT 685  
 ID AAA08343 standard; DNA; 849 BP.  
 DE Human TGC-440 secretory protein nucleotide sequence.  
 PN WO200014226-A1.  
 PD 16-MAR-2000.  
 PA (TAKS-) TAKEDA CHEM IND LTD.  
 Query Match 77.1%; Score 670.8; DB 3; Length 849;  
 Best Local Similarity 89.1%; Pred. No. 3.4e-174;  
 RESULT 686  
 ID ADT50719 standard; DNA; 972 BP.  
 DE Cancer related nucleic acid sequence #23.  
 PN WO2004092338-A2.  
 PD 28-OCT-2004.  
 PA (DIAD-) DIADEXUS INC.  
 Query Match 73.3%; Score 637.6; DB 13; Length 972;  
 Best Local Similarity 99.1%; Pred. No. 5.1e-165;  
 RESULT 687  
 ID AAC59829 standard; DNA; 654 BP.  
 DE Human secreted protein encoding DNA clone vq8 1.  
 PN WO200055375-A1.  
 PD 21-SEP-2000.  
 PA (ALPH-) ALPHAGEN INC.

Query Match 72.4%; Score 630; DB 3; Length 654;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-163;  
 RESULT 688  
 ID ADT50720 standard; DNA; 942 BP.  
 DE Cancer related nucleic acid sequence #24.  
 PN WO2004092338-A2.  
 PD 28-OCT-2004.  
 PA (DIAD-) DIADEXUS INC.  
 Query Match 71.9%; Score 625.6; DB 13; Length 942;  
 Best Local Similarity 99.4%; Pred. No. 1e-161;  
 RESULT 689  
 ID ADT50721 standard; DNA; 877 BP.  
 DE Cancer related nucleic acid sequence #25.  
 PN WO2004092338-A2.  
 PD 28-OCT-2004.  
 PA (DIAD-) DIADEXUS INC.  
 Query Match 65.5%; Score 570; DB 13; Length 877;  
 Best Local Similarity 97.4%; Pred. No. 2.1e-146;  
 RESULT 690  
 ID AAF68195 standard; cDNA; 533 BP.  
 DE Human lung tumour protein related nucleotide sequence SEQ ID NO:113.  
 PN WO200100828-A2.  
 PD 04-JAN-2001.  
 PA (CORI-) CORIXA CORP.  
 Query Match 60.4%; Score 525.8; DB 5; Length 533;  
 Best Local Similarity 99.6%; Pred. No. 2.5e-134;  
 RESULT 691  
 ID ABK38106 standard; cDNA; 533 BP.  
 DE cDNA encoding clone #18471 of lung tumour protein.  
 PN WO200204514-A2.  
 PD 17-JAN-2002.  
 PA (CORI-) CORIXA CORP.  
 Query Match 60.4%; Score 525.8; DB 6; Length 533;  
 Best Local Similarity 99.6%; Pred. No. 2.5e-134;  
 RESULT 692  
 ID ACA10435 standard; cDNA; 533 BP.  
 DE Human lung cancer-associated cDNA, SEQ ID 113.  
 PN US2002197669-A1.  
 PD 26-DEC-2002.  
 PA (BANG-) BANGUR C S.  
 PA (FANG-) FANGER G R.  
 PA (WANG-) WANG A.  
 PA (SWIT-) SWITZER A P.  
 PA (MCNE-) MCNEILL P D.  
 PA (CLAP-) CLAPPER J D.  
 Query Match 60.4%; Score 525.8; DB 8; Length 533;  
 Best Local Similarity 99.6%; Pred. No. 2.5e-134;  
 RESULT 693  
 ID ABX99386 standard; cDNA; 533 BP.  
 DE Lung cancer therapyand diagnosis associated cDNA #113.  
 PN US2002172952-A1.  
 PD 21-NOV-2002.  
 PA (CORI-) CORIXA CORP.  
 Query Match 60.4%; Score 525.8; DB 8; Length 533;  
 Best Local Similarity 99.6%; Pred. No. 2.5e-134;  
 RESULT 694  
 ID ADH45632 standard; cDNA; 533 BP.  
 DE Human lung tumour cDNA clone, SEQ ID No 113.  
 PN WO2003037267-A2.  
 PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 60.4%; Score 525.8; DB 10; Length 533;  
 Best Local Similarity 99.6%; Pred. No. 2.5e-134;  
 RESULT 695  
 ID ADE72169 standard; cDNA; 533 BP.  
 DE Human lung tumour protein cDNA #113.  
 PN US2003125245-A1.  
 PD 03-JUL-2003.  
 PA (WANG-) WANG T.  
 PA (BANG-) BANGUR C S.  
 Query Match 60.4%; Score 525.8; DB 12; Length 533;  
 Best Local Similarity 99.6%; Pred. No. 2.5e-134;

RESULT 696  
ID ADJ19551 standard; cDNA; 533 BP.  
DE Human lung cancer-related cDNA - SEQ ID 113.  
PN US2003211510-A1.  
PD 13-NOV-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 60.4%; Score 525.8; DB 13; Length 533;  
Best Local Similarity 99.6%; Pred. No. 2.5e-134;  
RESULT 697  
ID ADP07674 standard; DNA; 569 BP.  
DE Human secreted protein encoding DNA, seq id 157.  
PN WO2004042000-A2.  
PD 21-MAY-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 59.7%; Score 519; DB 12; Length 569;  
Best Local Similarity 100.0%; Pred. No. 1.9e-132;  
RESULT 698  
ID ADM67834 standard; DNA; 569 BP.  
DE Human secreted protein encoding DNA, seq id 81.  
PN WO2004042000-A2.  
PD 21-MAY-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 59.7%; Score 519; DB 13; Length 569;  
Best Local Similarity 100.0%; Pred. No. 1.9e-132;  
RESULT 699  
ID ADP07670 standard; DNA; 573 BP.  
DE Human secreted protein encoding DNA, seq id 153.  
PN WO2004042000-A2.  
PD 21-MAY-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 59.7%; Score 519; DB 12; Length 573;  
Best Local Similarity 100.0%; Pred. No. 2e-132;  
RESULT 700  
ID ADP07619 standard; DNA; 569 BP.  
DE Human secreted protein encoding DNA, seq id 102.  
PN WO2004042000-A2.  
PD 21-MAY-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 59.6%; Score 518.2; DB 12; Length 569;  
Best Local Similarity 99.6%; Pred. No. 3.2e-132;  
RESULT 701  
ID ACF58052 standard; DNA; 524 BP.  
DE Human VCC-1 expressed sequence tag (EST) fragment.  
PN WO2003087157-A2.  
PD 23-OCT-2003.  
PA (PHAA) PHARMACIA CORP.  
Query Match 51.4%; Score 447.2; DB 10; Length 524;  
Best Local Similarity 97.7%; Pred. No. 1.2e-112;  
RESULT 702  
ID ABK87217 standard; DNA; 30709 BP.  
DE Human lipase, hormone-sensitive (LIPE) gene sequence.  
Query Match 50.9%; Score 443; DB 6; Length 30709;  
Best Local Similarity 98.9%; Pred. No. 1e-110;  
RESULT 703  
ID ABL64634 standard; DNA; 419 BP.  
DE Stomach cancer related gene sequence SEQ ID NO:2971.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 47.8%; Score 415.8; DB 6; Length 419;  
Best Local Similarity 99.5%; Pred. No. 4.7e-104;  
RESULT 704  
ID AAV69618 standard; DNA; 511 BP.  
DE Human secreted protein gene 8 clone HLHCM89.  
PN WO9845712-A2.  
PD 15-OCT-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 46.2%; Score 402.2; DB 2; Length 511;  
Best Local Similarity 97.7%; Pred. No. 2.9e-100;  
RESULT 705  
ID AAX40454 standard; cDNA; 365 BP.  
DE Human secreted protein 5' EST SEQ ID No: 54.  
PN WO9906550-A2.  
PD 13-NOV-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 35.9%; Score 312; DB 12; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.7e-75;  
RESULT 706  
ID AAA08344 standard; DNA; 357 BP.  
DE Human TGC-440 secretory protein nucleotide sequence SEQ ID NO:4.  
PN WO200014226-A1.  
PD 16-MAR-2000.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Query Match 41.0%; Score 357; DB 3; Length 357;  
Best Local Similarity 100.0%; Pred. No. 7.1e-88;  
RESULT 707  
ID AAF68125 standard; cDNA; 312 BP.  
DE Human lung tumour protein related nucleotide sequence SEQ ID NO:43.  
PN WO200100828-A2.  
PD 04-JAN-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 35.9%; Score 312; DB 5; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.7e-75;  
RESULT 708  
ID ABK38036 standard; cDNA; 312 BP.  
DE cDNA encoding clone #18950 of lung tumour protein.  
PN WO200204514-A2.  
PD 17-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 35.9%; Score 312; DB 6; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.7e-75;  
RESULT 709  
ID ACA10365 standard; cDNA; 312 BP.  
DE Human lung cancer-associated cDNA, SEQ ID 43.  
PN US2002197669-A1.  
PD 26-DEC-2002.  
PA (BANG/) BANGUR C S.  
PA (FANG/) FANGER G R.  
PA (WANG/) WANG A.  
PA (WANG/) WANG T.  
PA (SWIT/) SWITZER A P.  
PA (MCNE/) MCNEILL P D.  
PA (CLAP/) CLAPPER J D.  
Query Match 35.9%; Score 312; DB 8; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.7e-75;  
RESULT 710  
ID ABX99316 standard; cDNA; 312 BP.  
DE Lung cancer therapyand diagnosis associated cDNA #43.  
PN US2002172952-A1.  
PD 21-NOV-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 35.9%; Score 312; DB 8; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.7e-75;  
RESULT 711  
ID ADH45562 standard; cDNA; 312 BP.  
DE Human lung tumour cDNA clone, SEQ ID No 43.  
PN WO2003037267-A2.  
PD 08-MAY-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 35.9%; Score 312; DB 10; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.7e-75;  
RESULT 712  
ID ADE72099 standard; cDNA; 312 BP.  
DE Human lung tumour protein cDNA #43.  
PN US2003125245-A1.  
PD 03-JUL-2003.  
PA (WANG/) WANG T.  
PA (BANG/) BANGUR C S.  
Query Match 35.9%; Score 312; DB 12; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.7e-75;  
RESULT 713  
ID ADJ19481 standard; cDNA; 312 BP.  
DE Human lung cancer-related cDNA - SEQ ID 43.  
PN US2003211510-A1.  
PD 13-NOV-2003.  
PA (CORI-) CORIXA CORP.

Query Match  
Best Local Similarity 35.9%; Score 312; DB 13; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.7e-75;  
RESULT 714  
ID AAA08345 standard; DNA; 291 BP.  
DE Mature human TGC-440 secretory protein nucleotide sequence SEQ ID NO:10.  
PN WO200014226-A1.  
PD 16-MAR-2000.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match  
Best Local Similarity 100.0%; Score 291; DB 3; Length 291;  
Best Local Similarity 100.0%; Pred. No. 1e-69;  
RESULT 715  
ID AAA08349 standard; DNA; 764 BP.  
DE Mouse TGC-440 secretory protein nucleotide sequence.  
PN WO200014226-A1.  
PD 16-MAR-2000.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match  
Best Local Similarity 30.1%; Score 262.2; DB 3; Length 764;  
Best Local Similarity 70.2%; Pred. No. 1.3e-61;  
RESULT 716  
ID ACF58051 standard; cDNA; 829 BP.  
DE Mouse VCC-1 polypeptide encoding cDNA.  
PN WO2003087157-A2.  
PD 23-OCT-2003.  
PA (PHAA ) PHARMACIA CORP.  
Query Match  
Best Local Similarity 30.1%; Score 261.8; DB 10; Length 829;  
Best Local Similarity 73.0%; Pred. No. 1.8e-61;  
RESULT 717  
ID AAA08350 standard; DNA; 357 BP.  
DE Mouse TGC-440 secretory protein nucleotide sequence SEQ ID NO:6.  
PN WO200014226-A1.  
PD 16-MAR-2000.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match  
Best Local Similarity 28.2%; Score 245.6; DB 3; Length 357;  
Best Local Similarity 80.8%; Pred. No. 3.6e-57;  
RESULT 718  
ID AAA08346 standard; DNA; 959 BP.  
DE Rat TGC-440 secretory protein nucleotide sequence.  
PN WO200014226-A1.  
PD 16-MAR-2000.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match  
Best Local Similarity 27.8%; Score 241.8; DB 3; Length 959;  
Best Local Similarity 73.1%; Pred. No. 6.2e-56;  
RESULT 719  
ID ABL82746 standard; cDNA; 242 BP.  
DE Human ovarian cancer related cDNA clone SEQ ID NO:5724.  
PN WO200192581-A2.  
PD 06-DEC-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 100.0%; Score 238; DB 6; Length 242;  
Best Local Similarity 100.0%; Pred. No. 3.7e-55;  
RESULT 720  
ID ABL82746 standard; DNA; 242 BP.  
DE Human ovarian cancer related cDNA clone SEQ ID NO:5724.  
PN WO200192581-A2.  
PD 06-DEC-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 27.4%; Score 231.8; DB 10; Length 553;  
Best Local Similarity 97.0%; Pred. No. 2.8e-53;  
RESULT 721  
ID AAX40453 standard; cDNA; 235 BP.  
DE Human secreted protein 5' EST SEQ ID NO: 53.  
PN WO9906550-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match  
Best Local Similarity 26.3%; Score 228.4; DB 2; Length 235;  
Best Local Similarity 98.7%; Pred. No. 1.6e-52;  
RESULT 722  
ID AAA08347 standard; DNA; 357 BP.  
DE Rat TGC-440 secretory protein nucleotide sequence SEQ ID NO:5.  
PN WO200014226-A1.  
PD 16-MAR-2000.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match  
Best Local Similarity 26.2%; Score 228; DB 3; Length 357;  
Best Local Similarity 100.0%; Pred. No. 1.7e-75;  
Best Local Similarity 100.0%; Pred. No. 1.5e-52;  
ID ADL84236 standard; DNA; 403 BP.  
DE DNA up-regulated in murine common lymphoid progenitor cells SeqID 629.  
PN WO2003093445-A2.  
PD 13-NOV-2003.  
PA (STOW-) STOWERS INST MEDICAL RES.  
Query Match  
Best Local Similarity 25.1%; Score 218; DB 12; Length 403;  
Best Local Similarity 74.0%; Pred. No. 1.5e-49;  
RESULT 724  
ID ADL84235 standard; DNA; 403 BP.  
DE DNA up-regulated in murine common lymphoid progenitor cells SeqID 628.  
PN WO2003093445-A2.  
PD 13-NOV-2003.  
PA (STOW-) STOWERS INST MEDICAL RES.  
Query Match  
Best Local Similarity 25.1%; Score 218; DB 12; Length 403;  
Best Local Similarity 74.0%; Pred. No. 1.5e-49;  
RESULT 725  
ID ABT22609 standard; DNA; 357 BP.  
DE Breast cancer marker gene SEQ ID NO 982.  
PN WO200285298-A2.  
PD 31-OCT-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 23.4%; Score 203.2; DB 10; Length 357;  
Best Local Similarity 71.7%; Pred. No. 1.7e-45;  
RESULT 726  
ID AAA08351 standard; DNA; 291 BP.  
DE Mature mouse TGC-440 secretory protein nucleotide sequence SEQ ID NO:12.  
PN WO200014226-A1.  
PD 16-MAR-2000.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match  
Best Local Similarity 23.0%; Score 200.4; DB 3; Length 291;  
Best Local Similarity 80.7%; Pred. No. 9.4e-45;  
RESULT 727  
ID AAT25820 standard; cDNA to mRNA; 195 BP.  
DE Human gene signature HUMG08049.  
PN WO9514772-A1.  
PD 01-JUN-1995.  
PA (MATS/) MATSUBARA K.  
PA (OKUB/) OKUBO K.  
Query Match  
Best Local Similarity 22.1%; Score 192; DB 2; Length 195;  
Best Local Similarity 98.5%; Pred. No. 1.6e-42;  
RESULT 728  
ID AAA08348 standard; DNA; 291 BP.  
DE Mature rat TGC-440 secretory protein nucleotide sequence SEQ ID NO:11.  
PN WO200014226-A1.  
PD 16-MAR-2000.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match  
Best Local Similarity 21.7%; Score 189.2; DB 3; Length 291;  
Best Local Similarity 78.3%; Pred. No. 1.1e-41;  
RESULT 729  
ID AED3177 standard; DNA; 81 BP.  
DE Contig 510 amplicon.  
PN WO2005100606-A2.  
PD 27-OCT-2005.  
PA (GENO-) GENOMIC HEALTH INC.  
Query Match  
Best Local Similarity 9.3%; Score 81; DB 14; Length 81;  
Best Local Similarity 100.0%; Pred. No. 4.3e-12;  
RESULT 730  
ID AAS07713 standard; DNA; 97 BP.  
DE Cervical cancer pre-malignant condition DNA marker #12.  
PN WO200142792-A2.  
PD 14-JUN-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 8.4%; Score 73.4; DB 4; Length 97;  
Best Local Similarity 86.0%; Pred. No. 5.7e-10;  
RESULT 731  
ID AAH70020 standard; cDNA; 518 BP.  
DE Human cervical cancer marker nucleic acid 1294.  
PN WO200142467-A2.  
PD 14-JUN-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 5.3%; Score 45.8; DB 4; Length 518;

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Best Local Similarity 74.3%; Pred. No. 0.05;
RESULT 732
ID AAA08356 standard; DNA; 51 BP.
DE Human TGC-440 secretory protein PCR primer SEQ ID NO:17.
PN WO200014226-A1.
PD 16-MAR-2000.
PA (TAKE ) TAKEDA CHEM IND LTD.
Query Match 5.1%; Score 44.6; DB 3; Length 51;
Best Local Similarity 92.2%; Pred. No. 0.037;
RESULT 733
ID AAF23906 standard; cDNA; 1484 BP.
DE Human secreted protein cDNA #13.
PN WO20007173-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.0%; Score 43.8; DB 4; Length 1484;
Best Local Similarity 62.2%; Pred. No. 0.28;
RESULT 734
ID ABD33526 standard; DNA; 31312 BP.
DE Murine cancer-associated (CA) gene MD07-104.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 5.0%; Score 43.2; DB 13; Length 31312;
Best Local Similarity 51.6%; Pred. No. 1.7;
RESULT 735
ID AAH71445 standard; cDNA; 456 BP.
DE Human cervical cancer marker nucleic acid 2719.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.9%; Score 42.8; DB 4; Length 456;
Best Local Similarity 86.8%; Pred. No. 0.31;
RESULT 736
ID ACN5539 standard; cDNA; 526 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-025-Q6-N6-B7, SEQ:10320.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 42.4; DB 13; Length 526;
Best Local Similarity 49.5%; Pred. No. 0.43;
RESULT 737
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
Query Match 4.8%; Score 42; DB 8; Length 2000;
Best Local Similarity 9.2%; Pred. No. 1;
RESULT 738
ID ACN91732 standard; DNA; 631 BP.
DE Breast cancer related marker, seq id 2882.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.8%; Score 41.8; DB 11; Length 631;
Best Local Similarity 41.4%; Pred. No. 0.69;
RESULT 739
ID ABQ74348 standard; DNA; 27359 BP.
DE Human transporter protein encoding gene SEQ ID NO:3.
Query Match 4.8%; Score 41.8; DB 6; Length 27359;
Best Local Similarity 59.8%; Pred. No. 3.8;
RESULT 740
ID ACN52919 standard; cDNA; 428 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-019-Q1-N6-D7, SEQ:7700.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.8%; Score 41.6; DB 13; Length 428;
Best Local Similarity 48.3%; Pred. No. 1.1;
RESULT 741
ID ADR63959 standard; cDNA; 574 BP.
DE Cotton cDNA sequence, SEQ ID 4740.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
Query Match 4.8%; Score 41.6; DB 13; Length 574;
Best Local Similarity 62.5%; Pred. No. 0.75;
RESULT 742
ID ADI69792 standard; DNA; 384 BP.
DE Human ovarian cancer DNA marker #2534.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.8%; Score 41.4; DB 5; Length 384;
Best Local Similarity 43.8%; Pred. No. 0.71;
RESULT 743
ID ADI76128 standard; DNA; 384 BP.
DE Human ovarian cancer DNA marker #8870.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.8%; Score 41.4; DB 5; Length 384;
Best Local Similarity 43.8%; Pred. No. 0.71;
RESULT 744
ID ACN53688 standard; cDNA; 421 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-K6-E3, SEQ:8469.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 40.8; DB 13; Length 421;
Best Local Similarity 48.3%; Pred. No. 1.1;
RESULT 745
ID ACN55836 standard; cDNA; 509 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-029-Q6-N6-B5, SEQ:10617.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 40.8; DB 13; Length 509;
Best Local Similarity 49.1%; Pred. No. 1.2;
RESULT 746
ID ACN58719 standard; cDNA; 534 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-011-Q6-N6-B7, SEQ:13500.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.7%; Score 40.6; DB 13; Length 534;
Best Local Similarity 48.9%; Pred. No. 1.4;
RESULT 747
ID ADL62362 standard; DNA; 1588 BP.
DE Human ovarian cancer DNA marker #20574.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.7%; Score 40.6; DB 5; Length 1588;
Best Local Similarity 58.8%; Pred. No. 2.2;
RESULT 748
ID ACN89723 standard; DNA; 2436 BP.
DE Breast cancer related marker, seq id 10873.
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PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 4.7%; Score 40.6; DB 11; Length 2436;  
Best Local Similarity 58.8%; Pred. No. 2.7;  
RESULT 749  
ID ADF82105 standard; DNA; 2619 BP.  
DE Leukaemia-related DNA sequence #2661.  
PN WO2003039443-A2.  
PD 15-MAY-2003.  
PA (DEK-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.  
PA (HAPE-) HAFERLACH T.  
PA (SCHO-) SCHOCH C.  
PA (KERN-) KERN W.  
Query Match 4.7%; Score 40.6; DB 10; Length 2619;  
Best Local Similarity 58.8%; Pred. No. 2.8;  
RESULT 750  
ID AED14464 standard; DNA; 2619 BP.  
DE Human cumulus cell differentially expressed gene.  
PN WO2005094306-A2.  
PD 13-OCT-2005.  
PA (UNMS) UNIV MICHIGAN STATE.  
Query Match 4.7%; Score 40.6; DB 14; Length 2619;  
Best Local Similarity 58.8%; Pred. No. 2.8;  
RESULT 751  
ID ABL33011 standard; DNA; 6171 BP.  
DE Human immune system associated gene SEQ ID NO: 984.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.6%; Score 40.4; DB 6; Length 6171;  
Best Local Similarity 46.2%; Pred. No. 4.7;  
RESULT 752  
ID ACN58276 standard; cDNA; 508 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-008-Q6-N6-D10, SEQ:13057.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK-) DEIKMAN J.  
PA (FENG-) FENG P C C.  
PA (FINC-) FINCHER K L.  
PA (ZIEG-) ZIEGLER T E.  
Query Match 4.6%; Score 40.2; DB 13; Length 508;  
Best Local Similarity 49.8%; Pred. No. 1.7;  
RESULT 753  
ID ABT42211 standard; DNA; 1186 BP.  
DE Toxicity modelling related rat gene SEQ ID No 1913.  
PN WO200295000-A2.  
PD 28-NOV-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 4.6%; Score 39.6; DB 10; Length 1186;  
Best Local Similarity 58.5%; Pred. No. 3.7;  
RESULT 754  
ID ADP72715 standard; DNA; 1186 BP.  
DE Renal toxin progression gene marker #1304.  
PN WO2004048598-A2.  
PD 10-JUN-2004.  
PA (GENE-) GENE LOGIC INC.  
Query Match 4.6%; Score 39.6; DB 12; Length 1186;  
Best Local Similarity 58.5%; Pred. No. 3.7;  
RESULT 755  
ID ABV55803 standard; cDNA; 428 BP.  
DE Human prostate expression marker cDNA 55794.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.5%; Score 39.4; DB 5; Length 428;  
Best Local Similarity 67.9%; Pred. No. 2.6;  
RESULT 756  
ID ABV51376 standard; cDNA; 488 BP.  
DE Human prostate expression marker cDNA 51367.  
PN WO200160860-A2.  
PD 23-AUG-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.5%; Score 39.4; DB 5; Length 488;  
Best Local Similarity 59.3%; Pred. No. 2.8;  
RESULT 757  
ID ABV44994 standard; cDNA; 309 BP.  
DE Human prostate expression marker cDNA 44985.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.5%; Score 39.2; DB 5; Length 309;  
Best Local Similarity 48.6%; Pred. No. 2.6;  
RESULT 758  
ID ACN52334 standard; cDNA; 571 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-E11, SEQ:7115.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK-) DEIKMAN J.  
PA (FENG-) FENG P C C.  
PA (FINC-) FINCHER K L.  
PA (ZIEG-) ZIEGLER T E.  
Query Match 4.5%; Score 39.2; DB 13; Length 571;  
Best Local Similarity 49.5%; Pred. No. 3.4;  
RESULT 759  
ID ACN60732 standard; cDNA; 587 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-027-Q6-K6-B6, SEQ:15513.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK-) DEIKMAN J.  
PA (FENG-) FENG P C C.  
PA (FINC-) FINCHER K L.  
PA (ZIEG-) ZIEGLER T E.  
Query Match 4.5%; Score 39.2; DB 13; Length 587;  
Best Local Similarity 49.1%; Pred. No. 3.5;  
RESULT 760  
ID ADQ23418 standard; DNA; 1873 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6238.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.5%; Score 39.2; DB 12; Length 1873;  
Best Local Similarity 58.6%; Pred. No. 5.9;  
RESULT 761  
ID ADV34961 standard; cDNA; 1873 BP.  
DE Human cDNA differentially expressed in the presence of valproate SeqID37.  
PN US2003096264-A1.  
PD 22-MAY-2003.  
PA (PSYC-) PSYCHIATRIC GENOMICS INC.  
Query Match 4.5%; Score 39.2; DB 13; Length 1873;  
Best Local Similarity 58.6%; Pred. No. 5.9;  
RESULT 762  
ID ABK39934 standard; DNA; 5321 BP.  
DE Human chemically pretreated gene sequence #8 strand 1.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.5%; Score 39.2; DB 6; Length 5321;  
Best Local Similarity 64.1%; Pred. No. 9.4;  
RESULT 763  
ID ABL92194 standard; DNA; 5321 BP.  
DE Chemically treated DNA repair gene fragment#2.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.5%; Score 39.2; DB 6; Length 5321;  
Best Local Similarity 64.1%; Pred. No. 9.4;  
RESULT 764  
ID AAK71873 standard; DNA; 775 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26685.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.5%; Score 39; DB 4; Length 775;  
Best Local Similarity 58.0%; Pred. No. 4.5;

RESULT 765  
ID AAK71874 standard; DNA; 775 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26686.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 58.0%; Score 39; DB 4; Length 775;  
RESULT 766  
ID ABV78103 standard; DNA; 1790 BP.  
DE Hypoxia-regulated protein coding sequence #123.  
PN WO200246465-A2.  
PD 13-JUN-2002.  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
Query Match  
Best Local Similarity 4.5%; Score 39; DB 6; Length 1790;  
Best Local Similarity 68.4%; Pred. No. 6.5;  
RESULT 767  
ID ADQ23564 standard; DNA; 2249 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6384.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match  
Best Local Similarity 4.5%; Score 39; DB 12; Length 2249;  
Best Local Similarity 59.5%; Pred. No. 7.2;  
RESULT 768  
ID ACH30440 standard; cDNA; 413 BP.  
DE Human testis cDNA #826.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRNA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match  
Best Local Similarity 4.5%; Score 38.8; DB 9; Length 413;  
Best Local Similarity 62.2%; Pred. No. 3.8;  
RESULT 769  
ID ACN49737 standard; cDNA; 546 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-026-Q6-N6-B2, SEQ:4518.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.5%; Score 38.8; DB 13; Length 546;  
Best Local Similarity 48.6%; Pred. No. 4.3;  
RESULT 770  
ID ABQ54479 standard; cDNA; 862 BP.  
DE Human ovarian antigen RHORE03 cDNA, SEQ ID NO:359.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 4.5%; Score 38.8; DB 6; Length 862;  
Best Local Similarity 55.1%; Pred. No. 5.3;  
RESULT 771  
ID ADN05367 standard; cDNA; 1913 BP.  
DE Antipsoriatic cDNA sequence #906.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH/) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 38.8; DB 12; Length 1913;  
Best Local Similarity 58.8%; Pred. No. 7.6;  
RESULT 772  
ID ABN79984 standard; DNA; 16633 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 1.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.5%; Score 38.8; DB 6; Length 16633;  
Best Local Similarity 67.1%; Pred. No. 20;  
RESULT 773  
ID ADQ17536 standard; DNA; 332 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 353.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match  
Best Local Similarity 4.4%; Score 38.6; DB 12; Length 332;  
Best Local Similarity 55.6%; Pred. No. 3.9;  
RESULT 774  
ID AAK58069 standard; cDNA; 356 BP.  
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:3129.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 4.4%; Score 38.6; DB 4; Length 356;  
Best Local Similarity 57.1%; Pred. No. 4;  
RESULT 775  
ID ADQ22236 standard; DNA; 1083 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5056.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match  
Best Local Similarity 4.4%; Score 38.6; DB 12; Length 1083;  
Best Local Similarity 55.6%; Pred. No. 6.7;  
RESULT 776  
ID ABN95915 standard; DNA; 2125 BP.  
DE Gene #2413 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match  
Best Local Similarity 4.4%; Score 38.6; DB 6; Length 2125;  
Best Local Similarity 63.4%; Pred. No. 9.1;  
RESULT 777  
ID AAL57274 standard; DNA; 2125 BP.  
DE IGFALS 'human modifier of p53 pathway' DNA.  
PN WO2003035833-A2.  
PD 01-MAY-2003.  
PA (EXEL-) EXELIXIS INC.  
Query Match  
Best Local Similarity 4.4%; Score 38.6; DB 8; Length 2125;  
Best Local Similarity 63.4%; Pred. No. 9.1;  
RESULT 778  
ID ABL33883 standard; DNA; 6609 BP.  
DE Human immune system associated gene SEQ ID NO: 1856.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.4%; Score 38.6; DB 6; Length 6609;  
Best Local Similarity 54.0%; Pred. No. 15;  
RESULT 779  
ID ABN80247 standard; DNA; 6609 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 264.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.4%; Score 38.6; DB 6; Length 6609;  
Best Local Similarity 54.0%; Pred. No. 15;  
RESULT 780  
ID AAL11578 standard; cDNA; 337 BP.  
DE Human breast cancer expressed polynucleotide 4035.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 4.4%; Score 38.4; DB 4; Length 337;  
Best Local Similarity 42.1%; Pred. No. 4.5;  
RESULT 781  
ID ACN81779 standard; DNA; 424 BP.  
DE Breast cancer related marker, seq id 2929.  
PN US200309974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 4.4%; Score 38.4; DB 11; Length 424;  
Best Local Similarity 42.1%; Pred. No. 5;  
RESULT 782  
ID ACN46935 standard; cDNA; 499 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-005-Q1-N6-D10, SEQ:1716.

PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIRMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.4%; Score 38.4; DB 13; Length 499;  
Best Local Similarity 47.8%; Pred. No. 5.3;  
RESULT 783  
ID ACD07397 standard; cDNA; 1072 BP.  
DE Bread wheat Myb-related transcription factor #2 cDNA.  
PN US2003024007-A1.  
PD 30-JAN-2003.  
PA (CAHO/) CAHOON R E.  
PA (ODEL/) ODELL J T.  
Query Match 4.4%; Score 38.4; DB 8; Length 1072;  
Best Local Similarity 57.5%; Pred. No. 7.6;  
RESULT 784  
ID ADJ77758 standard; cDNA; 1072 BP.  
DE cDNA encoding wheat Myb-related transcription factor #2.  
PN US2004040057-A1.  
PD 26-FEB-2004.  
PA (CAHO/) CAHOON R E.  
PA (FANG/) FANG Y.  
PA (ODEL/) ODELL J T.  
PA (WENG/) WENG Z.  
Query Match 4.4%; Score 38.4; DB 12; Length 1072;  
Best Local Similarity 57.5%; Pred. No. 7.6;  
RESULT 785  
ID ADF82072 standard; DNA; 1815 BP.  
DE Leukemia-related DNA sequence #2628.  
PN WO2003039443-A2.  
PD 15-MAY-2003.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (UYLO-) UNIV LUDWIG MAXIMILIANS.  
PA (HAFE/) HAFERLACH T.  
PA (SCHO/) SCHOCH C.  
PA (KERN/) KERN W.  
Query Match 4.4%; Score 38.4; DB 10; Length 1815;  
Best Local Similarity 58.9%; Pred. No. 9.6;  
RESULT 786  
ID ADQ24756 standard; DNA; 1954 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7576.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.4%; Score 38.4; DB 12; Length 1954;  
Best Local Similarity 58.9%; Pred. No. 9.9;  
RESULT 787  
ID ACC79092 standard; cDNA; 2490 BP.  
DE Human secreted protein SSCP-67 encoding cDNA SEQ ID NO:147.  
PN WO2003016508-A2.  
PD 27-FEB-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 4.4%; Score 38.4; DB 10; Length 2490;  
Best Local Similarity 49.0%; Pred. No. 11;  
RESULT 788  
ID ABL33597 standard; DNA; 5195 BP.  
DE Human immune system associated gene SEQ ID NO: 1570.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.4%; Score 38.4; DB 6; Length 5195;  
Best Local Similarity 60.6%; Pred. No. 15;  
RESULT 789  
ID ABK28395 standard; DNA; 15743 BP.  
DE DNA transcription associated genomic DNA #135.  
PN WO200192565-A2.  
PD 08-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.4%; Score 38.4; DB 6; Length 15743;  
Best Local Similarity 56.2%; Pred. No. 26;  
RESULT 790  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIRMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.4%; Score 38.4; DB 13; Length 499;  
Best Local Similarity 47.8%; Pred. No. 5.3;  
RESULT 783  
ID ACD07397 standard; cDNA; 1072 BP.  
DE Bread wheat Myb-related transcription factor #2 cDNA.  
PN US2003024007-A1.  
PD 30-JAN-2003.  
PA (CAHO/) CAHOON R E.  
PA (ODEL/) ODELL J T.  
Query Match 4.4%; Score 38.4; DB 8; Length 1072;  
Best Local Similarity 57.5%; Pred. No. 7.6;  
RESULT 784  
ID ADJ77758 standard; cDNA; 1072 BP.  
DE cDNA encoding wheat Myb-related transcription factor #2.  
PN US2004040057-A1.  
PD 26-FEB-2004.  
PA (CAHO/) CAHOON R E.  
PA (FANG/) FANG Y.  
PA (ODEL/) ODELL J T.  
PA (WENG/) WENG Z.  
Query Match 4.4%; Score 38.4; DB 12; Length 1072;  
Best Local Similarity 57.5%; Pred. No. 7.6;  
RESULT 785  
ID ADF82072 standard; DNA; 1815 BP.  
DE Leukemia-related DNA sequence #2628.  
PN WO2003039443-A2.  
PD 15-MAY-2003.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (UYLO-) UNIV LUDWIG MAXIMILIANS.  
PA (HAFE/) HAFERLACH T.  
PA (SCHO/) SCHOCH C.  
PA (KERN/) KERN W.  
Query Match 4.4%; Score 38.4; DB 10; Length 1815;  
Best Local Similarity 58.9%; Pred. No. 9.6;  
RESULT 786  
ID ADQ24756 standard; DNA; 1954 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7576.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.4%; Score 38.4; DB 12; Length 1954;  
Best Local Similarity 58.9%; Pred. No. 9.9;  
RESULT 787  
ID ACC79092 standard; cDNA; 2490 BP.  
DE Human secreted protein SSCP-67 encoding cDNA SEQ ID NO:147.  
PN WO2003016508-A2.  
PD 27-FEB-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 4.4%; Score 38.4; DB 10; Length 2490;  
Best Local Similarity 49.0%; Pred. No. 11;  
RESULT 788  
ID ABL33597 standard; DNA; 5195 BP.  
DE Human immune system associated gene SEQ ID NO: 1570.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.4%; Score 38.4; DB 6; Length 5195;  
Best Local Similarity 60.6%; Pred. No. 15;  
RESULT 789  
ID ABK28395 standard; DNA; 15743 BP.  
DE DNA transcription associated genomic DNA #135.  
PN WO200192565-A2.  
PD 08-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.4%; Score 38.4; DB 6; Length 15743;  
Best Local Similarity 56.2%; Pred. No. 26;  
RESULT 790  
ID AAL34680 standard; cDNA; 277 BP.  
DE Human musculoskeletal system related polynucleotide SEQ ID NO 22.  
PN WO200155367-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.4%; Score 38.2; DB 4; Length 277;  
Best Local Similarity 56.6%; Pred. No. 4.7;  
RESULT 791  
ID ABX57668 standard; cDNA; 277 BP.  
DE cDNA encoding novel human musculoskeletal system antigen #12.  
PN US2002147140-A1.  
PD 10-OCT-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 4.4%; Score 38.2; DB 8; Length 277;  
Best Local Similarity 56.8%; Pred. No. 4.7;  
RESULT 792  
ID ADJ27395 standard; DNA; 277 BP.  
DE Human musculoskeletal system-associated contig DNA - SEQ ID 22.  
PN US2004009488-A1.  
PD 15-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.4%; Score 38.2; DB 12; Length 277;  
Best Local Similarity 56.6%; Pred. No. 4.7;  
RESULT 793  
ID ABV55135 standard; cDNA; 279 BP.  
DE Human prostate expression marker cDNA 55126.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.4%; Score 38.2; DB 5; Length 279;  
Best Local Similarity 55.7%; Pred. No. 4.7;  
RESULT 794  
ID AAV80671 standard; cDNA; 1557 BP.  
DE Partial human DNAX toll-like receptor DTLR7 encoding cDNA.  
PN WO9850547-A2.  
PD 12-NOV-1998.  
PA (SCHE-) SCHERING CORP.  
Query Match 4.4%; Score 38.2; DB 2; Length 1557;  
Best Local Similarity 61.6%; Pred. No. 10;  
RESULT 795  
ID AAD26303 standard; cDNA; 1557 BP.  
DE Human DNAX Toll like receptor (DTLR) 7 cDNA #2, alternative form.  
PN WO200190151-A2.  
PD 29-NOV-2001.  
PA (SCHE-) SCHERING CORP.  
Query Match 4.4%; Score 38.2; DB 6; Length 1557;  
Best Local Similarity 61.6%; Pred. No. 10;  
RESULT 796  
ID RAD26288 standard; cDNA; 1557 BP.  
DE Human DNAX Toll like receptor (DTLR) 7 cDNA #2.  
PN WO200190151-A2.  
PD 29-NOV-2001.  
PA (SCHE-) SCHERING CORP.  
Query Match 4.4%; Score 38.2; DB 6; Length 1557;  
Best Local Similarity 61.6%; Pred. No. 10;  
RESULT 797  
ID AAD02321 standard; cDNA; 1939 BP.  
DE Human serine protease #2, encoding HMGBM65 cDNA clone.  
PN WO200068247-A2.  
PD 16-NOV-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.4%; Score 38.2; DB 3; Length 1939;  
Best Local Similarity 50.6%; Pred. No. 11;  
RESULT 798  
ID ABK90492 standard; cDNA; 1939 BP.  
DE Human serine protease cDNA #1.  
PN US2002119925-A1.  
PD 29-AUG-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.4%; Score 38.2; DB 6; Length 1939;  
Best Local Similarity 50.6%; Pred. No. 11;

RESULT 799  
ID AAD28647 standard; cDNA; 1939 BP.  
DE Human serine protease encoding gene 1 cDNA clone HMG6M5.  
PN WO200198476-A1.  
PD 27-DEC-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.4%; Score 38.2; DB 6; Length 1939;  
Best Local Similarity 50.6%; Pred. No. 11;  
RESULT 800  
ID AAC98572 standard; cDNA; 260 BP.  
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:582.  
PN WO200055351-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.4%; Score 38; DB 3; Length 260;  
Best Local Similarity 60.8%; Pred. No. 5.1;  
RESULT 801  
ID ACN55408 standard; cDNA; 499 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-023-Q6-N6-C10, SEQ:10189.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.4%; Score 38; DB 13; Length 499;  
Best Local Similarity 48.2%; Pred. No. 6.9;  
RESULT 802  
ID AAD02118 standard; cDNA; 1474 BP.  
DE Maize RAD51 orthologue #1 cDNA.  
PN WO200058370-A2.  
PD 16-NOV-2000.  
PA (PTON-) PTONEER HI-BRED INT INC.  
Query Match 4.4%; Score 38; DB 4; Length 1474;  
Best Local Similarity 54.2%; Pred. No. 11;  
RESULT 803  
ID ADQ25148 standard; DNA; 1533 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7968.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.4%; Score 38; DB 12; Length 1533;  
Best Local Similarity 55.2%; Pred. No. 11;  
RESULT 804  
ID ABQ67122 standard; DNA; 5164 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 152.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.4%; Score 38; DB 6; Length 5164;  
Best Local Similarity 59.1%; Pred. No. 20;  
RESULT 805  
ID ABL33642 standard; DNA; 6319 BP.  
DE Human immune system associated gene SEQ ID NO: 1615.  
PN WO20020928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.4%; Score 38; DB 6; Length 6319;  
Best Local Similarity 56.3%; Pred. No. 22;  
RESULT 806  
ID AEA61217 standard; DNA; 294575 BP.  
DE Human STK39 gene genomic sequence SEQ ID NO:127.  
PN US2005130172-A1.  
PD 16-JUN-2005.  
PA (FARB-) BAYER CORP.  
Query Match 4.4%; Score 38; DB 14; Length 294575;  
Best Local Similarity 46.0%; Pred. No. 1.2e+02;  
RESULT 807  
ID ABD33100 standard; DNA; 313287 BP.  
DE Human cancer-associated (CA) gene HD07-008.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.

Query Match 4.4%; Score 38; DB 13; Length 313287;  
Best Local Similarity 46.0%; Pred. No. 1.3e+02;  
RESULT 808  
ID AAL01787 standard; cDNA; 344 BP.  
DE Human reproductive system related antigen cDNA SEQ ID NO: 1788.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.3%; Score 37.8; DB 4; Length 344;  
Best Local Similarity 52.3%; Pred. No. 6.6;  
RESULT 809  
ID ABL97080 standard; cDNA; 344 BP.  
DE Human testicular antigen encoding cDNA SEQ ID NO: 748.  
PN WO200155317-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.3%; Score 37.8; DB 4; Length 344;  
Best Local Similarity 52.3%; Pred. No. 6.6;  
RESULT 810  
ID AAI82206 standard; cDNA; 480 BP.  
DE Human polynucleotide SEQ ID NO 2266.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.3%; Score 37.8; DB 4; Length 480;  
Best Local Similarity 49.7%; Pred. No. 7.7;  
RESULT 811  
ID ABV56463 standard; cDNA; 332 BP.  
DE Human prostate expression marker cDNA 56454.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.3%; Score 37.6; DB 5; Length 332;  
Best Local Similarity 65.5%; Pred. No. 7.4;  
RESULT 812  
ID ACN49835 standard; cDNA; 450 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-031-Q6-N6-E4, SEQ:4616.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.3%; Score 37.6; DB 13; Length 450;  
Best Local Similarity 48.2%; Pred. No. 8.5;  
RESULT 813  
ID ACN48235 standard; cDNA; 560 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-021-Q1-N6-B5, SEQ:3016.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.3%; Score 37.6; DB 13; Length 560;  
Best Local Similarity 48.2%; Pred. No. 9.4;  
RESULT 814  
ID ACN51616 standard; cDNA; 579 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-005-Q1-N6-D1, SEQ:6397.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.3%; Score 37.6; DB 13; Length 579;  
Best Local Similarity 48.2%; Pred. No. 9.5;  
RESULT 815  
ID AEC06158 standard; DNA; 3151 BP.  
DE Mouse Smad1 DNA SEQ ID NO 12.  
PN WO2005077403-A1.  
PD 25-AUG-2005.  
PA (STYC) STRYKER CORP.



Query Match 4.3%; Score 37.6; DB 14; Length 3151;  
 Best Local Similarity 48.2%; Pred. No. 20;  
 RESULT 816  
 ID AAS46329 standard; DNA; 8649 BP.  
 DE Tumour suppressor gene derived chemically modified sequence #51.  
 PN WO200169912-A2.  
 PD 20-SEP-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.3%; Score 37.6; DB 4; Length 8649;  
 Best Local Similarity 68.4%; Pred. No. 32;  
 RESULT 817  
 ID ABK31246 standard; DNA; 8649 BP.  
 DE Signal transduction associated gene modified DNA #45.  
 PN WO200200926-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.3%; Score 37.6; DB 6; Length 8649;  
 Best Local Similarity 68.4%; Pred. No. 32;  
 RESULT 818  
 ID ABL70201 standard; DNA; 8649 BP.  
 DE Chemically treated cell signalling DNA sequence#46.  
 PN WO200202807-A2.  
 PD 10-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.3%; Score 37.6; DB 6; Length 8649;  
 Best Local Similarity 68.4%; Pred. No. 32;  
 RESULT 819  
 ID AAS61159 standard; DNA; 8649 BP.  
 DE Human gene regulation-associated gene oligonucleotide #114.  
 PN WO200177375-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.3%; Score 37.6; DB 6; Length 8649;  
 Best Local Similarity 68.4%; Pred. No. 32;  
 RESULT 820  
 ID AAS58467 standard; cDNA; 16132 BP.  
 DE Mouse peroxisomal acetylpolymine oxidase (mPAO) genomic DNA.  
 PN WO2003068167-A2.  
 PD 21-AUG-2003.  
 PA (REGC ) UNIV CALIFORNIA.  
 Query Match 4.3%; Score 37.6; DB 9; Length 16132;  
 Best Local Similarity 56.5%; Pred. No. 43;  
 RESULT 821  
 ID AAS23328 standard; cDNA; 158 BP.  
 DE Human prostate cancer marker #50.  
 PN WO200153836-A2.  
 PD 26-JUL-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 4.3%; Score 37.4; DB 5; Length 158;  
 Best Local Similarity 57.1%; Pred. No. 6;  
 RESULT 822  
 ID ADE59443 standard; DNA; 305 BP.  
 DE Human gene AAS21144, SEQ ID NO 5338.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 Query Match 4.3%; Score 37.4; DB 10; Length 305;  
 Best Local Similarity 67.1%; Pred. No. 8.1;  
 RESULT 823  
 ID AAI91834 standard; cDNA; 411 BP.  
 DE Human polynucleotide SEQ ID NO 11894.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 4.3%; Score 37.4; DB 4; Length 411;  
 Best Local Similarity 57.1%; Pred. No. 9.2;  
 RESULT 824  
 ID ACH30697 standard; cDNA; 416 BP.  
 DE Human testis cDNA #1083.  
 PN US2003073623-A1.  
 PD 17-APR-2003.  
 PA (DRMA/) DRMANAC R T.

PA (LABA/) LABAT I.  
 PA (STAC/) STACHE-CRAIN B.  
 PA (DICK/) DICKSON M C.  
 PA (JONE/) JONES L W.  
 Query Match 4.3%; Score 37.4; DB 9; Length 416;  
 Best Local Similarity 58.0%; Pred. No. 9.3;  
 RESULT 825  
 ID AAI86835 standard; cDNA; 435 BP.  
 DE Human polynucleotide SEQ ID NO 6895.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 4.3%; Score 37.4; DB 4; Length 435;  
 Best Local Similarity 57.1%; Pred. No. 9.5;  
 RESULT 826  
 ID AAL01335 standard; cDNA; 439 BP.  
 DE Human reproductive system related antigen cDNA SEQ ID NO: 1336.  
 PN WO200155320-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 4.3%; Score 37.4; DB 4; Length 439;  
 Best Local Similarity 48.8%; Pred. No. 9.5;  
 RESULT 827  
 ID ABL96789 standard; cDNA; 439 BP.  
 DE Human testicular antigen encoding cDNA SEQ ID NO: 457.  
 PN WO200155317-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 4.3%; Score 37.4; DB 4; Length 439;  
 Best Local Similarity 48.8%; Pred. No. 9.5;  
 RESULT 828  
 ID AAS34169 standard; cDNA; 1035 BP.  
 DE Human cDNA encoding a novel foetal antigen, SEQ ID No 693.  
 PN WO200155312-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 4.3%; Score 37.4; DB 5; Length 1035;  
 Best Local Similarity 67.1%; Pred. No. 14;  
 RESULT 829  
 ID ABZ68674 standard; cDNA; 2398 BP.  
 DE Nucleotide sequence of a membrane steroid receptor.  
 PN WO2002101016-A2.  
 PD 19-DEC-2002.  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 Query Match 4.3%; Score 37.4; DB 8; Length 2398;  
 Best Local Similarity 57.1%; Pred. No. 21;  
 RESULT 830  
 ID ADP25184 standard; cDNA; 2398 BP.  
 DE PRO polypeptide encoding cDNA SEQ ID NO:2362.  
 PN WO2004041170-A2.  
 PD 21-MAY-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.3%; Score 37.4; DB 13; Length 2398;  
 Best Local Similarity 57.1%; Pred. No. 21;  
 RESULT 831  
 ID AEB48498 standard; DNA; 2398 BP.  
 DE DNA encoding human steroid progesterin receptor gamma (mSR-gamma).  
 PN WO2005068999-A1.  
 PD 28-JUL-2005.  
 PA (FARB ) BAYER HEALTHCARE AG.  
 Query Match 4.3%; Score 37.4; DB 14; Length 2398;  
 Best Local Similarity 57.1%; Pred. No. 21;  
 RESULT 832  
 ID ABN80324 standard; DNA; 8047 BP.  
 DE Human chemically modified disease associated gene SEQ ID NO 341.  
 PN WO200200927-A2.  
 PD 03-JAN-2002.  
 PA (EPIC-) EPIGENOMICS AG.  
 Query Match 4.3%; Score 37.4; DB 6; Length 8047;  
 Best Local Similarity 50.7%; Pred. No. 36;  
 RESULT 833  
 ID ABK33999 standard; DNA; 8111 BP.  
 DE Human DNA for staging of Astrocytomas #43.

PN WO200202808-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.3%; Score 37.4; DB 6; Length 8111;  
Best Local Similarity 67.1%; Pred. No. 36;  
RESULT 834  
ID ADA20390 standard; DNA; 8111 BP.  
DE Prostate tumour related genomic DNA sample #28.  
PN WO2002103042-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.3%; Score 37.4; DB 8; Length 8111;  
Best Local Similarity 67.1%; Pred. No. 36;  
RESULT 835  
ID ADA84197 standard; DNA; 8111 BP.  
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:55.  
PN WO2002103041-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.3%; Score 37.4; DB 8; Length 8111;  
Best Local Similarity 67.1%; Pred. No. 36;  
RESULT 836  
ID ABL33257 standard; DNA; 14950 BP.  
DE Human immune system associated gene SEQ ID NO: 1230.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.3%; Score 37.4; DB 6; Length 14950;  
Best Local Similarity 55.9%; Pred. No. 47;  
RESULT 837  
ID ABL18650 standard; DNA; 80226 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 7423.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NV.  
Query Match 4.3%; Score 37.4; DB 4; Length 80226;  
Best Local Similarity 53.0%; Pred. No. 1e+02;  
RESULT 838  
ID ABD33102 standard; DNA; 111836 BP.  
DE Murine cancer-associated (CA) gene MD07-009.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 4.3%; Score 37.4; DB 13; Length 111836;  
Best Local Similarity 57.1%; Pred. No. 1.2e+02;  
RESULT 839  
ID ABX48652 standard; cDNA; 426 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #13817.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 4.3%; Score 37.2; DB 8; Length 426;  
Best Local Similarity 54.3%; Pred. No. 11;  
RESULT 840  
ID ACN56344 standard; cDNA; 565 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-034-Q6-N6-B10, SEQ:11125.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.3%; Score 37.2; DB 13; Length 565;  
Best Local Similarity 48.2%; Pred. No. 12;  
RESULT 841  
ID AAS26890 standard; cDNA; 2549 BP.  
DE Human cDNA encoding a novel secreted protein, SEQ ID 82.  
PN WO200155441-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 4.3%; Score 37.2; DB 4; Length 2549;  
Best Local Similarity 57.9%; Pred. No. 24;  
RESULT 842  
ID ADR41347 standard; cDNA; 2644 BP.  
DE Human CD-like molecule HDTEJ03 cDNA, SEQ ID NO:146.  
PN WO200226930-A2.  
PD 04-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.3%; Score 37.2; DB 7; Length 2644;  
Best Local Similarity 57.9%; Pred. No. 24;  
RESULT 843  
ID ABO54403 standard; cDNA; 2911 BP.  
DE Human ovarian antigen HAOE30 cDNA, SEQ ID NO:283.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.3%; Score 37.2; DB 6; Length 2911;  
Best Local Similarity 51.9%; Pred. No. 25;  
RESULT 844  
ID ABL33356 standard; DNA; 6577 BP.  
DE Human immune system associated gene SEQ ID NO: 1329.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.3%; Score 37.2; DB 6; Length 6577;  
Best Local Similarity 56.6%; Pred. No. 37;  
RESULT 845  
ID ABL70561 standard; DNA; 6577 BP.  
DE Chemically treated cell signalling DNA sequence#226.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.3%; Score 37.2; DB 6; Length 6577;  
Best Local Similarity 56.6%; Pred. No. 37;  
RESULT 846  
ID AAS61221 standard; DNA; 6577 BP.  
DE Human gene regulation-associated gene oligonucleotide #176.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.3%; Score 37.2; DB 6; Length 6577;  
Best Local Similarity 56.6%; Pred. No. 37;  
RESULT 847  
ID ADS17402 standard; DNA; 78064 BP.  
DE Nucleotide sequence of zebrafish MAP2K6.  
PN WO2004078713-A2.  
PD 16-SEP-2004.  
PA (EXEL-) EXELIXIS INC.  
Query Match 4.3%; Score 37.2; DB 13; Length 78064;  
Best Local Similarity 65.9%; Pred. No. 1.1e+02;  
RESULT 848  
ID ADD69391 standard; DNA; 240823 BP.  
DE Human PG-3 DNA - SEQ ID 127.  
PN WO2003048185-A2.  
PD 12-JUN-2003.  
PA (GENV-) GENVEC INC.  
Query Match 4.3%; Score 37.2; DB 10; Length 240823;  
Best Local Similarity 44.9%; Pred. No. 1.9e+02;  
RESULT 849  
ID AAF24497 standard; cDNA; 240825 BP.  
DE Human PG-3 gene.  
Query Match 4.3%; Score 37.2; DB 4; Length 240825;  
Best Local Similarity 44.9%; Pred. No. 1.9e+02;  
RESULT 850  
ID ABO81802 standard; DNA; 240825 BP.  
DE Human PG-3 gene SEQ ID NO:1.  
Query Match 4.3%; Score 37.2; DB 6; Length 240825;  
Best Local Similarity 44.9%; Pred. No. 1.9e+02;  
RESULT 851  
ID ADJ76070 standard; DNA; 127 BP.  
DE Marker gene SEQ ID NO:1322.  
PN EPI394274-A2.  
PD 03-MAR-2004.

PA (GENO-) GENOX RES INC.  
Query Match 4.3%; Score 37; DB 12; Length 127;  
Best Local Similarity 62.4%; Pred. No. 7;  
RESULT 852  
ID ADL11530 standard; cDNA; 291 BP.  
DE Cat flea hindgut and malpighian tubule (HMT) protein cDNA #1935.  
PN US2004067516-A1.  
PD 08-APR-2004.  
PA (BRAN/) BRANDT K S.  
PA (GAIN/) GAINES P J.  
PA (STIN/) STINCHCOMB D T.  
PA (WISN/) WISNEWSKI N.  
Query Match 4.3%; Score 37; DB 12; Length 291;  
Best Local Similarity 60.4%; Pred. No. 10;  
RESULT 853  
ID ACH49203 standard; cDNA; 409 BP.  
DE Human leukocyte cDNA #797.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 4.3%; Score 37; DB 9; Length 409;  
Best Local Similarity 53.1%; Pred. No. 12;  
RESULT 854  
ID AAI98819 standard; cDNA; 444 BP.  
DE Human excretory related polynucleotide SEQ ID NO 263.  
PN WO200155313-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.3%; Score 37; DB 4; Length 444;  
Best Local Similarity 63.2%; Pred. No. 12;  
RESULT 855  
ID AAI63215 standard; cDNA; 444 BP.  
DE Human kidney related polynucleotide SEQ ID NO 255.  
PN WO200155323-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.3%; Score 37; DB 5; Length 444;  
Best Local Similarity 63.2%; Pred. No. 12;  
RESULT 856  
ID ACN62215 standard; cDNA; 516 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-026-Q6-N6-F3, SEQ:16996.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.3%; Score 37; DB 13; Length 516;  
Best Local Similarity 48.8%; Pred. No. 13;  
RESULT 857  
ID ABL32171 standard; DNA; 3973 BP.  
DE Human immune system associated gene SEQ ID NO: 144.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.3%; Score 37; DB 6; Length 3973;  
Best Local Similarity 62.4%; Pred. No. 33;  
RESULT 858  
ID ABL34205 standard; DNA; 5397 BP.  
DE Human immune system associated gene SEQ ID NO: 2178.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.3%; Score 37; DB 6; Length 5397;  
Best Local Similarity 67.5%; Pred. No. 38;  
RESULT 859  
ID ABK40041 standard; DNA; 6136 BP.  
DE Human chemically pretreated gene sequence #62 strand 1.  
PN WO200202806-A2.

PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.3%; Score 37; DB 6; Length 6136;  
Best Local Similarity 57.3%; Pred. No. 41;  
RESULT 860  
ID ABL33649 standard; DNA; 8234 BP.  
DE Human immune system associated gene SEQ ID NO: 1622.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.3%; Score 37; DB 6; Length 8234;  
Best Local Similarity 62.4%; Pred. No. 46;  
RESULT 861  
ID ABL34042 standard; DNA; 10039 BP.  
DE Human immune system associated gene SEQ ID NO: 2015.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.3%; Score 37; DB 6; Length 10039;  
Best Local Similarity 57.3%; Pred. No. 51;  
RESULT 862  
ID ABV47775 standard; cDNA; 282 BP.  
DE Human prostate expression marker cDNA 47766.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.2%; Score 36.8; DB 5; Length 282;  
Best Local Similarity 63.6%; Pred. No. 11;  
RESULT 863  
ID ABV59054 standard; cDNA; 360 BP.  
DE Human prostate expression marker cDNA 59045.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.2%; Score 36.8; DB 5; Length 360;  
Best Local Similarity 51.9%; Pred. No. 13;  
RESULT 864  
ID ABV07958 standard; cDNA; 370 BP.  
DE Human prostate expression marker cDNA 7949.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.2%; Score 36.8; DB 5; Length 370;  
Best Local Similarity 54.0%; Pred. No. 13;  
RESULT 865  
ID ADQ20928 standard; DNA; 391 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3748.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.2%; Score 36.8; DB 12; Length 391;  
Best Local Similarity 66.2%; Pred. No. 13;  
RESULT 866  
ID ADL43518 standard; DNA; 445 BP.  
DE Human ovarian cancer DNA marker #17408.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.2%; Score 36.8; DB 5; Length 445;  
Best Local Similarity 58.0%; Pred. No. 14;  
RESULT 867  
ID ACN58685 standard; cDNA; 483 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-011-Q6-K6-C8, SEQ:13466.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.2%; Score 36.8; DB 13; Length 483;  
Best Local Similarity 47.4%; Pred. No. 15;  
RESULT 868  
ID ABQ25138 standard; DNA; 631 BP.

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 11729.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.2%; Score 36.8; DB 6; Length 631;  
Best Local Similarity 66.2%; Pred. No. 16;  
RESULT 869  
ID ABQ25139 standard; DNA; 631 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 11730.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.2%; Score 36.8; DB 6; Length 631;  
Best Local Similarity 66.2%; Pred. No. 16;  
RESULT 870  
ID AAD57083 standard; DNA; 1290 BP.  
DE Human aldo-keto reductase IC, AKRIC2 DNA #1.  
PN WO2003051182-A2.  
PD 26-JUN-2003.  
PA (META-) METABOLEX INC.  
Query Match 4.2%; Score 36.8; DB 9; Length 1290;  
Best Local Similarity 58.0%; Pred. No. 23;  
RESULT 871  
ID ADP24450 standard; cDNA; 1290 BP.  
DE PRO polypeptide encoding cDNA SEQ ID NO:1628.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 4.2%; Score 36.8; DB 13; Length 1290;  
Best Local Similarity 58.0%; Pred. No. 23;  
RESULT 872  
ID ADU05984 standard; DNA; 1290 BP.  
DE Novel bronchial cancer-associated human gene SeqID206.  
PN DE10316701-A1.  
PD 04-NOV-2004.  
PA (HINZ/) HINZMANN B.  
PA (HERN/) HERMANN K.  
PA (CAST/) HEIDEN CASTANOS-VELEZ E.  
Query Match 4.2%; Score 36.8; DB 13; Length 1290;  
Best Local Similarity 58.0%; Pred. No. 23;  
RESULT 873  
ID ABA93750 standard; cDNA; 1316 BP.  
DE Human cell structure and motility cDNA clone tes3\_16b5.  
PN WO200198454-A2.  
PD 27-DEC-2001.  
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
Query Match 4.2%; Score 36.8; DB 6; Length 1316;  
Best Local Similarity 55.5%; Pred. No. 23;  
RESULT 874  
ID AAV07665 standard; cDNA; 1508 BP.  
DE Maize Bx1 cDNA (DIMBOA biosynthetic gene).  
PN WO9840505-A1.  
PD 17-SEP-1998.  
PA (DEKA-) DEKALB GENETICS CORP.  
Query Match 4.2%; Score 36.8; DB 2; Length 1508;  
Best Local Similarity 58.0%; Pred. No. 24;  
RESULT 875  
ID AAF29898 standard; DNA; 1697 BP.  
DE Human h15590 DNA.  
PN WO200100879-A1.  
PD 04-JAN-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 4.2%; Score 36.8; DB 5; Length 1697;  
Best Local Similarity 61.5%; Pred. No. 26;  
RESULT 876  
ID ADJ77843 standard; cDNA; 1725 BP.  
DE Corn lipase cDNA #3.  
PN US6673988-B1.  
PD 06-JAN-2004.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 4.2%; Score 36.8; DB 12; Length 1725;  
Best Local Similarity 53.5%; Pred. No. 26;  
RESULT 877

ID AAT79634 standard; DNA; 1898 BP.  
DE DNA encoding human ubiquitous nuclear receptor polypeptide.  
PN US5639616-A.  
PD 17-JUN-1997.  
PA (ARCH-) ARCH DEV CORP.  
Query Match 4.2%; Score 36.8; DB 2; Length 1898;  
Best Local Similarity 63.6%; Pred. No. 27;  
RESULT 878  
ID AAC76167 standard; cDNA; 2070 BP.  
DE Human ORFX ORF1722 polynucleotide sequence SEQ ID NO:3443.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.2%; Score 36.8; DB 3; Length 2070;  
Best Local Similarity 53.5%; Pred. No. 28;  
RESULT 879  
ID ADR99088 standard; DNA; 2100 BP.  
DE Tudor repeat associator with PCTAIRE 2, PCTAIRE2BP, DNA SEQ ID 94.  
PN WO2004078035-A2.  
PD 16-SEP-2004.  
PA (FARB) BAYER PHARM CORP.  
Query Match 4.2%; Score 36.8; DB 13; Length 2100;  
Best Local Similarity 53.5%; Pred. No. 28;  
RESULT 880  
ID ACN92771 standard; DNA; 2111 BP.  
DE Breast cancer related marker, seq id 13921.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 4.2%; Score 36.8; DB 11; Length 2111;  
Best Local Similarity 61.5%; Pred. No. 28;  
RESULT 881  
ID AEF55813 standard; DNA; 2182 BP.  
DE Human genomic DNA #420.  
PN WO2006008128-A2.  
PD 26-JAN-2006.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.2%; Score 36.8; DB 15; Length 2182;  
Best Local Similarity 59.6%; Pred. No. 29;  
RESULT 882  
ID ABL33871 standard; DNA; 5511 BP.  
DE Human immune system associated gene SEQ ID NO: 1844.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.2%; Score 36.8; DB 6; Length 5511;  
Best Local Similarity 53.5%; Pred. No. 44;  
RESULT 883  
ID ABL70480 standard; DNA; 9742 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#185.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.2%; Score 36.8; DB 6; Length 9742;  
Best Local Similarity 53.5%; Pred. No. 57;  
RESULT 884  
ID AAS46478 standard; DNA; 14112 BP.  
DE Tumour suppressor gene derived chemically modified sequence #200.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.2%; Score 36.8; DB 4; Length 14112;  
Best Local Similarity 63.6%; Pred. No. 67;  
RESULT 885  
ID ABL33443 standard; DNA; 14112 BP.  
DE Human immune system associated gene SEQ ID NO: 1416.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.2%; Score 36.8; DB 6; Length 14112;  
Best Local Similarity 63.6%; Pred. No. 67;  
RESULT 886  
ID ABK31333 standard; DNA; 14112 BP.

DE Signal transduction associated gene modified complementary DNA #88.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.2%; Score 36.8; DB 6; Length 14112;  
Best Local Similarity 63.8%; Pred. No. 67;  
RESULT 887  
ID ABO66980 standard; DNA; 14112 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 10.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.2%; Score 36.8; DB 6; Length 14112;  
Best Local Similarity 63.6%; Pred. No. 67;  
RESULT 888  
ID ADQ97025 standard; DNA; 57889 BP.  
DE Mouse cancer associated sequence MD10-002, SEQ ID 1.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 4.2%; Score 36.8; DB 12; Length 57889;  
Best Local Similarity 69.4%; Pred. No. 1.3e+02;  
RESULT 889  
ID ADQ97557 standard; DNA; 254396 BP.  
DE Human cancer associated sequence HD09-013, SEQ ID 534.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 4.2%; Score 36.8; DB 12; Length 254396;  
Best Local Similarity 55.5%; Pred. No. 2.5e+02;  
RESULT 890  
ID ABV48821 standard; cDNA; 265 BP.  
DE Human prostate expression marker cDNA 48812.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.2%; Score 36.6; DB 5; Length 265;  
Best Local Similarity 63.5%; Pred. No. 13;  
RESULT 891  
ID AAH70126 standard; cDNA; 545 BP.  
DE Human cervical cancer marker nucleic acid 1400.  
PN WO200142467-A2.  
PD 14-JUN-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.2%; Score 36.6; DB 4; Length 545;  
Best Local Similarity 42.7%; Pred. No. 17;  
RESULT 892  
ID ADT17571 standard; cDNA; 1054 BP.  
DE Plant cDNA, Seq ID 2897.  
PN US2004216190-A1.  
PD 28-OCT-2004.  
PA (KOVA/) KOVALIC D K.  
Query Match 4.2%; Score 36.6; DB 13; Length 1054;  
Best Local Similarity 62.6%; Pred. No. 24;  
RESULT 893  
ID AAV28734 standard; cDNA; 1102 BP.  
DE Murine smooth muscle cell specific SM22 alpha gene cDNA.  
PN WO9815575-A1.  
PD 16-APR-1998.  
PA (ARCH-) ARCH DEV CORP.  
Query Match 4.2%; Score 36.6; DB 2; Length 1102;  
Best Local Similarity 71.6%; Pred. No. 24;  
RESULT 894  
ID AAH26695 standard; cDNA; 1102 BP.  
DE Mouse smooth muscle 22 alpha (SM22-alpha) cDNA.  
PN US6284743-B1.  
PD 04-SEP-2001.  
PA (ARCH-) ARCH DEV CORP.  
Query Match 4.2%; Score 36.6; DB 4; Length 1102;  
Best Local Similarity 71.8%; Pred. No. 24;  
RESULT 895  
ID AAD20564 standard; cDNA; 1102 BP.  
DE Murine SM22alpha cDNA.

PN US6291211-B1.  
PD 18-SEP-2001.  
PA (ARCH-) ARCH DEV CORP.  
Query Match 4.2%; Score 36.6; DB 4; Length 1102;  
Best Local Similarity 71.6%; Pred. No. 24;  
RESULT 896  
ID AAD21105 standard; cDNA; 1102 BP.  
DE Murine SM22 alpha cDNA.  
PN US6297221-B1.  
PD 02-OCT-2001.  
PA (ARCH-) ARCH DEV CORP.  
Query Match 4.2%; Score 36.6; DB 4; Length 1102;  
Best Local Similarity 71.6%; Pred. No. 24;  
RESULT 897  
ID ABK33330 standard; cDNA; 1102 BP.  
DE Mouse cDNA encoding SM22alpha.  
PN US6331527-B1.  
PD 18-DEC-2001.  
PA (ARCH-) ARCH DEV CORP.  
Query Match 4.2%; Score 36.6; DB 6; Length 1102;  
Best Local Similarity 71.6%; Pred. No. 24;  
RESULT 898  
ID ADN04573 standard; cDNA; 1342 BP.  
DE Antipsooriatic cDNA sequence #492.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 4.2%; Score 36.6; DB 12; Length 1342;  
Best Local Similarity 68.0%; Pred. No. 26;  
RESULT 899  
ID ADU06264 standard; DNA; 1342 BP.  
DE Novel bronchial cancer-associated human gene SeqID488.  
PN DE10316701-A1.  
PD 04-NOV-2004.  
PA (HINZ/) HINZMANN B.  
PA (HERM/) HERMANN K.  
PA (CAST/) HEIDEN CASTANOS-VELEZ E.  
Query Match 4.2%; Score 36.6; DB 13; Length 1342;  
Best Local Similarity 68.0%; Pred. No. 26;  
RESULT 900  
ID ABE83780 standard; cDNA; 3623 BP.  
DE Human cDNA differentially expressed in asthma, SEQ ID NO:188.  
PN WO2005118403-A2.  
PD 15-DEC-2005.  
PA (LINK-) LINKAGENE LTD.  
Query Match 4.2%; Score 36.6; DB 15; Length 3623;  
Best Local Similarity 56.1%; Pred. No. 41;  
RESULT 901  
ID ABL33169 standard; DNA; 7781 BP.  
DE Human immune system associated gene SEQ ID NO: 1142.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.2%; Score 36.6; DB 6; Length 7781;  
Best Local Similarity 62.6%; Pred. No. 58;  
RESULT 902  
ID ABL32887 standard; DNA; 16439 BP.  
DE Human immune system associated gene SEQ ID NO: 860.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.2%; Score 36.6; DB 6; Length 16439;  
Best Local Similarity 68.0%; Pred. No. 82;  
RESULT 903  
ID AAF22297 standard; DNA; 96583 BP.  
DE BAC containing repeats from centromeres 1-4 #20.  
PN WO200055325-A2.  
PD 21-SEP-2000.  
PA (UYCH-) UNIV CHICAGO.  
Query Match 4.2%; Score 36.6; DB 3; Length 96583;  
Best Local Similarity 54.0%; Pred. No. 1.8e+02;  
RESULT 904  
ID AAL08212 standard; cDNA; 220 BP.

DE Human breast cancer expressed polynucleotide 669.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.2%; Score 36.4; DB 4; Length 220;  
Best Local Similarity 58.2%; Pred. No. 13;  
RESULT 905  
ID AAL25957 standard; cDNA; 313 BP.  
DE Human breast cancer expressed polynucleotide 18414.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.2%; Score 36.4; DB 4; Length 313;  
Best Local Similarity 58.2%; Pred. No. 15;  
RESULT 906  
ID AAI82408 standard; cDNA; 391 BP.  
DE Human polynucleotide SEQ ID NO 2468.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.2%; Score 36.4; DB 4; Length 391;  
Best Local Similarity 61.7%; Pred. No. 17;  
RESULT 907  
ID ADI69469 standard; DNA; 424 BP.  
DE Human ovarian cancer DNA marker #2211.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.2%; Score 36.4; DB 5; Length 424;  
Best Local Similarity 47.3%; Pred. No. 18;  
RESULT 908  
ID ADI75809 standard; DNA; 424 BP.  
DE Human ovarian cancer DNA marker #8551.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.2%; Score 36.4; DB 5; Length 424;  
Best Local Similarity 47.3%; Pred. No. 18;  
RESULT 909  
ID AAL19122 standard; cDNA; 472 BP.  
DE Human breast cancer expressed polynucleotide 11579.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.2%; Score 36.4; DB 4; Length 472;  
Best Local Similarity 58.2%; Pred. No. 19;  
RESULT 910  
ID AAC79470 standard; cDNA; 578 BP.  
DE cDNA sequence of human breast tumour clone B511S.  
PN WO200061756-A2.  
PD 19-OCT-2000.  
PA (CORI-) CORIXA CORP.  
Query Match 4.2%; Score 36.4; DB 3; Length 578;  
Best Local Similarity 49.0%; Pred. No. 20;  
RESULT 911  
ID AAI67224 standard; cDNA; 578 BP.  
DE B511S cDNA sequence.  
PN WO200175171-A2.  
PD 11-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 4.2%; Score 36.4; DB 4; Length 578;  
Best Local Similarity 49.0%; Pred. No. 20;  
RESULT 912  
ID ABK29014 standard; cDNA; 578 BP.  
DE Human breast tumour polypeptide full length cDNA clone #1.  
PN WO200198339-A2.  
PD 27-DEC-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 4.2%; Score 36.4; DB 6; Length 578;  
Best Local Similarity 49.0%; Pred. No. 20;  
RESULT 913  
ID ADT94972 standard; cDNA; 624 BP.  
DE Colon cancer associated human cDNA sequence #491.  
PN US2003087818-A1.  
PD 08-MAY-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 4.2%; Score 36.4; DB 11; Length 624;  
Best Local Similarity 57.1%; Pred. No. 21;  
RESULT 914  
ID ADX41454 standard; cDNA; 624 BP.  
DE Human cDNA encoding colon cancer protein SEQ ID NO 491.  
PN WO200274156-A2.  
PD 26-SEP-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.2%; Score 36.4; DB 11; Length 624;  
Best Local Similarity 57.1%; Pred. No. 21;  
RESULT 915  
ID ACN87147 standard; DNA; 627 BP.  
DE Breast cancer related marker, seq id 8297.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 4.2%; Score 36.4; DB 11; Length 627;  
Best Local Similarity 58.2%; Pred. No. 21;  
RESULT 916  
ID AAF72823 standard; DNA; 826 BP.  
DE Secreted protein gene #25.  
PN WO200107459-A1.  
PD 01-FEB-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.2%; Score 36.4; DB 4; Length 826;  
Best Local Similarity 49.5%; Pred. No. 24;  
RESULT 917  
ID ABL90008 standard; cDNA; 1350 BP.  
DE Human polynucleotide SEQ ID NO 570.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.2%; Score 36.4; DB 6; Length 1350;  
Best Local Similarity 49.5%; Pred. No. 30;  
RESULT 918  
ID ADD47667 standard; DNA; 1450 BP.  
DE Human gene BC004560, SEQ ID NO 13363.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match 4.2%; Score 36.4; DB 10; Length 1450;  
Best Local Similarity 50.0%; Pred. No. 31;  
RESULT 919  
ID AEA26104 standard; DNA; 1640 BP.  
DE Human renal cell carcinoma-related LSAMP gene SeqID124.  
PN WO2005047519-A2.  
PD 26-MAY-2005.  
PA (VAND-) VAN ANDEL RES INST.  
Query Match 4.2%; Score 36.4; DB 14; Length 1640;  
Best Local Similarity 59.8%; Pred. No. 33;  
RESULT 920  
ID ACN92828 standard; DNA; 2304 BP.  
DE Breast cancer related marker, seq id 13978.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 4.2%; Score 36.4; DB 11; Length 2304;  
Best Local Similarity 54.5%; Pred. No. 38;  
RESULT 921  
ID ACA92424 standard; DNA; 2463 BP.  
DE DNA encoding human PMMW-9.  
PN WO2003031939-A2.  
PD 17-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 4.2%; Score 36.4; DB 10; Length 2463;  
Best Local Similarity 52.7%; Pred. No. 39;  
RESULT 922  
ID ADR73483 standard; DNA; 2479 BP.  
DE Human Lutheran blood group, LU, gene.

PN WO2004076682-A2.  
PD 10-SEP-2004.  
PA (SURR-) SURROMED INC. 4.2%; Score 36.4; DB 13; Length 2479;  
Query Match 50.8%; Pred. No. 39;  
Best Local Similarity  
RESULT 923  
ID ADV97196 standard; cDNA; 2479 BP.  
DE Human Lutheran blood group glycoprotein (LU) cDNA, SEQ:51.  
PN US2005003390-A1.  
PD 06-JAN-2005.  
PA (AXEN/) AXENOVICH S A.  
PA (STUL/) STULL R.  
PA (GELM/) GELMAN M.  
PA (CHUI/) CHUI K.  
PA (NGDD/) NG D.  
Query Match 4.2%; Score 36.4; DB 14; Length 2479;  
Best Local Similarity 50.8%; Pred. No. 39;  
RESULT 924  
ID ADZ26456 standard; cDNA; 2479 BP.  
DE Human Lutheran blood group antigen cDNA.  
PN WO2005030999-A1.  
PD 07-APR-2005.  
PA (DAND) DANA FARBER CANCER INST INC.  
Query Match 4.2%; Score 36.4; DB 14; Length 2479;  
Best Local Similarity 50.6%; Pred. No. 39;  
RESULT 925  
ID AEE60841 standard; DNA; 2479 BP.  
DE Human pathological responsiveness gene SEQ ID NO:50.  
PN US2005266420-A1.  
PD 01-DEC-2005.  
PA (TEXA) UNIV TEXAS SYSTEM.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 4.2%; Score 36.4; DB 15; Length 2479;  
Best Local Similarity 50.6%; Pred. No. 39;  
RESULT 926  
ID AAS46320 standard; DNA; 2865 BP.  
DE Tumour suppressor gene derived chemically modified sequence #42.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.2%; Score 36.4; DB 4; Length 2865;  
Best Local Similarity 59.8%; Pred. No. 42;  
RESULT 927  
ID ABN80051 standard; DNA; 2865 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 68.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.2%; Score 36.4; DB 6; Length 2865;  
Best Local Similarity 59.8%; Pred. No. 42;  
RESULT 928  
ID ABN80022 standard; DNA; 6636 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 39.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.2%; Score 36.4; DB 6; Length 6636;  
Best Local Similarity 55.6%; Pred. No. 61;  
RESULT 929  
ID ABL33568 standard; DNA; 8305 BP.  
DE Human immune system associated gene SEQ ID NO: 1541.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.2%; Score 36.4; DB 6; Length 8305;  
Best Local Similarity 55.6%; Pred. No. 68;  
RESULT 930  
ID ADQ22695 standard; DNA; 12010 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5515.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.2%; Score 36.4; DB 12; Length 12010;

Best Local Similarity 61.7%; Pred. No. 80;  
RESULT 931  
ID ADO22739 standard; DNA; 12010 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5559.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.2%; Score 36.4; DB 12; Length 12010;  
Best Local Similarity 61.7%; Pred. No. 80;  
RESULT 932  
ID ADQ97056 standard; DNA; 169865 BP.  
DE Human cancer associated sequence HD11-007, SEQ ID 32.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 4.2%; Score 36.4; DB 12; Length 169865;  
Best Local Similarity 49.5%; Pred. No. 2.7e+02;  
RESULT 933  
ID AAS63092 standard; cDNA; 139 BP.  
DE Cell death protective sequence CNI-00728, ORF #24.  
PN WO200176532-A2.  
PD 18-OCT-2001.  
PA (COGE-) COSENT NEUROSCIENCE INC.  
Query Match 4.2%; Score 36.2; DB 6; Length 139;  
Best Local Similarity 65.4%; Pred. No. 12;  
RESULT 934  
ID ABV60296 standard; cDNA; 238 BP.  
DE Human prostate expression marker cDNA 60287.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENIUM PREDICTIVE MEDICINE INC.  
Query Match 4.2%; Score 36.2; DB 5; Length 238;  
Best Local Similarity 68.5%; Pred. No. 15;  
RESULT 935  
ID ACN59994 standard; cDNA; 282 BP.  
DE Cotton gynoecium tissue EST Clone ID: L1B3829-036-Q1-N6-D2, SEQ:14775.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.2%; Score 36.2; DB 13; Length 282;  
Best Local Similarity 47.9%; Pred. No. 17;  
RESULT 936  
ID ACN33051 standard; cDNA; 328 BP.  
DE Cotton androecium tissue EST Clone ID: L1B3828-021-Q1-N6-C4, SEQ:7832.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.2%; Score 36.2; DB 13; Length 328;  
Best Local Similarity 47.9%; Pred. No. 18;  
RESULT 937  
ID ABX40394 standard; cDNA; 358 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #5559.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 4.2%; Score 36.2; DB 8; Length 358;  
Best Local Similarity 59.0%; Pred. No. 19;  
RESULT 938  
ID AAI30868 standard; cDNA; 369 BP.  
DE Human polynucleotide SEQ ID NO 10928.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.2%; Score 36.2; DB 4; Length 369;

Best Local Similarity 65.4%; Pred. No. 19;  
RESULT 939  
ID ADQ04292 standard; DNA; 439 BP.  
DE Maize transcription factor seqid 1138.  
PN US2004123339-A1.  
PD 24-JUN-2004.  
PA (CONN//) CONNER T W.  
PA (HECK//) HECK G R.  
PA (LIUJ//) LIU J.  
Query Match  
Best Local Similarity 4.2%; Score 36.2; DB 12; Length 439;  
RESULT 940  
ID ADZ61999 standard; DNA; 673 BP.  
DE Murine Tscap91a gene, SEQ ID 1723.  
PN US2005084872-A1.  
PD 21-APR-2005.  
PA (LUMP//) LUM P Y.  
PA (TANY//) TAN Y.  
PA (DAIH//) DAI H.  
PA (MUIS//) MUISE E S.  
PA (BERG//) BERGER J P.  
PA (THOM//) THOMPSON J R.  
Query Match  
Best Local Similarity 4.2%; Score 36.2; DB 14; Length 673;  
RESULT 941  
ID AAC59830 standard; DNA; 1176 BP.  
DE Human secreted protein encoding DNA clone vq9 1.  
PN WO20005375-A1.  
PD 21-SEP-2000.  
PA (ALPH-) ALPHAGENE INC.  
Query Match  
Best Local Similarity 4.2%; Score 36.2; DB 3; Length 1176;  
RESULT 942  
ID AAG63068 standard; cDNA; 1466 BP.  
DE Cell death protective sequence CNI-00728.  
PN WO200176532-A2.  
PD 18-OCT-2001.  
PA (COGE-) COGENT NEUROSCIENCE INC.  
Query Match  
Best Local Similarity 4.2%; Score 36.2; DB 6; Length 1466;  
RESULT 943  
ID ADP04700 standard; cDNA; 2275 BP.  
DE Sea squirt cDNA with tissue specific expression in development Seq 295.  
PN JP2004057129-A.  
PD 26-FEB-2004.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Query Match  
Best Local Similarity 52.2%; Pred. No. 43;  
RESULT 944  
ID ADG75808 standard; DNA; 2534 BP.  
DE Human protein modification and maintenance molecule DNA SeqID132.  
PN WO2003083084-A2.  
PD 09-OCT-2003.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 4.2%; Score 36.2; DB 10; Length 2534;  
RESULT 945  
ID ADZ49479 standard; DNA; 2867 BP.  
DE Insulin signaling pathway related gene, SEQ ID 808.  
PN US2005085436-A1.  
PD 21-APR-2005.  
PA (LIHH//) LI H.  
PA (MAJJ//) MA J.  
Query Match  
Best Local Similarity 4.2%; Score 36.2; DB 14; Length 2867;  
RESULT 946  
ID ABB69145 standard; DNA; 2867 BP.  
DE Human modulator of IGF1R pathway polynucleotide #22.  
PN WO2005073723-A1.  
PD 11-AUG-2005.  
PA (EXEL-) EXELIXIS INC.  
PA (NICO//) NICOLL M.  
Query Match  
Best Local Similarity 4.2%; Score 36.2; DB 14; Length 2867;  
Best Local Similarity 59.0%; Pred. No. 48;  
RESULT 947  
ID AAF15852 standard; cDNA; 2873 BP.  
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:287.  
PN WO200055174-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE//) ROSEN C A.  
Query Match  
Best Local Similarity 4.2%; Score 36.2; DB 3; Length 2873;  
RESULT 948  
ID ABO67152 standard; DNA; 5867 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 182.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.2%; Score 36.2; DB 6; Length 5867;  
RESULT 949  
ID ABR39967 standard; DNA; 8943 BP.  
DE Human chemically pretreated gene sequence #24 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.2%; Score 36.2; DB 6; Length 8943;  
RESULT 950  
ID ABL33501 standard; DNA; 9157 BP.  
DE Human immune system associated gene SEQ ID NO: 1474.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.2%; Score 36.2; DB 6; Length 9157;  
RESULT 951  
ID ABL34178 standard; DNA; 13084 BP.  
DE Human immune system associated gene SEQ ID NO: 2151.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.2%; Score 36.2; DB 6; Length 13084;  
RESULT 952  
ID ABV44994 standard; cDNA; 309 BP.  
DE Human prostate expression marker cDNA 44985.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 4.1%; Score 36; DB 5; Length 309;  
RESULT 953  
ID AAL19599 standard; cDNA; 405 BP.  
DE Human breast cancer expressed polynucleotide 12056.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 4.1%; Score 36; DB 4; Length 405;  
RESULT 954  
ID ABV23693 standard; cDNA; 489 BP.  
DE Human prostate expression marker cDNA 23684.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 4.1%; Score 36; DB 5; Length 489;  
RESULT 955  
ID ABV29562 standard; cDNA; 489 BP.  
DE Human prostate expression marker cDNA 29553.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 4.1%; Score 36; DB 5; Length 489;



Best Local Similarity 52.7%; Pred. No. 24;  
RESULT 956  
ID ACN55766 standard; cDNA; 513 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-028-Q6-N6-C2, SEQ:10547.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.1%; Score 36; DB 13; Length 513;  
Best Local Similarity 47.7%; Pred. No. 25;  
RESULT 957  
ID ACN62215 standard; cDNA; 516 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-026-Q6-N6-F3, SEQ:16996.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.1%; Score 36; DB 13; Length 516;  
Best Local Similarity 47.7%; Pred. No. 25;  
RESULT 958  
ID ACN53350 standard; cDNA; 528 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-006-Q1-N6-F8, SEQ:8131.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.1%; Score 36; DB 13; Length 528;  
Best Local Similarity 47.7%; Pred. No. 25;  
RESULT 959  
ID ACN45364 standard; cDNA; 533 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-A8, SEQ:145.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.1%; Score 36; DB 13; Length 533;  
Best Local Similarity 64.3%; Pred. No. 25;  
RESULT 960  
ID ACN53339 standard; cDNA; 537 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-006-Q1-N6-D9, SEQ:8120.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.1%; Score 36; DB 13; Length 537;  
Best Local Similarity 47.7%; Pred. No. 25;  
RESULT 961  
ID ACN51258 standard; cDNA; 554 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-013-Q1-N6-B2, SEQ:6039.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.1%; Score 36; DB 13; Length 554;  
Best Local Similarity 47.7%; Pred. No. 26;  
RESULT 962  
ID ACN46001 standard; cDNA; 559 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-012-Q1-N6-F6, SEQ:782.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.1%; Score 36; DB 13; Length 559;  
Best Local Similarity 49.0%; Pred. No. 26;  
RESULT 963  
ID ACN52090 standard; cDNA; 571 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-B9, SEQ:6871.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.1%; Score 36; DB 13; Length 571;  
Best Local Similarity 47.7%; Pred. No. 26;  
RESULT 964  
ID ACN52875 standard; cDNA; 576 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-018-Q1-N6-H5, SEQ:7656.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.1%; Score 36; DB 13; Length 576;  
Best Local Similarity 47.7%; Pred. No. 26;  
RESULT 965  
ID ACN51619 standard; cDNA; 579 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-005-Q1-N6-D4, SEQ:6400.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.1%; Score 36; DB 13; Length 579;  
Best Local Similarity 47.4%; Pred. No. 26;  
RESULT 966  
ID ACN50136 standard; cDNA; 636 BP.  
DE Cotton non-primed seed EST Clone ID: LIB3826-001-Q1-K6-F4, SEQ:4917.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.1%; Score 36; DB 13; Length 636;  
Best Local Similarity 67.1%; Pred. No. 27;  
RESULT 967  
ID AAQ86744 standard; cDNA; 1285 BP.  
DE TIMP-3 metalloproteinase inhibitor coding sequence.  
PN WO9509913-A1.  
PD 13-APR-1995.  
PA (INCY-) INCVTE PHARM INC.  
Query Match 4.1%; Score 36; DB 2; Length 1285;  
Best Local Similarity 58.3%; Pred. No. 38;  
RESULT 968  
ID AAD07709 standard; cDNA; 1328 BP.  
DE Human secreted protein-encoding gene 5 cDNA clone HPMGR66, SEQ ID NO:15.  
PN WO200134800-A1.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 36; DB 5; Length 1328;  
Best Local Similarity 54.5%; Pred. No. 38;  
RESULT 969  
ID AAD08331 standard; cDNA; 1355 BP.  
DE Human secreted protein-encoding gene 20 cDNA clone HMEJL08, SEQ ID NO:59.  
PN WO200136440-A1.  
PD 25-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 36; DB 4; Length 1355;  
Best Local Similarity 54.5%; Pred. No. 39;

RESULT 970  
ID AAD07732 standard; cDNA; 1355 BP.  
DE Human secreted protein-encoding Gene 5 cDNA clone HPMGR66, SEQ ID NO:38.  
PN WO200134800-A1.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 36; DB 5; Length 1355;  
Best Local Similarity 54.5%; Pred. No. 39;  
RESULT 971  
ID ADD71195 standard; cDNA; 2200 BP.  
DE Human intracellular signalling molecule INTSIG-32 cDNA SEQ ID NO:84.  
PN WO2003039348-A2.  
PD 15-MAY-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 4.1%; Score 36; DB 10; Length 2200;  
Best Local Similarity 58.3%; Pred. No. 48;  
RESULT 972  
ID ADB62738 standard; cDNA; 2390 BP.  
DE Human cDNA encoding clone NT2NE20069580.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 4.1%; Score 36; DB 10; Length 2390;  
Best Local Similarity 45.7%; Pred. No. 50;  
RESULT 973  
ID AEF65450 standard; DNA; 3332 BP.  
DE Mouse G protein-coupled receptor kinase 2 (GRK2) homolog gene sequence.  
PN WO2006009890-A2.  
PD 26-JAN-2006.  
PA (RECG) UNIV CALIFORNIA.  
Query Match 4.1%; Score 36; DB 15; Length 3332;  
Best Local Similarity 50.0%; Pred. No. 58;  
RESULT 974  
ID ABL06562 standard; cDNA; 4453 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 14168.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 4.1%; Score 36; DB 4; Length 4453;  
Best Local Similarity 55.6%; Pred. No. 66;  
RESULT 975  
ID ABQ67069 standard; DNA; 5611 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 99.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 36; DB 6; Length 5611;  
Best Local Similarity 62.0%; Pred. No. 73;  
RESULT 976  
ID ABL34078 standard; DNA; 6062 BP.  
DE Human immune system associated gene SEQ ID NO: 2051.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 36; DB 6; Length 6062;  
Best Local Similarity 67.1%; Pred. No. 76;  
RESULT 977  
ID ABQ67048 standard; DNA; 14362 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 78.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 36; DB 6; Length 14362;  
Best Local Similarity 54.5%; Pred. No. 1.1e+02;  
RESULT 978  
ID AAS45514 standard; DNA; 14708 BP.  
DE Chemically pretreated genomic DNA associated with cell cycle #110.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 36; DB 4; Length 14708;  
Best Local Similarity 54.5%; Pred. No. 1.1e+02;

RESULT 979  
ID ABL34245 standard; DNA; 14708 BP.  
DE Human immune system associated gene SEQ ID NO: 2218.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 36; DB 6; Length 14708;  
Best Local Similarity 54.5%; Pred. No. 1.1e+02;  
RESULT 980  
ID ABL92325 standard; DNA; 14708 BP.  
DE Chemically treated DNA repair gene fragment complementary to #67.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 36; DB 6; Length 14708;  
Best Local Similarity 54.5%; Pred. No. 1.1e+02;  
RESULT 981  
ID ABK28450 standard; DNA; 14708 BP.  
DE DNA transcription associated complementary genomic DNA #162.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 36; DB 6; Length 14708;  
Best Local Similarity 54.5%; Pred. No. 1.1e+02;  
RESULT 982  
ID ABL32654 standard; DNA; 17211 BP.  
DE Human immune system associated gene SEQ ID NO: 627.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 36; DB 6; Length 17211;  
Best Local Similarity 49.2%; Pred. No. 1.2e+02;  
RESULT 983  
ID ABL32767 standard; DNA; 19659 BP.  
DE Human immune system associated gene SEQ ID NO: 740.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 36; DB 6; Length 19659;  
Best Local Similarity 67.1%; Pred. No. 1.3e+02;  
RESULT 984  
ID AAK90436 standard; DNA; 21860 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 4012.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 36; DB 4; Length 21860;  
Best Local Similarity 67.1%; Pred. No. 1.4e+02;  
RESULT 985  
ID AAK7599 standard; DNA; 21860 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32411.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 36; DB 4; Length 21860;  
Best Local Similarity 67.1%; Pred. No. 1.4e+02;  
RESULT 986  
ID AAL37438 standard; DNA; 21860 BP.  
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3803.  
PN WO200155367-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 36; DB 4; Length 21860;  
Best Local Similarity 67.1%; Pred. No. 1.4e+02;  
RESULT 987  
ID AAD16680 standard; DNA; 21860 BP.  
DE Human pancreatic related protein-encoding genomic DNA, SEQ ID NO:44.  
PN WO200155327-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 36; DB 5; Length 21860;  
Best Local Similarity 67.1%; Pred. No. 1.4e+02;  
RESULT 988  
ID ABX60426 standard; cDNA; 21860 BP.

DE cDNA encoding novel human musculoskeletal system antigen #2770.  
PN US2002147140-A1.  
PD 10-OCT-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 4.1%; Score 36; DB 8; Length 21860;  
Best Local Similarity 67.1%; Pred. No. 1.4e+02;  
RESULT 989  
ID ADJ31176 standard; DNA; 21860 BP.  
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3803.  
PN US2004009488-A1.  
PD 15-JAN-2004.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 36; DB 12; Length 21860;  
Best Local Similarity 67.1%; Pred. No. 1.4e+02;  
RESULT 990  
ID ABL07108 standard; cDNA; 48452 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 15806.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 4.1%; Score 36; DB 4; Length 48452;  
Best Local Similarity 60.0%; Pred. No. 1.9e+02;  
RESULT 991  
ID AAL28691 standard; DNA; 41 BP.  
DE Human SNP oligonucleotide #1899.  
PN WO200147944-A2.  
PD 05-JUL-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.1%; Score 35.8; DB 4; Length 41;  
Best Local Similarity 94.9%; Pred. No. 9;  
RESULT 992  
ID AAA08355 standard; DNA; 47 BP.  
DE Human TGC-440 secretory protein PCR primer SEQ ID NO:16.  
PN WO200014226-A1.  
PD 16-MAR-2000.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match 4.1%; Score 35.8; DB 3; Length 47;  
Best Local Similarity 85.1%; Pred. No. 9.6;  
RESULT 993  
ID ABX44678 standard; cDNA; 368 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #9843.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 4.1%; Score 35.8; DB 8; Length 368;  
Best Local Similarity 65.8%; Pred. No. 24;  
RESULT 994  
ID AAI86808 standard; cDNA; 377 BP.  
DE Human polynucleotide SEQ ID NO 6868.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.1%; Score 35.8; DB 4; Length 377;  
Best Local Similarity 61.1%; Pred. No. 25;  
RESULT 995  
ID AAI88641 standard; cDNA; 384 BP.  
DE Human polynucleotide SEQ ID NO 8701.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.1%; Score 35.8; DB 4; Length 384;  
Best Local Similarity 61.1%; Pred. No. 25;  
RESULT 996  
ID ABV59190 standard; cDNA; 460 BP.  
DE Human prostate expression marker cDNA 59181.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 4.1%; Score 35.8; DB 5; Length 460;  
Best Local Similarity 63.2%; Pred. No. 27;  
RESULT 997  
ID ACN51760 standard; cDNA; 467 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-007-Q1-N6-P9, SEQ:6541.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.1%; Score 35.8; DB 13; Length 467;  
Best Local Similarity 48.7%; Pred. No. 27;  
RESULT 998  
ID ABK5238 standard; cDNA; 486 BP.  
DE Human colon cancer-associated cDNA, SEQ ID NO 708.  
PN WO200212280-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.1%; Score 35.8; DB 6; Length 486;  
Best Local Similarity 57.1%; Pred. No. 28;  
RESULT 999  
ID ADT94877 standard; cDNA; 563 BP.  
DE Colon cancer associated human cDNA sequence #396.  
PN US2003087818-A1.  
PD 08-MAY-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 4.1%; Score 35.8; DB 11; Length 563;  
Best Local Similarity 57.1%; Pred. No. 29;  
RESULT 1000  
ID ADX41359 standard; cDNA; 563 BP.  
DE Human cDNA encoding colon cancer protein SEQ ID NO 396.  
PN WO200274156-A2.  
PD 26-SEP-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.1%; Score 35.8; DB 11; Length 563;  
Best Local Similarity 57.1%; Pred. No. 29;  
RESULT 1001  
ID ADT95504 standard; cDNA; 587 BP.  
DE Colon cancer associated human cDNA sequence #1023.  
PN US2003087818-A1.  
PD 08-MAY-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 4.1%; Score 35.8; DB 11; Length 587;  
Best Local Similarity 57.1%; Pred. No. 30;  
RESULT 1002  
ID ADX41986 standard; cDNA; 587 BP.  
DE Human cDNA encoding colon cancer protein SEQ ID NO 1023.  
PN WO200274156-A2.  
PD 26-SEP-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.1%; Score 35.8; DB 11; Length 587;  
Best Local Similarity 57.1%; Pred. No. 30;  
RESULT 1003  
ID AAV58362 standard; cDNA; 618 BP.  
DE Coding sequence for secreted protein of clone DO19\_1.  
PN WO9837094-A2.  
PD 27-AUG-1998.  
PA (GEMY ) GENETICS INST INC.  
Query Match 4.1%; Score 35.8; DB 2; Length 618;  
Best Local Similarity 61.1%; Pred. No. 31;  
RESULT 1004  
ID ADT95765 standard; cDNA; 644 BP.  
DE Colon cancer associated human cDNA sequence #1284.  
PN US2003087818-A1.  
PD 08-MAY-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 4.1%; Score 35.8; DB 11; Length 644;  
Best Local Similarity 57.1%; Pred. No. 31;  
RESULT 1005  
ID ADX42247 standard; cDNA; 644 BP.  
DE Human cDNA encoding colon cancer protein SEQ ID NO 1284.  
PN WO200274156-A2.

PD 26-SEP-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.1%; Score 35.8; DB 11; Length 644;  
Best Local Similarity 57.1%; Pred. No. 31;  
RESULT 1006  
ID ADF76748 standard; cDNA; 963 BP.  
DE Novel human secreted and transmembrane protein cDNA SeqID 423.  
PN WO2003072035-A2.  
PD 04-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.1%; Score 35.8; DB 10; Length 963;  
Best Local Similarity 65.8%; Pred. No. 38;  
RESULT 1007  
ID AAD05534 standard; cDNA; 1011 BP.  
DE Human secreted protein-encoding gene 7 cDNA clone HOFMQ33, SEQ ID NO:53.  
PN WO200134767-A2.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 35.8; DB 4; Length 1011;  
Best Local Similarity 65.8%; Pred. No. 38;  
RESULT 1008  
ID ADA40429 standard; cDNA; 1011 BP.  
DE Human secreted protein encoding cDNA.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 35.8; DB 8; Length 1011;  
Best Local Similarity 65.8%; Pred. No. 38;  
RESULT 1009  
ID ACC50793 standard; cDNA; 1011 BP.  
DE Human secreted protein coding sequence, SEQ ID 460.  
PN WO200295010-A2.  
PD 28-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 35.8; DB 8; Length 1011;  
Best Local Similarity 65.8%; Pred. No. 38;  
RESULT 1010  
ID ABZ71437 standard; cDNA; 1011 BP.  
DE Secreted protein-encoding gene 129 cDNA clone HOFMQ33, SEQ ID NO:258.  
PN WO200276488-A1.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 35.8; DB 8; Length 1011;  
Best Local Similarity 65.8%; Pred. No. 38;  
RESULT 1011  
ID ADB91395 standard; cDNA; 1011 BP.  
DE Human secreted protein cDNA #SEQ ID 341.  
PN WO2003004622-A2.  
PD 16-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 35.8; DB 9; Length 1011;  
Best Local Similarity 65.8%; Pred. No. 38;  
RESULT 1012  
ID ADC73895 standard; cDNA; 1011 BP.  
DE Human secreted protein-related DNA - SEQ ID 528.  
PN WO2003038063-A2.  
PD 08-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 35.8; DB 10; Length 1011;  
Best Local Similarity 65.8%; Pred. No. 38;  
RESULT 1013  
ID ADA56594 standard; cDNA; 1011 BP.  
DE Gene encoding human secreted protein #404.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 35.8; DB 10; Length 1011;  
Best Local Similarity 65.8%; Pred. No. 38;  
RESULT 1014  
ID ABQ54241 standard; cDNA; 1106 BP.  
DE Human ovarian antigen HRACW30 cDNA, SEQ ID NO:121.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 35.8; DB 6; Length 1106;  
Best Local Similarity 52.0%; Pred. No. 40;  
RESULT 1015  
ID ADD78282 standard; DNA; 1612 BP.  
DE Human CGDD-24 coding sequence.  
PN WO2003077875-A2.  
PD 25-SEP-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 4.1%; Score 35.8; DB 10; Length 1612;  
Best Local Similarity 63.2%; Pred. No. 47;  
RESULT 1016  
ID ABK43722 standard; cDNA; 1887 BP.  
DE DNA encoding novel central nervous system protein #302.  
PN WO200155318-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 35.8; DB 4; Length 1887;  
Best Local Similarity 61.1%; Pred. No. 51;  
RESULT 1017  
ID ADI54109 standard; cDNA; 1887 BP.  
DE cDNA encoding novel human protein seq id 312.  
PN US2004018969-A1.  
PD 29-JAN-2004.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 4.1%; Score 35.8; DB 12; Length 1887;  
Best Local Similarity 61.1%; Pred. No. 51;  
RESULT 1018  
ID ADI32345 standard; DNA; 1944 BP.  
DE Mouse OAS1b DNA.  
PN US2003235575-A1.  
PD 25-DEC-2003.  
PA (AMHP) WYETH.  
PA (BAYU) BAYLOR COLLEGE MEDICINE.  
Query Match 4.1%; Score 35.8; DB 12; Length 1944;  
Best Local Similarity 51.6%; Pred. No. 52;  
RESULT 1019  
ID AAT59700 standard; DNA; 2001 BP.  
DE PTH-like peptide DNA clone HHM-8.  
PN US5605815-A.  
PD 25-FEB-1997.  
PA (UYVA) UNIV YALE.  
Query Match 4.1%; Score 35.8; DB 2; Length 2001;  
Best Local Similarity 59.2%; Pred. No. 52;  
RESULT 1020  
ID AAC79959 standard; cDNA; 2329 BP.  
DE Human secreted protein encoding cDNA for gene 12.  
PN WO200058357-A1.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 35.8; DB 3; Length 2329;  
Best Local Similarity 57.7%; Pred. No. 56;  
RESULT 1021  
ID AA251555 standard; cDNA; 3535 BP.  
DE Human hypoxia response regulating gene, 95 cDNA.  
PN WO200012525-A1.  
PD 09-MAR-2000.  
PA (QUAR-) QUARK BIOTECH INC.  
PA (KOHN/) KOHN K.  
Query Match 4.1%; Score 35.8; DB 3; Length 3535;  
Best Local Similarity 54.1%; Pred. No. 68;  
RESULT 1022  
ID ADQ22432 standard; DNA; 3982 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5252.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.1%; Score 35.8; DB 12; Length 3982;  
Best Local Similarity 52.3%; Pred. No. 71;  
RESULT 1023  
ID ACN88609 standard; DNA; 4296 BP.

DE Breast cancer related marker, seq id 9759.  
PN US200309974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 4.1%; Score 35.8; DB 11; Length 4296;  
Best Local Similarity 51.8%; Pred. No. 74;  
RESULT 1024  
ID ACN90377 standard; DNA; 4552 BP.  
DE Breast cancer related marker, seq id 11527.  
PN US200309974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 4.1%; Score 35.8; DB 11; Length 4552;  
Best Local Similarity 65.8%; Pred. No. 76;  
RESULT 1025  
ID AAS60872 standard; cDNA; 4877 BP.  
DE Human cancer agent-resistance marker #531.  
PN WO200179556-A2.  
PD 25-OCT-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.1%; Score 35.8; DB 4; Length 4877;  
Best Local Similarity 63.2%; Pred. No. 78;  
RESULT 1026  
ID AAS60871 standard; cDNA; 4877 BP.  
DE Human cancer agent-resistance marker #530.  
PN WO200179556-A2.  
PD 25-OCT-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.1%; Score 35.8; DB 4; Length 4877;  
Best Local Similarity 63.2%; Pred. No. 78;  
RESULT 1027  
ID AAS60883 standard; cDNA; 4877 BP.  
DE Human cancer agent-resistance marker #542.  
PN WO200179556-A2.  
PD 25-OCT-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.1%; Score 35.8; DB 4; Length 4877;  
Best Local Similarity 63.2%; Pred. No. 78;  
RESULT 1028  
ID ABN80020 standard; DNA; 6561 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 37.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 35.8; DB 6; Length 6561;  
Best Local Similarity 52.9%; Pred. No. 89;  
RESULT 1029  
ID ABL32638 standard; DNA; 6650 BP.  
DE Human immune system associated gene SEQ ID NO: 611.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 35.8; DB 6; Length 6650;  
Best Local Similarity 65.8%; Pred. No. 90;  
RESULT 1030  
ID AAS46727 standard; DNA; 7244 BP.  
DE Tumour suppressor gene derived chemically modified sequence #450.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 35.8; DB 4; Length 7244;  
Best Local Similarity 55.1%; Pred. No. 94;  
RESULT 1031  
ID ABL92323 standard; DNA; 10762 BP.  
DE Chemically treated DNA repair gene fragment complementary to#66.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 35.8; DB 6; Length 10762;  
Best Local Similarity 65.8%; Pred. No. 1.1e+02;  
RESULT 1032  
ID ABL33451 standard; DNA; 19787 BP.  
DE Human immune system associated gene SEQ ID NO: 1424.

PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 35.8; DB 6; Length 19787;  
Best Local Similarity 44.2%; Pred. No. 1.5e+02;  
RESULT 1033  
ID ABD33498 standard; DNA; 23503 BP.  
DE Murine cancer-associated (CA) gene MD07-097.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 4.1%; Score 35.8; DB 13; Length 23503;  
Best Local Similarity 56.3%; Pred. No. 1.6e+02;  
RESULT 1034  
ID AAS46787 standard; DNA; 61020 BP.  
DE Tumour suppressor gene derived chemically modified sequence #513.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 35.8; DB 4; Length 61020;  
Best Local Similarity 65.8%; Pred. No. 2.5e+02;  
RESULT 1035  
ID AAF22293 standard; DNA; 101786 BP.  
DE BAC containing repeats from centromeres 1-4 #16.  
PN WO200055325-A2.  
PD 21-SEP-2000.  
PA (UYCH-) UNIV CHICAGO.  
Query Match 4.1%; Score 35.8; DB 3; Length 101786;  
Best Local Similarity 65.8%; Pred. No. 3.1e+02;  
RESULT 1036  
ID ADI76910 standard; DNA; 250 BP.  
DE Human ovarian cancer DNA marker #9652.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.1%; Score 35.6; DB 5; Length 250;  
Best Local Similarity 39.4%; Pred. No. 23;  
RESULT 1037  
ID ADI70589 standard; DNA; 250 BP.  
DE Human ovarian cancer DNA marker #3331.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.1%; Score 35.6; DB 5; Length 250;  
Best Local Similarity 39.4%; Pred. No. 23;  
RESULT 1038  
ID ABVI9977 standard; cDNA; 295 BP.  
DE Human prostate expression marker cDNA i9968.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.1%; Score 35.6; DB 5; Length 295;  
Best Local Similarity 62.2%; Pred. No. 25;  
RESULT 1039  
ID ABV49738 standard; cDNA; 303 BP.  
DE Human prostate expression marker cDNA 49729.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.1%; Score 35.6; DB 5; Length 303;  
Best Local Similarity 62.2%; Pred. No. 25;  
RESULT 1040  
ID ADM16713 standard; DNA; 346 BP.  
DE PRM-P5-H4 encoding sequence.  
PN WO2004027041-A2.  
PD 01-APR-2004.  
PA (MERI-) MERIAL LTD.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 4.1%; Score 35.6; DB 12; Length 346;  
Best Local Similarity 58.5%; Pred. No. 27;  
RESULT 1041  
ID ABV54410 standard; cDNA; 462 BP.  
DE Human prostate expression marker cDNA 54401.

PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.1%; Score 35.6; DB 5; Length 462;  
Best Local Similarity 62.2%; Pred. No. 31;  
RESULT 1042  
ID AA193637 standard; cDNA; 478 BP.  
DE Human polynucleotide SEQ ID NO 13697.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.1%; Score 35.6; DB 4; Length 478;  
Best Local Similarity 47.7%; Pred. No. 31;  
RESULT 1043  
ID AA187737 standard; cDNA; 481 BP.  
DE Human polynucleotide SEQ ID NO 7797.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.1%; Score 35.6; DB 4; Length 481;  
Best Local Similarity 53.6%; Pred. No. 31;  
RESULT 1044  
ID ACH38616 standard; cDNA; 481 BP.  
DE Human endothelial cell cDNA #6749.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 4.1%; Score 35.6; DB 9; Length 481;  
Best Local Similarity 53.6%; Pred. No. 31;  
RESULT 1045  
ID ACN48060 standard; cDNA; 487 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-018-Q1-N6-F4, SEQ:2841.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.1%; Score 35.6; DB 13; Length 487;  
Best Local Similarity 47.3%; Pred. No. 31;  
RESULT 1046  
ID AAK57064 standard; cDNA; 532 BP.  
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:2124.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 35.6; DB 4; Length 532;  
Best Local Similarity 57.4%; Pred. No. 33;  
RESULT 1047  
ID ACN62126 standard; cDNA; 533 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-025-Q6-N6-E11, SEQ:16907.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.1%; Score 35.6; DB 13; Length 533;  
Best Local Similarity 47.9%; Pred. No. 33;  
RESULT 1048  
ID ABV14236 standard; cDNA; 545 BP.  
DE Human prostate expression marker cDNA 14227.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.1%; Score 35.6; DB 5; Length 545;  
Best Local Similarity 53.6%; Pred. No. 33;  
RESULT 1049  
ID AAH31453 standard; cDNA; 632 BP.

DE Human olfactory receptor polynucleotide, SEQ ID NO: 25.  
PN WO200127158-A2.  
PD 19-APR-2001.  
PA (DIGI-) DIGISCENTS.  
Query Match 4.1%; Score 35.6; DB 4; Length 632;  
Best Local Similarity 49.5%; Pred. No. 35;  
RESULT 1050  
ID ADE29043 standard; DNA; 683 BP.  
DE Human selected interacting domain DNA - SEQ ID 29.  
PN WO2003046176-A2.  
PD 05-JUN-2003.  
PA (HYBR-) HYBRIGENICS.  
Query Match 4.1%; Score 35.6; DB 10; Length 683;  
Best Local Similarity 60.2%; Pred. No. 36;  
RESULT 1051  
ID ABN98603 standard; DNA; 936 BP.  
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 371.  
PN US2002023281-A1.  
PD 21-FEB-2002.  
PA (GORL/) GORLACH J.  
PA (ANY/) AN Y.  
PA (HAMI/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (YUY/) YU Y.  
PA (RAME/) RAMEAKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHWEA A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRIC/) KRICKER M.  
PA (SLAT/) SLATER T.  
PA (DAVI/) DAVIS K R.  
PA (ALLE/) ALLEN K.  
PA (HOFF/) HOFFMAN N.  
PA (HURB/) HURBAN P.  
Query Match 4.1%; Score 35.6; DB 6; Length 936;  
Best Local Similarity 62.5%; Pred. No. 42;  
RESULT 1052  
ID ADF82222 standard; DNA; 1084 BP.  
DE Leukaemia-related DNA sequence #2778.  
PN WO2003039443-A2.  
PD 15-MAY-2003.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.  
PA (HAPE/) HAERLACH T.  
PA (SCHO/) SCHOCH C.  
PA (KERN/) KERN W.  
Query Match 4.1%; Score 35.6; DB 10; Length 1084;  
Best Local Similarity 64.6%; Pred. No. 45;  
RESULT 1053  
ID ADJ80201 standard; cDNA; 1103 BP.  
DE Novel human nucleic acid-associated protein coding sequence #19.  
PN WO2003038052-A2.  
PD 08-MAY-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 4.1%; Score 35.6; DB 10; Length 1103;  
Best Local Similarity 62.2%; Pred. No. 45;  
RESULT 1054  
ID AEC20303 standard; DNA; 1103 BP.  
DE Human nucleic acid-associated protein (NAAP) coding sequence - SEQ ID 77.  
PN US2005186569-A1.  
PD 25-AUG-2005.  
PA (BECH/) BECHA S D.  
PA (BORO/) BOROMSKY M L.  
PA (BURF/) BURFORD N.  
PA (CHAW/) CHAWLA N K.  
PA (ELLI/) ELLIOTT V S.  
PA (EMER/) EMERLING B M.  
PA (FORS/) FORSYTHE I J.

PA (GIET/) GIETZEN K J.  
 PA (GORV/) GORVAD A E.  
 PA (GRIF/) GRIFFIN J A.  
 PA (HAFI/) HAFALIA A J A.  
 PA (ISON/) ISON C H.  
 PA (LALP/) LAL P.  
 PA (LEES/) LEE E A.  
 PA (LEES/) LEE S.  
 PA (LEES/) LEE S Y.  
 PA (MARQ/) MARQUIS J P.  
 PA (RAMK/) RAMKOMAR J.  
 PA (SPRA/) SPRAGUE W W.  
 PA (SWAR/) SWARNAKAR A.  
 PA (TANG/) TANG Y T.  
 PA (WARR/) WARREN B A.  
 PA (YANG/) YANG J.  
 PA (YUEH/) YUE H.  
 PA (ZEBR/) ZEBARJADIAN Y.  
 Query Match 4.1%; Score 35.6; DB 14; Length 1103;  
 Best Local Similarity 62.2%; Pred. No. 45;  
 RESULT 1055  
 ID AAC59836 standard; DNA; 1204 BP.  
 DE Human secreted protein encoding DNA clone vq21 1.  
 PN WO200055375-A1.  
 PD 21-SEP-2000.  
 PA (ALPH-) ALPHAGENE INC.  
 Query Match 4.1%; Score 35.6; DB 3; Length 1204;  
 Best Local Similarity 58.5%; Pred. No. 47;  
 RESULT 1056  
 ID ADT99265 standard; DNA; 1233 BP.  
 DE Mouse parkin protein encoding DNA.  
 PN US2004214763-A1.  
 PD 28-OCT-2004.  
 PA (AVET) AVENTIS PHARMA SA.  
 PA (INRM) INST NAT SANTE & RECH MEDICALE.  
 Query Match 4.1%; Score 35.6; DB 13; Length 1233;  
 Best Local Similarity 58.5%; Pred. No. 48;  
 RESULT 1057  
 ID ADP55498 standard; cDNA; 1284 BP.  
 DE Human PRO cDNA sequence SEQ ID NO:1474.  
 PN WO2004039956-A2.  
 PD 13-MAY-2004.  
 PA (GETH) GENENTECH INC.  
 Query Match 4.1%; Score 35.6; DB 13; Length 1284;  
 Best Local Similarity 60.2%; Pred. No. 49;  
 RESULT 1058  
 ID ABE83638 standard; cDNA; 1284 BP.  
 DE Human cDNA differentially expressed in asthma, SEQ ID NO:46.  
 PN WO2005118403-A2.  
 PD 15-DEC-2005.  
 PA (LINK-) LINKAGENE LTD.  
 Query Match 4.1%; Score 35.6; DB 15; Length 1284;  
 Best Local Similarity 60.2%; Pred. No. 49;  
 RESULT 1059  
 ID AAS26060 standard; cDNA; 1801 BP.  
 DE Human cDNA encoding a novel secreted protein, Seq ID 239.  
 PN WO200155322-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 4.1%; Score 35.6; DB 4; Length 1801;  
 Best Local Similarity 58.5%; Pred. No. 57;  
 RESULT 1060  
 ID ABX73401 standard; DNA; 1801 BP.  
 DE Human novel polynucleotide #229.  
 PN US2002132753-A1.  
 PD 19-SEP-2002.  
 PA (ROSE/) ROSEN C A.  
 PA (RUBE/) RUBEN S M.  
 PA (BARA/) BARASH S C.  
 Query Match 4.1%; Score 35.6; DB 8; Length 1801;  
 Best Local Similarity 58.5%; Pred. No. 57;  
 RESULT 1061  
 ID AAL45822 standard; cDNA; 2185 BP.

DE Human secreted protein coding sequence SEQ ID NO: 27.  
 PN WO200228877-A1.  
 PD 11-APR-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 4.1%; Score 35.6; DB 6; Length 2185;  
 Best Local Similarity 60.2%; Pred. No. 62;  
 RESULT 1062  
 ID AAQ05055 standard; DNA; 2400 BP.  
 DE Placenta-specific protein Pp11 encoding DNA.  
 PN EP374909-A.  
 PD 27-JUN-1990.  
 PA (BEHW) BEHRINGERWERKE AG.  
 Query Match 4.1%; Score 35.6; DB 2; Length 2400;  
 Best Local Similarity 58.5%; Pred. No. 64;  
 RESULT 1063  
 ID AEF55950 standard; DNA; 2500 BP.  
 DE Human genomic DNA #557.  
 PN WO2006008128-A2.  
 PD 26-JAN-2006.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.1%; Score 35.6; DB 15; Length 2500;  
 Best Local Similarity 55.7%; Pred. No. 66;  
 RESULT 1064  
 ID AEF55714 standard; DNA; 2500 BP.  
 DE Human genomic DNA #321.  
 PN WO2006008128-A2.  
 PD 26-JAN-2006.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.1%; Score 35.6; DB 15; Length 2500;  
 Best Local Similarity 55.7%; Pred. No. 66;  
 RESULT 1065  
 ID AEF55557 standard; DNA; 2646 BP.  
 DE Human genomic DNA #164.  
 PN WO2006008128-A2.  
 PD 26-JAN-2006.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.1%; Score 35.6; DB 15; Length 2646;  
 Best Local Similarity 54.6%; Pred. No. 67;  
 RESULT 1066  
 ID ADE29042 standard; DNA; 2890 BP.  
 DE Human AIM1 selected interacting domain DNA - SEQ ID 28.  
 PN WO2003046176-A2.  
 PD 05-JUN-2003.  
 PA (HYBR-) HYBRIGENICS.  
 Query Match 4.1%; Score 35.6; DB 10; Length 2890;  
 Best Local Similarity 60.2%; Pred. No. 70;  
 RESULT 1067  
 ID ADA53524 standard; cDNA; 3266 BP.  
 DE Human coding sequence, SEQ ID 1092.  
 PN EP1293569-A2.  
 PD 19-MAR-2003.  
 PA (HELI-) HELIX RES INST.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Query Match 4.1%; Score 35.6; DB 10; Length 3266;  
 Best Local Similarity 60.2%; Pred. No. 74;  
 RESULT 1068  
 ID AAX87412 standard; cDNA; 3607 BP.  
 DE Hepatocellular carcinoma marker gene L4 cDNA.  
 PN WO9939200-A1.  
 PD 05-AUG-1999.  
 PA (UYJE-) UNIV JEFFERSON THOMAS.  
 Query Match 4.1%; Score 35.6; DB 2; Length 3607;  
 Best Local Similarity 58.5%; Pred. No. 77;  
 RESULT 1069  
 ID ACN91230 standard; DNA; 3811 BP.  
 DE Breast cancer related marker, seq id 12380.  
 PN US200309974-A1.  
 PD 29-MAY-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 4.1%; Score 35.6; DB 11; Length 3811;  
 Best Local Similarity 64.6%; Pred. No. 79;  
 RESULT 1070  
 ID ADQ63590 standard; cDNA; 4092 BP.

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DE Novel human cDNA sequence #751.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.1%; Score 35.6; DB 12; Length 4092;
Best Local Similarity 60.2%; Pred. No. 82;
RESULT 1071
ID AA234304 standard; cDNA; 4199 BP.
DE Human PRO286 nucleotide sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 2; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1072
ID AAX58296 standard; cDNA; 4199 BP.
DE Human Toll protein PRO286 cDNA.
PN WO9920756-A2.
PD 29-APR-1999.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 2; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1073
ID AAC78584 standard; cDNA; 4199 BP.
DE Human PRO286 nucleotide sequence SEQ ID NO:497.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 3; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1074
ID ACA63872 standard; cDNA; 4199 BP.
DE Novel human secreted and transmembrane protein PRO286 cDNA.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 8; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1075
ID ACA72036 standard; cDNA; 4199 BP.
DE Human secreted and transmembrane PRO polypeptide #32 cDNA.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 8; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1076
ID ABX92676 standard; cDNA; 4199 BP.
DE cDNA encoding human PRO286 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 8; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1077
ID ACA66417 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO286.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 8; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1078
ID ACAG2618 standard; cDNA; 4199 BP.
DE Human cDNA encoding Toll protein PRO286.
PN US2003027260-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 8; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1079
ID ADA25036 standard; cDNA; 4199 BP.
DE Novel human secreted and transmembrane protein PRO286 cDNA.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 9; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1080
ID ACJ30018 standard; cDNA; 4199 BP.
DE Novel human secreted and transmembrane protein PRO286 cDNA.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 9; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1081
ID ADA12697 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO586.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 9; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1082
ID ACD29433 standard; cDNA; 4199 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #127.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 9; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1083
ID ADS74003 standard; cDNA; 4199 BP.
DE Human PRO polynucleotide sequence #127.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1084
ID ADB76719 standard; cDNA; 4199 BP.
DE Human PRO polynucleotide sequence #127.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1085
ID ADC44145 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1086
ID ADC61905 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1087
ID ADC63869 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 10; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1088
ID ADC66969 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003060406-A1.
PD 27-MAR-2003.
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PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 10; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1089  
ID ADC65093 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003064407-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 10; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1090  
ID ADC63153 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003068648-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 10; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1091  
ID ADC68218 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003069178-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 10; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1092  
ID ADC41538 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003072745-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 10; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1093  
ID ADC67593 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003073131-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 10; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1094  
ID ADC62529 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003073624-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 10; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1095  
ID ADC42162 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003104998-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 10; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1096  
ID ADE49531 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003096744-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 10; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1097  
ID ADE35585 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003203434-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.

Query Match 4.1%; Score 35.6; DB 10; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1098  
ID ADE16699 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003203435-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 10; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1099  
ID ADD73314 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003203436-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 10; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1100  
ID ADD72672 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003194781-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 10; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1101  
ID ADE17323 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003203433-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 10; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1102  
ID ADF47337 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003195333-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 10; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1103  
ID ADG53094 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003216561-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 10; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1104  
ID ADG60414 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003206915-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 10; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1105  
ID ADI61174 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003077700-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 10; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1106  
ID ADC42837 standard; cDNA; 4199 BP.  
DE Novel human secreted and transmembrane protein PRO286 cDNA.  
PN US2003050239-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 10; Length 4199;

Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1107  
ID ADE48831 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003104536-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 12; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1108  
ID ADE89932 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003130181-A1.  
PD 10-JUL-2003.  
PA (ASHK/) ASHKENAZI A J.  
PA (BAKE/) BAKER K P.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOM/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M B.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOSKI P J.  
PA (GIRM/) GIRMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (KUOS/) KUO S S.  
PA (NAPI/) NAPIER M A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROIM/) ROY M A.  
PA (SHEL/) SHELTON D L.  
PA (STEW/) STEWART T A.  
PA (TUNA/) TUNAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 4.1%; Score 35.6; DB 12; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1109  
ID ADF61572 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003195345-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 12; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1110  
ID ADF40264 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003198994-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 12; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1111  
ID ADF46060 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003195148-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 12; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1112  
ID ADF24456 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003204055-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 12; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1113  
ID ADF40888 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003199021-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 12; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1114  
ID ADF23832 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003203402-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 12; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1115  
ID ADF33815 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003194780-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 12; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1116  
ID ADF27282 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003199436-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 12; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1117  
ID ADF27918 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003199437-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 12; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1118  
ID ADF41512 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003199435-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 12; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1119  
ID ADF33191 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003211091-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 12; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1120  
ID ADF25557 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003211092-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 12; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1121  
ID ADF26658 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003199674-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 12; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1122  
ID ADF24456 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2003204055-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.

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Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1122
ID ADF34447 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1123
ID ADF46684 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1124
ID ADG50670 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1125
ID ADG50046 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1126
ID ADG51918 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1127
ID ADG49422 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1128
ID ADG48798 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1129
ID ADG51294 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1130
ID ADG59238 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1131
ID ADG62694 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1132
ID ADH25719 standard; cDNA; 4199 BP.
DE Human neurotrophin homologue related nucleotide sequence SEQ ID NO:497.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1133
ID ADL07330 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1134
ID ADL07330 standard; cDNA; 4199 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO286.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 12; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1135
ID ADU50452 standard; cDNA; 4199 BP.
DE PRO286 coding sequence, SEQ ID 497.
PN US2004223964-A1.
PD 11-NOV-2004.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.6; DB 13; Length 4199;
Best Local Similarity 60.2%; Pred. No. 83;
RESULT 1136
ID ADM49731 standard; cDNA; 4199 BP.
DE PRO286 cDNA, SEQ ID 497.
PN US2005014226-A1.
PD 20-JAN-2005.
PA (ASHK/) ASHENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERE/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODD/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 4.1%; Score 35.6; DB 14; Length 4199;
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Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1137  
ID AD523392 standard; cDNA; 4199 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO286.  
PN US2005084935-A1.  
PD 21-APR-2005.  
PA (ASHK/) ASHKENAZI A J.  
PA (BAKE/) BAKER K P.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOM/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODO/) GODDARD A.  
PA (GODO/) GODONSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (KUOS/) KUO S S.  
PA (NAPI/) NAPIER M A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (SHEL/) SHELTON D L.  
PA (STEW/) STEWART T A.  
PA (TUNA/) TUNAS D. P M.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 4.1%; Score 35.6; DB 14; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1138  
ID AED48220 standard; cDNA; 4199 BP.  
DE Human PRO286 cDNA, clone DNA426631154.  
PN US2005227342-A1.  
PD 13-OCT-2005.  
PA (GETH/) GENENTECH INC.  
Query Match 4.1%; Score 35.6; DB 14; Length 4199;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1139  
ID ADU23156 standard; cDNA; 4211 BP.  
DE Human Toll-like receptor 8 (TLR8) cDNA sequence - SEQ ID 48.  
PN WO2004094671-A2.  
PD 04-NOV-2004.  
PA (COLE-) COLEY PHARM GMBH.  
PA (COLE-) COLEY PHARM GROUP INC.  
Query Match 4.1%; Score 35.6; DB 13; Length 4211;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1140  
ID AEF77703 standard; cDNA; 4211 BP.  
DE Human toll-like receptor 8 (TLR8) variant 2 cDNA.  
PN WO20060171-A2.  
PD 16-FEB-2006.  
PA (META-) METABOLEX INC.  
Query Match 4.1%; Score 35.6; DB 15; Length 4211;  
Best Local Similarity 60.2%; Pred. No. 83;  
RESULT 1141  
ID ABL34030 standard; DNA; 6048 BP.  
DE Human immune system associated gene SEQ ID NO: 2003.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 35.6; DB 6; Length 6048;  
Best Local Similarity 55.7%; Pred. No. 98;  
RESULT 1142  
ID AAG63352 standard; DNA; 6048 BP.  
DE Chemically pretreated metabolism associated gene #47.  
PN WO200176451-A2.  
PD 18-OCT-2001.

PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 35.6; DB 6; Length 6048;  
Best Local Similarity 55.7%; Pred. No. 98;  
RESULT 1143  
ID AAG46338 standard; DNA; 6063 BP.  
DE Tumour suppressor gene derived chemically modified sequence #60.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 35.6; DB 4; Length 6063;  
Best Local Similarity 58.5%; Pred. No. 98;  
RESULT 1144  
ID AAK52133 standard; cDNA; 6792 BP.  
DE Human polynucleotide SEQ ID NO 678.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.1%; Score 35.6; DB 4; Length 6792;  
Best Local Similarity 60.2%; Pred. No. 1e+02;  
RESULT 1145  
ID AED73524 standard; cDNA; 6802 BP.  
DE Human placental protein encoding cDNA SEQ ID NO:352.  
PN US2005255114-A1.  
PD 17-NOV-2005.  
PA (NUVE-) NUVELO INC.  
Query Match 4.1%; Score 35.6; DB 14; Length 6802;  
Best Local Similarity 60.2%; Pred. No. 1e+02;  
RESULT 1146  
ID AAH90035 standard; cDNA; 6815 BP.  
DE Human bone marrow cDNA, SEQ ID NO: 279.  
PN WO200153453-A2.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.1%; Score 35.6; DB 5; Length 6815;  
Best Local Similarity 60.2%; Pred. No. 1e+02;  
RESULT 1147  
ID ABZ35054 standard; cDNA; 6817 BP.  
DE Human gene expression profile polynucleotide SEQ ID NO 166.  
PN WO200274979-A2.  
PD 26-SEP-2002.  
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.  
Query Match 4.1%; Score 35.6; DB 6; Length 6817;  
Best Local Similarity 60.2%; Pred. No. 1e+02;  
RESULT 1148  
ID ABR84449 standard; cDNA; 6817 BP.  
DE Human cDNA differentially expressed in granulocytic cells #1020.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 4.1%; Score 35.6; DB 6; Length 6817;  
Best Local Similarity 60.2%; Pred. No. 1e+02;  
RESULT 1149  
ID ADE85674 standard; DNA; 6817 BP.  
DE Farnesyl transferase inhibitor modulated leukemia associated gene #893.  
PN WO2003038129-A2.  
PD 08-MAY-2003.  
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.  
Query Match 4.1%; Score 35.6; DB 10; Length 6817;  
Best Local Similarity 60.2%; Pred. No. 1e+02;  
RESULT 1150  
ID ADR26031 standard; DNA; 6817 BP.  
DE Breast cancer prognosis marker #1892.  
PN WO2004065545-A2.  
PD 05-AUG-2004.  
PA (ROSE-) ROSETTA INPHARMATICS LLC.  
PA (NECA-) NETHERLANDS CANCER INST.  
Query Match 4.1%; Score 35.6; DB 13; Length 6817;  
Best Local Similarity 60.2%; Pred. No. 1e+02;  
RESULT 1151  
ID AEC82974 standard; cDNA; 6817 BP.  
DE Breast cancer associated cDNA SEQ ID NO 542.  
PN WO2005083429-A2.  
PD 09-SEP-2005.

PA (VERI-) VERIDEX LLC.  
Query Match 4.1%; Score 35.6; DB 14; Length 6817;  
Best Local Similarity 60.2%; Pred. No. 1e+02;  
RESULT 1152  
ID AAH89922 standard; cDNA; 7317 BP.  
DE Human bone marrow cDNA, SEQ ID NO: 53.  
PN WO200153453-A2.  
PD 26-JUL-2001.  
PA (HYSB-) HYSBQ INC.  
Query Match 4.1%; Score 35.6; DB 5; Length 7317;  
Best Local Similarity 60.2%; Pred. No. 1.1e+02;  
RESULT 1153  
ID ABQ77419 standard; cDNA; 7364 BP.  
DE Human CGDD cDNA 3075937CB1 SEQ ID 33.  
PN WO2003014322-A2.  
PD 20-FEB-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 4.1%; Score 35.6; DB 8; Length 7364;  
Best Local Similarity 60.2%; Pred. No. 1.1e+02;  
RESULT 1154  
ID ABK28343 standard; DNA; 10138 BP.  
DE DNA transcription associated genomic DNA #109.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 35.6; DB 6; Length 10138;  
Best Local Similarity 60.2%; Pred. No. 1.2e+02;  
RESULT 1155  
ID ABL33900 standard; DNA; 11662 BP.  
DE Human immune system associated gene SEQ ID NO: 1873.  
PN WO20020928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 35.6; DB 6; Length 11662;  
Best Local Similarity 64.6%; Pred. No. 1.3e+02;  
RESULT 1156  
ID ABQ67059 standard; DNA; 34688 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 89.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 35.6; DB 6; Length 34688;  
Best Local Similarity 64.6%; Pred. No. 2.2e+02;  
RESULT 1157  
ID AAK78813 standard; DNA; 51469 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33625.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 35.6; DB 4; Length 51469;  
Best Local Similarity 54.8%; Pred. No. 2.6e+02;  
RESULT 1158  
ID AAK70270 standard; DNA; 51469 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25082.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 35.6; DB 4; Length 51469;  
Best Local Similarity 54.8%; Pred. No. 2.6e+02;  
RESULT 1159  
ID AAK69322 standard; DNA; 51469 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24134.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 35.6; DB 4; Length 51469;  
Best Local Similarity 54.8%; Pred. No. 2.6e+02;  
RESULT 1160  
ID ADQ97873 standard; DNA; 114454 BP.  
DE Mouse cancer associated sequence MD11-016, SEQ ID 850.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.

Query Match 4.1%; Score 35.6; DB 12; Length 114454;  
Best Local Similarity 48.1%; Pred. No. 3.7e+02;  
RESULT 1161  
ID AEF74795 standard; DNA; 178863 BP.  
DE Human polynucleotide #309.  
PN WO2006013561-A2.  
PD 09-FEB-2006.  
PA (VISS-) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.  
Query Match 4.1%; Score 35.6; DB 15; Length 178863;  
Best Local Similarity 53.6%; Pred. No. 4.5e+02;  
RESULT 1162  
ID ABD33364 standard; DNA; 203132 BP.  
DE Murine cancer-associated (CA) gene MD07-067.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 4.1%; Score 35.6; DB 13; Length 203132;  
Best Local Similarity 48.5%; Pred. No. 4.8e+02;  
RESULT 1163  
ID ADZ13443 standard; DNA; 203132 BP.  
DE Murine cancer-associated genomic DNA #84.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR-) CHIRON CORP.  
Query Match 4.1%; Score 35.6; DB 14; Length 203132;  
Best Local Similarity 48.5%; Pred. No. 4.8e+02;  
RESULT 1164  
ID ABV19042 standard; cDNA; 252 BP.  
DE Human prostate expression marker cDNA 19033.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.1%; Score 35.4; DB 5; Length 252;  
Best Local Similarity 63.5%; Pred. No. 26;  
RESULT 1165  
ID ABV49607 standard; cDNA; 302 BP.  
DE Human prostate expression marker cDNA 49598.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.1%; Score 35.4; DB 5; Length 302;  
Best Local Similarity 69.6%; Pred. No. 29;  
RESULT 1166  
ID AAL00078 standard; cDNA; 324 BP.  
DE Human reproductive system related antigen cDNA SEQ ID NO: 79.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 35.4; DB 4; Length 324;  
Best Local Similarity 62.8%; Pred. No. 30;  
RESULT 1167  
ID ABV48140 standard; cDNA; 350 BP.  
DE Human prostate expression marker cDNA 48131.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.1%; Score 35.4; DB 5; Length 350;  
Best Local Similarity 53.7%; Pred. No. 31;  
RESULT 1168  
ID ABX36333 standard; cDNA; 405 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #1498.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT-) BYATT J C.  
PA (MATH-) MATHIALAGAN N.  
PA (TAON-) TAO N.  
PA (WAR-) WARREN W C.  
Query Match 4.1%; Score 35.4; DB 8; Length 405;  
Best Local Similarity 66.2%; Pred. No. 33;  
RESULT 1169  
ID ABV57623 standard; cDNA; 488 BP.  
DE Human prostate expression marker cDNA 57614.

PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.1%; Score 35.4; DB 5; Length 488;  
Best Local Similarity 59.4%; Pred. No. 36;  
RESULT 1170  
ID ACN46717 standard; cDNA; 522 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-003-Q1-N6-C8, SEQ:1498.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.1%; Score 35.4; DB 13; Length 522;  
Best Local Similarity 48.3%; Pred. No. 37;  
RESULT 1171  
ID ACN47378 standard; cDNA; 574 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-010-Q1-N6-G2, SEQ:2159.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.1%; Score 35.4; DB 13; Length 574;  
Best Local Similarity 48.3%; Pred. No. 38;  
RESULT 1172  
ID ABQ22672 standard; DNA; 673 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 9263.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 35.4; DB 6; Length 673;  
Best Local Similarity 54.8%; Pred. No. 41;  
RESULT 1173  
ID ABQ22673 standard; DNA; 673 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 9264.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 35.4; DB 6; Length 673;  
Best Local Similarity 54.8%; Pred. No. 41;  
RESULT 1174  
ID AAS29157 standard; cDNA; 792 BP.  
DE cDNA encoding for human DNA-binding protein #128.  
PN WO20015162-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 35.4; DB 5; Length 792;  
Best Local Similarity 59.4%; Pred. No. 44;  
RESULT 1175  
ID ABS68297 standard; cDNA; 792 BP.  
DE cDNA encoding human DNA-binding protein #128.  
PN US2002102638-A1.  
PD 01-AUG-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 4.1%; Score 35.4; DB 6; Length 792;  
Best Local Similarity 59.4%; Pred. No. 44;  
RESULT 1176  
ID ADC25291 standard; cDNA; 792 BP.  
DE Human cDNA from extracellular matrix gene 128.  
PN US2003049650-A1.  
PD 13-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 35.4; DB 10; Length 792;  
Best Local Similarity 59.4%; Pred. No. 44;  
RESULT 1177  
ID ABQ54594 standard; cDNA; 1058 BP.  
DE Human ovarian antigen HCOM35 cDNA, SEQ ID NO:474.  
PN WO200200677-A1.

PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 35.4; DB 6; Length 1058;  
Best Local Similarity 56.4%; Pred. No. 50;  
RESULT 1178  
ID AAD08425 standard; cDNA; 1143 BP.  
DE Human secreted protein-encoding gene 22 cDNA clone HARNB17, SEQ ID NO:32.  
PN WO200134643-A1.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.1%; Score 35.4; DB 4; Length 1143;  
Best Local Similarity 54.1%; Pred. No. 52;  
RESULT 1179  
ID ACC74280 standard; cDNA; 1233 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1233;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1180  
ID AAS46043 standard; cDNA; 1234 BP.  
DE Human DNA encoding PRO polypeptide sequence #119.  
PN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GETH-) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 4; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1181  
ID AAF92089 standard; cDNA; 1234 BP.  
DE Human PRO3566 cDNA.  
PN WO200116318-A2.  
PD 08-MAR-2001.  
PA (GETH-) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 4; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1182  
ID ABS74409 standard; cDNA; 1234 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO3566.  
PN US2002119130-A1.  
PD 29-AUG-2002.  
PA (GETH-) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 6; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1183  
ID ACA89493 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1184  
ID ACA73503 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH-) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1185  
ID ACA05818 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH-) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1186  
ID ACA66852 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO protein #119.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH-) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;

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Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1187
ID ACA91195 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1188
ID ACD81572 standard; cDNA; 1234 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO3566.
PN US200309013-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1189
ID ACF20227 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1190
ID ACF19613 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1191
ID ACD21901 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1192
ID ACF13066 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1193
ID ACD25169 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1194
ID ACF00218 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1195
ID ACA60394 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1196
ID ACA72275 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.

Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1197
ID ACD04799 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1198
ID ACD18260 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1199
ID ACD08267 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1200
ID ACA88701 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1201
ID ACA70143 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1202
ID ACD12365 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1203
ID ACD15908 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1204
ID ACD25476 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1205
ID ACD17953 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1206
ID ACC98240 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
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RESULT 1207  
ID ACD21594 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1208  
ID ACD18661 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1209  
ID ACA58841 standard; cDNA; 1234 BP.  
DE cDNA encoding human secreted polypeptide PRO3566.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1210  
ID ABX98271 standard; cDNA; 1234 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 237.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1211  
ID ACD14022 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1212  
ID ACD09802 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1213  
ID ACC88547 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1214  
ID ACD21287 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1215  
ID ABX75659 standard; cDNA; 1234 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO3566.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1216  
ID ACA64017 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #32.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;

RESULT 1217  
ID ABX97862 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1218  
ID ACA97338 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1219  
ID ACA57801 standard; cDNA; 1234 BP.  
DE Human PRO3566 cDNA.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1220  
ID ACD14329 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1221  
ID ACC91112 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1222  
ID ACC88854 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1223  
ID ACD07051 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1224  
ID ACA67502 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1225  
ID ACC81557 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1226  
ID ACA91281 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #32.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;



RESULT 1227  
ID ACC89161 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1228  
ID ACC86517 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1229  
ID ACC89775 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1230  
ID ACC32954 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1231  
ID ACAT72582 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003022285-A1.  
PD 30-JAN-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1232  
ID ACA99100 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1233  
ID ACA9836 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1234  
ID ACA96979 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1235  
ID ACA90975 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1236  
ID ACA70757 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1237  
ID ACA95267 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1238  
ID ACC86210 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1239  
ID ACD45180 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane polypeptide PRO3566 cDNA.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1240  
ID ACC90082 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1241  
ID ACD12690 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1242  
ID ACF19920 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1243  
ID ABX76864 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1244  
ID ACA73196 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1245  
ID ACA86739 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1246  
ID ACA74583 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1247  
ID ACA70450 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.

PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1248  
ID ACD14636 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1249  
ID ACA93728 standard; cDNA; 1234 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO3566.  
PN US2003045694-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1250  
ID ACA68308 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1251  
ID ABX98773 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US20030316157-A1.  
PD 20-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1252  
ID ACA67302 standard; cDNA; 1234 BP.  
DE cDNA encoding human secreted polypeptide PRO3566.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1253  
ID ACC81250 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1254  
ID ACA95574 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US20030316155-A1.  
PD 20-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1255  
ID ACD04492 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1256  
ID ACC87933 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1257  
ID ACF12595 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.

PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1258  
ID ACH66275 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1259  
ID ACA96310 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1260  
ID ACA65084 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1261  
ID ACA73810 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1262  
ID ACA74222 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1263  
ID ACA96617 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1264  
ID ACD10723 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1265  
ID ACC91419 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1266  
ID ACD02754 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1267  
ID ACC87319 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003036165-A1.  
PD 20-FEB-2003.

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PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1278
ID ACA74890 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003022293-A1.
PD 30-JAN-2003.
ID ACC85903 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1279
ID ACA91761 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1280
ID ACA89320 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1281
ID ACA71405 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1282
ID ACC90805 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1283
ID ACA65815 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO protein #119.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1284
ID ACA68957 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1285
ID ACA94960 standard; cDNA; 1234 BP.
DE cDNA encoding human PRO polypeptide #119.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1286
ID ACD16522 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1287
ID ACD15601 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1288
ID ACD16215 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1274
ID ACD17376 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1275
ID ACD17376 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1276
ID ACC92033 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1277
ID ACD02329 standard; cDNA; 1234 BP.
DE Novel human secreted and transmembrane protein PRO3566 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 4.1%; Score 35.4; DB 8; Length 1234;
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RESULT 1288  
ID ACA98479 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #32.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1289  
ID ABX16704 standard; cDNA; 1234 BP.  
DE Human cDNA encoding secreted/transmembrane protein #119.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 8; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1290  
ID ACA33404 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #32.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1291  
ID ACA97645 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1292  
ID ACA99094 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1293  
ID ACC91726 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1294  
ID ACD11137 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1295  
ID ACD14987 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1296  
ID ACD11751 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1297  
ID ACC95880 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003036135-A1.  
PD 20-FEB-2003.

Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1298  
ID ACF16443 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1299  
ID ACF02561 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1300  
ID ACF02868 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1301  
ID ACF21455 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1302  
ID ACF10139 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1303  
ID ACF78032 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1304  
ID ACD46737 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1305  
ID ACD49500 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1306  
ID ACF28267 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;

Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1307  
ID ACD89957 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US200308682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1308  
ID ACD84352 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1309  
ID ACD99126 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1310  
ID ADA77989 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1311  
ID ACF48868 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1312  
ID ACD09188 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1313  
ID ACF11981 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1314  
ID ACF41215 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1315  
ID ACF15829 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1316  
ID ACF16136 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003040071-A1.

PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1317  
ID ACD31963 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1318  
ID ACF18771 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1319  
ID ACF09218 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1320  
ID ACF78339 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1321  
ID ACF51938 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064440-A1.  
PD 03-APR-2003.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1322  
ID ACF26425 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1323  
ID ACF24218 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1324  
ID ACF63529 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1325  
ID ACF50403 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
RESULT 1326  
ID ACH07874 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
RESULT 1327  
ID ACF13680 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
RESULT 1328  
ID ACD41606 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
RESULT 1329  
ID ACF32019 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
RESULT 1330  
ID ACF23297 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
RESULT 1331  
ID ACF39987 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
RESULT 1332  
ID ACD45509 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
RESULT 1333  
ID ACF53166 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
RESULT 1334  
ID ACF27346 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;

Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1335  
ID ACF45184 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
RESULT 1336  
ID ACF29802 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
RESULT 1337  
ID ACD89878 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
RESULT 1338  
ID ACD84659 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
RESULT 1339  
ID ACD98819 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
RESULT 1340  
ID ACF77111 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
RESULT 1341  
ID ACF76804 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
RESULT 1342  
ID ACF49789 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
RESULT 1343  
ID ACF50096 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
RESULT 1344  
ID ACD09495 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.

PN US2003036127-A1.  
PD 20-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1345  
ID ACD08574 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1346  
ID ACH03607 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane polypeptide PRO 3566 cDNA.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1347  
ID ACF12288 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1348  
ID ACC94796 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1349  
ID ACD22515 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1350  
ID ACF15215 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1351  
ID ACC97310 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1352  
ID ACC92340 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1353  
ID ACF13987 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1354

ID ACF14294 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1355  
ID ACF09525 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1356  
ID ACD45816 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1357  
ID ACD47965 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1358  
ID ACD67696 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1359  
ID ACF25504 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1360  
ID ACF29188 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1361  
ID ACD84966 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1362  
ID ACD84045 standard; cDNA; 1234 BP.  
DE Human PRO polynucleotide #119.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1363  
ID ACD88036 standard; cDNA; 1234 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1364  
ID ACF30723 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1365  
ID ACF32326 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1366  
ID ACHI1986 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1367  
ID ACHI2293 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1368  
ID ADA19925 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1369  
ID ACD40685 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1370  
ID ADB17308 standard; cDNA; 1234 BP.  
DE Human cDNA clone (SeqID 63) encoding the transmembrane PRO protein.  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1371  
ID ACF18157 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1372  
ID ACF08604 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003049778-A1.

PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1373  
ID ACF31405 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1374  
ID ACF52245 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1375  
ID ACD50114 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1376  
ID ACF38817 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1377  
ID ACF26732 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1378  
ID ACF24832 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1379  
ID ACF46412 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1380  
ID ACF27960 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1381  
ID ACD89264 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068684-A1.  
PD 10-APR-2003.



PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1382  
ID ACF63836 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1383  
ID ACF60476 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1384  
ID ACH12600 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1385  
ID ACH10023 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1386  
ID ACD03878 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1387  
ID ACD10416 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1388  
ID ACD12058 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1389  
ID ACF42443 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1390  
ID ACF18464 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1391  
ID ACF02254 standard; cDNA; 1234 BP.

DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1392  
ID ACF21762 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1393  
ID ACF10446 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1394  
ID ACF33898 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1395  
ID ACF44860 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1396  
ID ACD90492 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1397  
ID ACD91105 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1398  
ID ACF30416 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003087478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1399  
ID ACD87115 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1400  
ID ACF60169 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003073185-A1.

PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
PD 10-APR-2003.  
RESULT 1401  
ID ACF46719 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
PD 22-MAY-2003.  
RESULT 1402  
ID ACF75576 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
PD 17-APR-2003.  
RESULT 1403  
ID ADA79781 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003073173-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
PD 20-MAR-2003.  
RESULT 1404  
ID ACF17236 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
PD 27-MAR-2003.  
RESULT 1405  
ID ACF22990 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
PD 13-MAR-2003.  
RESULT 1406  
ID ACF07990 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
PD 13-MAR-2003.  
RESULT 1407  
ID ACF08297 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
PD 03-APR-2003.  
RESULT 1408  
ID ACF40601 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
PD 03-APR-2003.  
RESULT 1409  
ID ACF53780 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
PD 03-APR-2003.  
RESULT 1410  
ID ACF61397 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003096359-A1.

ID ACD47044 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
PD 10-APR-2003.  
RESULT 1411  
ID ACF47947 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
PD 10-APR-2003.  
RESULT 1412  
ID ACF47333 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
PD 10-APR-2003.  
RESULT 1413  
ID ACF46105 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
PD 10-APR-2003.  
RESULT 1414  
ID ACD86194 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
PD 01-MAY-2003.  
RESULT 1415  
ID ACF52552 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
PD 01-MAY-2003.  
RESULT 1416  
ID ACF52859 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
PD 01-MAY-2003.  
RESULT 1417  
ID ACF64852 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
PD 05-JUN-2003.  
RESULT 1418  
ID ACF76497 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
PD 05-JUN-2003.  
RESULT 1419  
ID ACF61397 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003096359-A1.

PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;  
Query Match  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1420  
ID ACF61704 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;  
Query Match  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1421  
ID ACD30735 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1422  
ID ACD31656 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1423  
ID ACD32577 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;  
Query Match  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1424  
ID ADA20097 standard; cDNA; 1234 BP.  
DE Novel human secreted and transmembrane protein PRO3566 cDNA.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;  
Query Match  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1425  
ID ACD82121 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane polypeptide PRO 3566 cDNA.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;  
Query Match  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1426  
ID ACF17543 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;  
Query Match  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1427  
ID ACF07376 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;  
Query Match  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1428  
ID ACF20534 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;  
Query Match

Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1429  
ID ACF20841 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1430  
ID ACF21148 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1431  
ID ACD47658 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;  
Query Match  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1432  
ID ACF47640 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;  
Query Match  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1433  
ID ACF53473 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;  
Query Match  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1434  
ID ACD86808 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;  
Query Match  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1435  
ID ACH05056 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;  
Query Match  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1436  
ID ACF44553 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;  
Query Match  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1437  
ID ADA81508 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;  
Query Match  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1438  
ID ACD22208 standard; cDNA; 1234 BP.

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DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PA (GETH ) GENENTECH INC. 50.3%; Pred. No. 54;
RESULT 1439
ID ACD24555 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US200304920-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PA (GETH ) GENENTECH INC. 50.3%; Pred. No. 54;
RESULT 1440
ID ACD39758 standard; cDNA; 1234 BP.
DE CDNA encoding human PRO polypeptide #119.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PA (GETH ) GENENTECH INC. 50.3%; Pred. No. 54;
RESULT 1441
ID ACD40065 standard; cDNA; 1234 BP.
DE CDNA encoding human PRO polypeptide #119.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1442
ID ACF13373 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1443
ID ACF03175 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1444
ID ACF78646 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1445
ID ACF11367 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PA (GETH ) GENENTECH INC. 50.3%; Pred. No. 54;
RESULT 1446
ID ACF50710 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PA (GETH ) GENENTECH INC. 50.3%; Pred. No. 54;
RESULT 1447
ID ACF34205 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1448
ID ACD46430 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1449
ID ACD48272 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1450
ID ACF27653 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1451
ID ACF24525 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1452
ID ACD85580 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1453
ID ACD90185 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1454
ID ACD83738 standard; cDNA; 1234 BP.
DE Human PRO polynucleotide #119.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1455
ID ACF49175 standard; cDNA; 1234 BP.
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;
PA (GETH ) GENENTECH INC. 50.3%; Pred. No. 54;
RESULT 1456
ID ACH07260 standard; cDNA; 1234 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #119.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC. 4.1%; Score 35.4; DB 9; Length 1234;
Best Local Similarity 50.3%; Pred. No. 54;
RESULT 1457
ID ACH07567 standard; cDNA; 1234 BP.
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DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1458  
ID ACH08181 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1459  
ID ACH11372 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1460  
ID ACH11679 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1461  
ID ACH10330 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1462  
ID ACF01333 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1463  
ID ACF40908 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1464  
ID ACD24248 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1465  
ID ACD31349 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1466  
ID ACF17850 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1467  
ID ACF32633 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1468  
ID ACF40294 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1469  
ID ACF48254 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064441-A1.  
PD 03-APR-2003.  
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Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1470  
ID ACF38203 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1471  
ID ACF25139 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1472  
ID ACF27039 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1473  
ID ACF29495 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1474  
ID ACD87729 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1475  
ID ACF76190 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1476

RESULT 1486  
ID ACC94489 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054467-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
Pred. No. 54;  
RESULT 1477  
ID ACC43939 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
Pred. No. 54;  
RESULT 1478  
ID ACH06284 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
Pred. No. 54;  
RESULT 1479  
ID ACH06591 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
Pred. No. 54;  
RESULT 1480  
ID ADA03306 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
Pred. No. 54;  
RESULT 1481  
ID ACC92647 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
Pred. No. 54;  
RESULT 1482  
ID ACC93261 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
Pred. No. 54;  
RESULT 1483  
ID ACF19306 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
Pred. No. 54;  
RESULT 1484  
ID ACD12997 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
Pred. No. 54;  
RESULT 1485  
ID ACF06455 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
Pred. No. 54;

RESULT 1486  
ID ACC94489 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
Pred. No. 54;  
RESULT 1487  
ID ACC97917 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
Pred. No. 54;  
RESULT 1488  
ID ACC94182 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
Pred. No. 54;  
RESULT 1489  
ID ACF42136 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
Pred. No. 54;  
RESULT 1490  
ID ACB31042 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
Pred. No. 54;  
RESULT 1491  
ID ACD43071 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
Pred. No. 54;  
RESULT 1492  
ID ACD43378 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
Pred. No. 54;  
RESULT 1493  
ID ACF14908 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
Pred. No. 54;  
RESULT 1494  
ID ACF01640 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.1%; Score 35.4; DB 9; Length 1234;  
Pred. No. 54;  
RESULT 1495  
ID ACF31712 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003064469-A1.  
PD 03-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1496  
ID ACD67389 standard; cDNA; 1234 BP.  
DE cDNA encoding human PRO polypeptide #119.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1497  
ID ACD48579 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1498  
ID ACD48886 standard; cDNA; 1234 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #119.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1499  
ID ACF51324 standard; cDNA; 1234 BP.  
DE Human secreted polypeptide PRO3566-encoding cDNA, SEQ ID NO:237.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.1%; Score 35.4; DB 9; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;  
RESULT 1500  
ID AEF74278 standard; cDNA; 1234 BP.  
DE Human PRO3566 encoding cDNA SEQ ID NO:63.  
PN US2005260647-A1.  
PD 24-NOV-2005.  
PA (EATO/) EATON D L.  
PA (FILV/) FILVAROFF E.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W L.  
Query Match 4.1%; Score 35.4; DB 15; Length 1234;  
Best Local Similarity 50.3%; Pred. No. 54;

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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 3, 2006, 09:03:50 ; Search time 5165 Seconds

(without alignments)  
9419.132 Million cell updates/sec

**Title:** US-10-015-967-1

**Perfect score:**

Sequence: 1 ctgcccctcaaatgggaacg.....tcaaaaaaaaaaaaaaaaaa 870

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1500 summaries

Database :

1: qb est1:\*

2: qb\_est3: \*

3: gb\_est4: \*

4: gb\_est5:★

5: gb\_est6:★

6: gb\_htc:\*

7: gb\_est2:\*

8: gb\_est7:\*

9: gb\_est8: \*

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10: gb_est9:
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11: gb\_gss1:

12: gb\_gss2:

13: gb\_gb3:

14: gb\_9884:

Prod No is the number

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Match	Score	Length	DB	ID	Description	
C	1	725	83.3	748	4	CB242167	UI - CF - FNO	
	2	685.8	78.8	715	3	BM982101	UI - CF - EN1	
	3	682.8	78.5	753	3	BM978124	UI - CF - EC1	
	4	679.4	78.1	693	10	DR422006	navo6g10	
	5	677	77.8	677	3	BM769732	K - EST0053	
	6	675.6	77.7	820	4	BI177094	603059769	
	7	671	77.1	671	4	EX102380	BK102380	
	8	666	76.6	666	3	BM831028	K - EST0104	
	9	664	76.3	664	3	BM854000	K - EST0136	
	10	622	71.5	628	9	DN998063	TC195256	
C	11	621.4	71.4	628	9	DN998245	TC124609	
	12	607.8	69.9	631	5	CD688783	EST5305 h	
	13	607.2	69.8	628	3	BU746867	K - EST0021	
	14	590.4	67.9	592	3	BU682452	UI - CF - EC1	
	15	589	67.7	589	9	DB236758	DB236758	
	16	582.6	67.0	613	2	BG536626	602566231	
	17	579	66.6	615	3	BM766904	K - EST0048	
	18	575.6	66.2	594	3	BM743525	K - EST0016	
	19	573.8	66.0	578	3	BM979898	UI - CF - EN1	

93 266.8 30.7 270 3 BM855784  
94 264.4 30.4 421 4 CB434699  
C 95 263 30.2 263 7 BF055365  
C 96 263 30.2 263 7 BE645174  
97 262.2 30.1 643 4 BV731153  
98 262.2 30.1 649 6 BK143005  
99 259.4 29.8 479 7 BE624584  
100 258.6 29.7 605 1 AA537274  
C 101 258.4 29.7 575 4 CB450481  
102 258.2 29.6 541 4 BX520414  
103 257.8 29.6 466 1 AA881969  
104 257.8 29.6 484 1 AA789593  
C 105 255 29.3 255 1 AI207071  
106 253.4 29.1 433 7 BE197231  
107 252.8 29.1 913 10 DV047460  
C 108 247.4 28.4 834 4 CB952075  
109 245.8 28.3 298 5 CD707468  
C 110 241.2 27.7 271 7 BE181362  
111 240.4 27.6 829 2 BI078998  
112 240.4 27.6 1279 2 BG535485  
C 113 239.2 27.5 556 8 CK980826  
114 238 27.4 242 1 AA477092  
115 234 26.9 251 2 BF743524  
116 224.4 25.8 390 10 DY092442  
C 117 220 25.3 533 4 CB420505  
C 118 219 25.2 254 7 AW389442  
119 218.2 25.1 267 2 BF743520  
C 120 218 25.1 232 1 AI747423  
121 213.8 24.6 227 1 AI680037  
122 210.6 24.2 273 10 DY071286  
C 123 209.6 24.1 242 7 BF089449  
C 124 203 23.3 472 4 CB435186  
125 201.2 23.1 579 12 CG691642  
C 126 195 22.2 253 7 BF088641  
C 127 193.2 22.2 279 1 AI758852  
C 128 190.4 21.9 241 7 BF089451  
129 189 21.7 191 4 CO0521  
130 185.4 21.3 422 7 BF652670  
131 176.2 20.3 223 7 AW797203  
C 132 175.6 20.2 311 4 CB696926  
C 133 139.8 16.1 144 2 AA074399  
C 134 136.4 15.7 424 2 BF945955  
135 136.2 15.7 213 2 BG938127  
C 136 133.6 15.4 415 3 BQ380575  
C 137 126.6 14.6 401 1 AI276273  
C 138 120.4 13.8 465 1 AI463349  
C 139 118 13.6 167 7 AW797186  
C 140 114 13.1 143 3 BU674435  
141 103.8 11.9 571 9 DA763751  
C 142 100.4 11.5 631 12 CB250770  
C 143 93.6 10.8 360 1 AI375133  
C 144 89.6 10.3 251 4 CB220287  
C 145 82.6 9.5 454 14 CR873527  
C 146 78.4 9.0 398 12 CG491802  
147 78 9.0 128 5 CD586654  
C 148 69.8 8.0 610 14 CR833969  
C 149 69.2 8.0 596 2 BG381659  
C 150 69 7.9 485 14 DU513069  
151 66.6 7.7 780 11 A2960058  
152 65.4 7.5 696 11 A2804554  
153 65 7.5 364 3 BU677228  
C 154 58.2 6.7 1080 14 CN000EPP  
C 155 55.8 6.4 1101 14 CN730176  
C 156 54 6.2 478 8 CN730176  
C 157 49.2 5.7 1272 9 DN810334  
C 158 49 5.6 329 1 AI810721  
C 159 48 5.5 863 7 BE964633  
C 160 47.8 5.5 569 9 DN900142  
C 161 47.8 5.5 836 10 DV785142  
C 162 47.4 5.4 1300 10 DV792998  
C 163 46.4 5.3 835 5 CJ442368  
C 164 46.2 5.3 371 3 BQ196067  
C 165 46.2 5.3 959 14 CNS01407

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167 45.6 5.2 1101 14 CNS00LOO  
C 168 45.6 5.2 1101 14 CNS0106X  
C 169 45.2 5.2 509 9 DN524243  
C 170 45.2 5.2 912 9 DN569400  
C 171 45.2 5.2 957 10 DT804263  
C 172 45 5.2 971 9 DN561756  
C 173 44.6 5.1 389 1 AI301631  
C 174 44.6 5.1 431 14 CNS04J60  
C 175 44.4 5.1 983 2 BG622358  
C 176 44.2 5.1 386 8 CV999880  
C 177 44.2 5.1 1316 7 BE955081  
C 178 44 5.1 465 9 CX803105  
C 179 44 5.1 808 14 DU958240  
C 180 44 5.1 837 8 CN169807  
C 181 44 5.1 989 11 AZ536271  
C 182 44 5.1 1033 9 DN573003  
C 183 44 5.1 3491 6 AK155463  
C 184 43.8 5.0 684 11 AQ894677  
C 185 43.8 5.0 892 9 DN573579  
C 186 43.8 5.0 895 14 CNS0071A  
C 187 43.8 5.0 898 14 CNS00JQC  
C 188 43.8 5.0 923 3 BU588149  
C 189 43.8 5.0 939 14 CNS00CNG  
C 190 43.8 5.0 1101 14 CNS0181N  
C 191 43.6 5.0 302 10 DY365008  
C 192 43.4 5.0 640 9 DN414095  
C 193 43.4 5.0 258 11 AZ808132  
C 194 43.4 5.0 355 2 BI111761  
C 195 43.4 5.0 428 5 CU310586  
C 196 43.4 5.0 640 8 CX331766  
C 197 43.4 5.0 652 9 DN873829  
C 198 43.2 5.0 456 3 BQ197844  
C 199 43.2 5.0 884 14 CNS00600  
C 200 43 4.9 615 2 BI521894  
C 201 43 4.9 661 9 DN872401  
C 202 43 4.9 873 5 CD251221  
C 203 43 4.9 967 11 BH154293  
C 204 42.8 4.9 412 9 DN903185  
C 205 42.8 4.9 474 7 BE848199  
C 206 42.8 4.9 485 14 DE136007  
C 207 42.8 4.9 683 4 BY724873  
C 208 42.8 4.9 761 14 CNS02MEY  
C 209 42.8 4.9 802 5 CK128354  
C 210 42.8 4.9 1322 7 BE966081  
C 211 42.6 4.9 155 1 AA162707  
C 212 42.6 4.9 354 9 CX428158  
C 213 42.6 4.9 379 7 BE231815  
C 214 42.6 4.9 410 5 CU321550  
C 215 42.6 4.9 413 5 CF404793  
C 216 42.6 4.9 425 1 AI796113  
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C 218 42.6 4.9 635 3 BU063136  
C 219 42.6 4.9 727 4 CA164504  
C 220 42.6 4.9 826 8 CR433419  
C 221 42.6 4.9 855 14 AG135519  
C 222 42.4 4.9 280 8 CN211523  
C 223 42.4 4.9 438 8 CO895118  
C 224 42.4 4.9 601 4 BX550992  
C 225 42.4 4.9 619 2 BI799499  
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C 228 42.4 4.9 821 1 AL047047  
C 229 42.4 4.9 866 5 CK413099  
C 230 42.4 4.9 913 14 AG396212  
C 231 42.4 4.9 926 2 BI524254  
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C 234 42.2 4.9 423 4 CB280289  
C 235 42.2 4.9 455 5 CJ263805  
C 236 42.2 4.9 508 4 CA365670  
C 237 42.2 4.9 517 9 DN868818  
C 238 42.2 4.9 534 3 BQ085821

C90175 C90175 Dict  
AL068607 Drosophil  
AL095895 Drosophil  
DN354243 Mesod2318  
DN569400 93812657  
DT804263 127363864  
DN561756 88080644  
AI301631 qn17h09.x  
AI290145 Tetraodon  
BG622358 602647045  
CV999880 1573904.b  
BE965081 601658868  
CX803105 JGI\_CAAJ1  
DU958240 225373 To  
CN169807 AGENCOURT  
DN573003 92937986  
AK155463 Mus muscu  
AO894677 HS\_3143\_B  
DN573579 92289141  
AL066286 Drosophil  
BU588149 AGENCOURT  
AL059400 Drosophil  
AI108773 Drosophil  
DY365008 ZO\_Ee000  
DN414095 LiBZ15-0  
AZ808132 2M0071H07  
BI111761 602897921  
CU310586 CJ310586  
CX331766 JGI\_XZT17  
DN873829 nad39a12  
BQ197844 NXLV121.D  
AL065923 Drosophil  
BI521894 603081323  
DN872401 nad19g07.  
CD251221 AGENCOURT  
BH154293 ENTQV43TF  
DN903185 naq44h08.  
BE848199 us36d05.y  
DE136007 Oryzias 1  
BY724873 BY724873  
AL204019 Tetraodon  
CK128354 AGENCOURT  
BE966081 601659991  
AA162707 mm4c02.r  
CX428158 JGI\_XZG18  
BE231815 136644 MA  
CU321550 CJ321550  
CF404793 CSECS068E  
AI796113 wh42e07.x  
DT396095 JGI\_CABH1  
BU063136 Fgr\_2\_L12  
CA164504 SCJFRT205  
CR433419 CR433419  
AG135519 Pan trogl  
CN211523 rzhewab0  
CO895118 Bxvgen\_23  
BX550992 US350992  
BI799499 H134B02.E  
DN886591 naf37h04.  
AL105420 Drosophil  
AL047047 DKF2p5860  
CK413099 AUF\_lpG11  
AG396212 Mus muscu  
BI524254 603052055  
BG555702 df19g02.x  
C90082 C90082 Dict  
CB280289 tu43h09.y  
CJ263805 CJ263805  
CA365670 640857 NC  
DN868818 nac36d04.  
BQ085821 1i10d05.y

239	42.2	4.9	536	9	CX733097	CX733097 oc39b09.y	312	4.7	41	4.7	353	5	CF382108	CF382108 lab96h07.
240	42.2	4.9	544	4	CB979855	CB979855 CAB70001_	313	4.7	41	4.7	412	5	CJ310210	CJ310210 CJ310210
241	42.2	4.9	694	10	DV624532	DV624532 94087.1.C	314	4.7	435	4.7	435	5	CJ305667	CJ305667 CJ305667
242	42.2	4.9	837	9	DN053786	DN053786 JGI CABAB	315	4.7	41	4.7	470	9	CX572103	CX572103 TT8000183
243	42.2	4.9	1000	12	CL111647	CL111647 TSB1-5539	316	4.7	41	4.7	502	10	DT928899	DT928899 BMSB11813
244	42	4.8	303	8	CO081908	CO081908 GR_R446E	317	4.7	41	4.7	544	5	CK789750	CK789750 AGENCOURT
245	42	4.8	342	9	CS168327	CS168327 LJB3731-0	318	4.7	41	4.7	548	4	CB723280	CB723280 UI-M-GKO-
246	42	4.8	419	3	BU551636	BU551636 mail18d05.	319	4.7	41	4.7	551	8	CO814978	CO814978 AGENCOURT
247	42	4.8	552	5	CK086699	CK086699 AmeF214.L	C 320	4.7	41	4.7	620	8	CR431617	CR431617 CR431617
248	42	4.8	859	14	CNS004YV	AL055406 Drosophil	321	4.7	41	4.7	652	10	DT101207	DT101207 JGI ANNS
249	42	4.8	1101	14	CNS00KCF	AL077499 Drosophil	322	4.7	41	4.7	688	8	CV529650	CV529650 ALV_011B
250	42	4.8	1238	13	CL646737	CL646737 CH213-122	323	4.7	41	4.7	717	8	CN842704	CN842704 AGENCOURT
251	41.8	4.8	176	5	CS176859	CR76859 lan68h02.	324	4.7	41	4.7	744	5	CK797902	CK797902 AGENCOURT
252	41.8	4.8	279	10	BR430456	BR430456 max30g06.	325	4.7	41	4.7	786	8	CX134193	CX134193 AGENCOURT
253	41.8	4.8	317	4	DX481768	DX481768 DXP2p6861	326	4.7	41	4.7	810	3	BU944974	BU944974 AGENCOURT
254	41.8	4.8	423	2	BF724797	BF724797 bx08g10.x	327	4.7	41	4.7	849	2	BG110577	BG110577 602281019
255	41.8	4.8	448	9	DN866491	DN866491 nsc22b04.	C 328	4.7	41	4.7	859	14	CNS00KLL	AL077728 Drosophil
256	41.8	4.8	635	10	DT841689	DT841689 LB00460.C	C 329	4.7	41	4.7	893	8	CR564211	CR564211 CR564211
257	41.8	4.8	678	14	CR003486	CR003486 Forward s	330	4.7	41	4.7	928	5	CK022959	CK022959 AGENCOURT
258	41.8	4.8	719	11	B21675	B21675 F17P15-Sp6	331	4.7	41	4.7	937	14	AG466365	AG466365 Mus muscu
259	41.8	4.8	913	5	CK416843	CK416843 AUF IpInt	C 332	4.7	41	4.7	938	10	DW637916	DW637916 CLJ368-C2
260	41.8	4.8	935	13	CZ519146	CZ519146 GNM2-8211	C 333	4.7	41	4.7	951	10	DT799609	DT799609 126446838
261	41.8	4.8	1030	13	CL492173	CL492173 SAIL_564	C 334	4.7	41	4.7	104	2	BJ366707	BJ366707 BJ366707
262	41.8	4.8	1041	10	DT798111	DT798111 126435162	335	4.7	41	4.7	195	5	CF546382	CF546382 labg72803.
263	41.8	4.8	1101	14	CNS000D1	AL065414 Drosophil	C 336	4.7	41	4.7	315	5	CF318708	CF318708 HD--08-P0
264	41.8	4.8	1101	14	CNS0167Y	AL106840 Drosophil	337	4.7	41	4.7	362	10	DV079721	DV079721 B15SFmidg
265	41.8	4.8	1766	7	BF683714	BF683714 602139978	338	4.7	41	4.7	384	8	CX311212	CX311212 JGI X2T11
266	41.6	4.8	158	5	CF383869	CF383869 lac11c07	C 339	4.7	41	4.7	386	8	CX125202	CX125202 1325194.N
267	41.6	4.8	316	10	DR446496	DR446496 AR1032E06	340	4.7	41	4.7	421	8	CX026756	CX026756 1338219.N
268	41.6	4.8	377	12	CE245314	CE245314 tigr-g88-	341	4.7	41	4.7	447	4	BY465334	BY465334 BY465334
269	41.6	4.8	381	5	CK381710	CK381710 lag29a09.	C 342	4.7	41	4.7	475	4	BX566461	BX566461 BX566461
270	41.6	4.8	385	5	CK381768	CK381768 lag29a04.	C 343	4.7	41	4.7	483	14	CR836821	CR836821 GR0AA471A
271	41.6	4.8	405	1	CF354661	CF354661 lac16b05.	C 344	4.7	41	4.7	507	4	CA344051	CA344051 B74365.NC
272	41.6	4.8	489	1	AL664772	AL664772 AL664772	345	4.7	41	4.7	510	4	CA344051	CA344051 B74365.NC
273	41.6	4.8	572	1	AL727326	AL727326 AL727326	346	4.7	41	4.7	547	8	CN728405	CN728405 13JKNW2
274	41.6	4.8	591	9	DN975655	DN975655 CT07_85.T	347	4.7	41	4.7	563	9	DN895807	DN895807 nap01C03.
275	41.6	4.8	596	9	DN870799	DN870799 nad09b10.	C 348	4.7	41	4.7	592	3	BM671350	BM671350 UI-E-CKI-
276	41.6	4.8	737	12	CC910523	CC910523 t061n19ba	C 349	4.7	41	4.7	617	4	BF560294	BF560294 BX560294
277	41.6	4.8	921	5	CF585473	CF585473 AGENCOURT	C 350	4.7	41	4.7	752	5	CF519392	CF519392 AGENCOURT
278	41.4	4.8	252	8	CX068628	CX068628 1320073.N	C 351	4.7	41	4.7	756	4	CB243933	CB243933 UI-CF-FN0
279	41.4	4.8	256	2	BJ680202	BJ680202 BJ680202	C 352	4.7	41	4.7	790	10	DT254385	DT254385 JGI_CAAU6
280	41.4	4.8	434	3	BU958142	BU958142 AGENCOURT	C 353	4.7	41	4.7	843	4	BX710027	BX710027 BX710027
281	41.4	4.8	462	1	AI125744	AI125744 q991b02.x	C 354	4.7	41	4.7	876	10	DR549024	DR549024 WS03214.C
282	41.4	4.8	496	10	DT424714	DT424714 JGI CABY5	C 355	4.7	41	4.7	921	10	DT068969	DT068969 AGENCOURT
283	41.4	4.8	595	1	AM035555	AM035555 AM035555	C 356	4.7	41	4.7	964	10	DT776388	DT776388 125250650
284	41.4	4.8	690	8	CV666124	CV666124 LCPB04EX0	C 357	4.7	41	4.7	1083	7	BE965014	BE965014 601658792
285	41.4	4.8	951	14	CNS0157Z	AL105905 Drosophil	358	4.7	41	4.7	1117	2	BG766575	BG766575 602733344
286	41.4	4.8	1056	12	CC306139	CC306139 CH261-129	C 359	4.7	41	4.7	1438	2	BF781133	BF781133 602108779
287	41.4	4.8	1101	14	CNS0039E	AL063919 Drosophil	C 360	4.7	41	4.7	1645	7	BE962684	BE962684 601656058
288	41.4	4.8	1101	14	CNS0180X	AL108747 Drosophil	C 361	4.7	41	4.7	4022	6	BC029662	BC029662 Homo sapi
289	41.2	4.7	234	5	CF511149	CF511149 Cabud0002	362	4.7	41	4.7	153	5	CK374496	CK374496 lai78c08.
290	41.2	4.7	289	2	EG018795	EG018795 daa56e11.	C 363	4.7	41	4.7	225	1	AA724507	AA724507 a104g08.8
291	41.2	4.7	405	5	CF639220	CF639220 D12.G10.F	364	4.7	41	4.7	235	3	BQ610416	BQ610416 sap41804.
292	41.2	4.7	430	8	CN831162	CN831162 EL845.Bra	C 365	4.7	41	4.7	245	2	BI291129	BI291129 UI-R-DK0-
293	41.2	4.7	544	8	CO881720	CO881720 BovGen.10	366	4.7	41	4.7	271	2	BG146874	BG146874 mab96f09.
294	41.2	4.7	566	7	BF410536	BF410536 UI-R-CAO-	367	4.7	41	4.7	314	5	CF754869	CF754869 lae07d02.
295	41.2	4.7	594	5	CK935674	CK935674 CGF100455	368	4.7	41	4.7	327	8	CO182751	CO182751 EC23873.5
296	41.2	4.7	599	3	BQ746546	BQ746546 UI-M-PAO-	369	4.7	41	4.7	332	5	CK384472	CK384472 lab25d06
297	41.2	4.7	625	14	CNS036A2	AL229763 Tetraodon	370	4.7	41	4.7	338	8	CO192780	CO192780 EC34473.5
298	41.2	4.7	706	10	DY360654	DY360654 ZO_Ed000	371	4.7	41	4.7	346	5	CF382593	CF382593 lac88g07.
299	41.2	4.7	716	13	CL514121	CL514121 SAIL_883	372	4.7	41	4.7	383	5	CF382551	CF382551 lac88a12.
300	41.2	4.7	792	10	DT773642	DT773642 125583905	373	4.7	41	4.7	385	5	CF356034	CF356034 lab77b02.
301	41.2	4.7	844	5	CF883043	CF883043 ttrc032x3	374	4.7	41	4.7	395	8	CR544106	CR544106 DKF2P470M
302	41.2	4.7	928	13	CZ510468	CZ510468 GNM2-5812	375	4.7	41	4.7	410	3	BM567429	BM567429 k15a09.y
303	41.2	4.7	960	4	BX375427	BX375427 BX375427	C 376	4.7	41	4.7	437	2	BI293909	BI293909 UI-R-DK0-
304	41.2	4.7	987	14	CNS000418	AL065537 Drosophil	C 377	4.7	41	4.7	439	7	AW632847	AW632847 b101a07.x
305	41.2	4.7	1004	10	DV072413	DV072413 VP01.12.O	378	4.7	41	4.7	448	5	CF803224	CF803224 r959g04.y
306	41.2	4.7	1334	10	DV786702	DV786702 Hw_liver_	379	4.7	41	4.7	448	5	CF803224	CF803224 r959g04.y
307	41.2	4.7	3347	6	AK139104	AK139104 Mus_muscu	380	4.7	41	4.7	449	3	BP483514	BP483514 BP483514
308	41	4.7	158	5	CF353009	CF353009 lab60e05.	C 381	4.7	41	4.7	471	1	AI890026	AI890026 wms0g06.x
309	41	4.7	273	7	AW164794	AW164794 se77h06.y	C 382	4.7	41	4.7	493	5	CF546442	CF546442 lae73f11.
310	41	4.7	277	1	AU261831	AU261831 AU261831	C 383	4.7	41	4.7	505	7	AW632884	AW632884 b101d08.x
311	41	4.7	300	4	BX476421	BX476421 DKF2p686A	384	4.7	41	4.7	509	8	CO883450	CO883450 BovGen_11

385	40.6	4.7	533	11	AZ052908	RPCI-23-4	458	40	4.6	394	5	CF383901	lac11903.
386	40.6	4.7	568	5	CF554171	AGENCOURT	459	40	4.6	414	5	CJ322462	CJ322462
387	40.6	4.7	596	3	BM936065	UI-N-B21-	c	460	4.6	416	9	DN872226	mad18f09.
388	40.6	4.7	636	12	CC563671	CH240.475	461	40	4.6	421	3	BU774346	SJEGKA06
389	40.6	4.7	652	2	B1274223	UI-R-CW0-	c	462	4.6	456	4	CA451405	UI-M-FV0-
390	40.6	4.7	662	1	AL889632	AL889632	c	463	4.6	455	4	CB461292	721246.MA
391	40.6	4.7	776	14	AG607515	Mus muscu	464	40	4.6	472	2	BJ338254	BJ338254
392	40.6	4.7	781	14	CNS009DO	AL053444	c	465	4.6	480	1	AA956345	UI-R-E1-f
393	40.6	4.7	792	8	CV470318	CV470318	466	40	4.6	485	1	AU051956	AU051956
394	40.6	4.7	851	3	BU954498	AGENCOURT	467	40	4.6	495	1	AM031205	AM031205
395	40.6	4.7	869	14	DX075355	KB-B086E2	468	40	4.6	508	8	CN986100	61682.125
396	40.6	4.7	872	4	BX752799	BX752799	c	469	4.6	512	14	CR801511	CR801511
397	40.6	4.7	904	10	DT770997	125680637	c	470	4.6	547	9	DN975983	CT12.22.T
398	40.6	4.7	929	4	DX760619	BX760619	c	471	4.6	550	2	BI293646	UI-R-DK0-
399	40.6	4.7	954	10	DT804783	127377390	472	40	4.6	558	1	AJ931852	AJ931852
400	40.6	4.7	1101	14	CNS00HTH	AL074023	473	40	4.6	563	8	CX328448	JGI.XZT67
401	40.6	4.7	1101	14	CNS01720	AL107514	c	474	4.6	573	4	CB615111	AMGNNUC:U
402	40.6	4.7	1149	10	DV623046	DV623046	475	40	4.6	591	10	DT835946	LB00432.C
403	40.6	4.7	1204	14	AG332691	AG332691	476	40	4.6	605	4	C8588300	AGENCOURT
404	40.4	4.6	174	5	CF606084	RADIC01_0	477	40	4.6	614	5	CJ793633	tr53d05.x
405	40.4	4.6	249	9	CX799674	CX799674	478	40	4.6	622	1	AI587114	AI587114
406	40.4	4.6	372	5	CF583967	AGENCOURT	c	479	4.6	637	10	DM260609	DM260609
407	40.4	4.6	389	2	BG237082	sa97a09.	c	480	4.6	645	11	AZ421486	IM0199G17
408	40.4	4.6	415	5	CJ304128	CJ304128	c	481	4.6	669	9	DN815169	DN815169
409	40.4	4.6	482	4	BX549422	BX549422	c	482	4.6	669	10	DM023562	UI-S-GB1-
410	40.4	4.6	500	5	CK379767	CK379767	483	40	4.6	697	1	AM006156	AM006156
411	40.4	4.6	578	10	DR404052	CSAG-PNP1	484	40	4.6	768	5	CJ439911	CJ439911
412	40.4	4.6	590	9	CX573023	CX573023	485	40	4.6	802	3	BU556118	BU556118
413	40.4	4.6	625	11	B29043	T24J14TF.TA	486	40	4.6	819	14	AG469163	Mus muscu
414	40.4	4.6	625	14	CNS036A2	AL229763	c	487	4.6	879	14	CNS00BVO	AG469163
415	40.4	4.6	753	9	DN838005	DN838005	c	488	4.6	897	10	DT772513	Drosophi1
416	40.4	4.6	838	3	BU587874	AGENCOURT	c	489	4.6	930	10	DV075519	125665216
417	40.4	4.6	851	9	DN582583	DN582583	490	40	4.6	935	10	DV055423	DT772513
418	40.4	4.6	931	5	CK413737	AUF.IPG11	c	491	4.6	951	10	DT782856	WT1291190
419	40.4	4.6	997	9	DN571222	DN571222	492	40	4.6	958	10	DV069817	DV055423
420	40.4	4.6	1037	10	DV075133	WT1291190	493	40	4.6	959	10	DV069681	125636838
421	40.4	4.6	1152	2	BG309087	BG309087	494	40	4.6	968	10	DV071065	VP01.02.L
422	40.4	4.6	1184	2	DT088615	DT088615	495	40	4.6	991	10	DV070926	VP01.02.C
423	40.4	4.6	1221	14	CNS0169U	AL106476	496	40	4.6	993	10	DV053532	VP01.08.I
424	40.4	4.6	1615	6	AK043740	Mus muscu	497	40	4.6	994	10	DV073491	VP01.16.L
425	40.2	4.6	155	5	CF331482	NACH.-07-	498	40	4.6	995	10	DV071636	VP01.10.C
426	40.2	4.6	180	5	CK377194	lah99e05.	499	40	4.6	1004	10	DV047751	DAV20.18
427	40.2	4.6	242	2	BM434360	BM434360	500	40	4.6	1022	10	DV051526	DAV35.03-
428	40.2	4.6	249	4	CB964409	Ac2282.Ra	501	40	4.6	1042	10	DV074506	DAV35.03-
429	40.2	4.6	275	10	DV769182	DV769182	502	40	4.6	1042	10	DV074507	VP01.19.J
430	40.2	4.6	291	3	BQ785586	BQ785586	503	40	4.6	1069	10	DV073397	VP01.13.J
431	40.2	4.6	340	5	CF529645	UI-1-BC1p	c	504	4.6	1101	14	CNS0006J	VP01.16.G
432	40.2	4.6	387	1	AI139546	AI139546	505	40	4.6	1101	14	CNS01844	AL108862
433	40.2	4.6	418	1	AI395043	MA002273.	506	40	4.6	1102	10	DV074951	Drosophi1
434	40.2	4.6	447	4	CA945634	CA945634	c	507	4.6	1147	9	DR124836	VP01.20.K
435	40.2	4.6	488	10	DV865683	DV865683	508	40	4.6	1167	10	DV047372	DR124836
436	40.2	4.6	494	3	BQ521094	BQ521094	c	509	4.6	1495	7	BF541123	49114046-
437	40.2	4.6	569	8	CO100558	CO100558	510	40	4.6	3138	6	HS807377	DAV20.17-
438	40.2	4.6	589	9	DN877170	nae1lg06.	511	39.8	4.6	172	1	AA162226	602068734
439	40.2	4.6	615	4	CB194319	CB194319	512	39.8	4.6	206	10	DV862573	AA162226
440	40.2	4.6	646	10	DT110892	DT110892	513	39.8	4.6	280	8	CN472566	CRP2305.C
441	40.2	4.6	713	1	AJ815888	AJ815888	514	39.8	4.6	305	9	DN798248	USDA-FP.1
442	40.2	4.6	849	10	DT771619	DT771619	515	39.8	4.6	356	5	CK936931	USDA-FP.7A
443	40.2	4.6	884	10	DT771925	DT771925	516	39.8	4.6	396	2	BI941650	CGF100451
444	40.2	4.6	943	4	CB202689	CB202689	517	39.8	4.6	396	3	BM999663	SC82c02.Y
445	40.2	4.6	1024	9	DN575349	DN575349	518	39.8	4.6	407	7	BE787416	UI-H-DI0-
446	40.2	4.6	1173	2	BG290683	BG290683	519	39.8	4.6	487	4	BX555510	UI-H-BI0p
447	40.2	4.6	1203	2	BM466037	BM466037	c	520	4.6	487	4	BX555510	601479554
448	40.2	4.6	2362	6	CR859135	Pong9.PVG	521	39.8	4.6	514	9	CX368966	BX555510
449	40.2	4.6	130	1	AU037910	AU037910	522	39.8	4.6	546	9	CK740718	JGI.XZT54
450	40.2	4.6	152	5	CK428770	CK428770	523	39.8	4.6	553	3	BM860273	fy36c02.Y
451	40.2	4.6	162	8	CN796620	DN801055	524	39.8	4.6	580	4	CA337315	NISC.lv11
452	40.2	4.6	169	8	CN797086	DN800781	525	39.8	4.6	580	8	CO804381	AGENCOURT
453	40.2	4.6	245	9	DN237176	EST00301	526	39.8	4.6	620	8	CV920665	PH048A.C
454	40.2	4.6	251	2	BU702291	BU702291	c	527	4.6	733	4	CB510691	98a1rwH50
455	40.2	4.6	298	3	BU587978	AGENCOURT	528	39.8	4.6	753	4	C8599054	AGENCOURT
456	40.2	4.6	375	5	CF425838	lad45a03.	529	39.8	4.6	845	5	CK397453	CK397453
457	40.2	4.6	377	5	CF804787	lad79h06.	530	39.8	4.6	857	8	CN384732	LE2TR01L1

C 531	39.8	4.6	954	10	DT802126	DT802126 126488246	C 604	39.6	4.6	1193	2	BG428284	BG428284 602498959
C 532	39.8	4.6	996	10	DT784459	DT784459 127494684	C 605	39.6	4.6	1207	9	DR149283	DR149283 49350707
C 533	39.8	4.6	997	14	CNS0005TE	AL060767 Drosophila	C 606	39.6	4.6	2769	6	CR858102	CR858102 Pongo pyg
534	39.8	4.6	1025	10	DT780188	DT780188 125260844	607	39.4	4.5	166	2	BI703589	BI703589 rs73c03.y
535	39.6	4.6	185	2	BI943092	BI943092 8n28g12.y	608	39.4	4.5	186	9	DN872128	DN872128 nad18a08.
536	39.6	4.6	200	1	AU038268	AU038268 AU038268	609	39.4	4.5	209	3	BUS30885	BUS30885 AGENCOURT
537	39.6	4.6	210	5	CF123088	CF123088 UT-HF-CHO	C 610	39.4	4.5	212	5	CF613319	CF613319 1a1f27h09.
538	39.6	4.6	220	10	DM445757	DM445757 HHAGE0434	C 611	39.4	4.5	231	7	AW235745	AW235745 xm45c08.x
539	39.6	4.6	241	10	DN076574	DN076574 F21SFmldg	C 612	39.4	4.5	296	8	CV953285	CV953285 pVrpbv.98
C 540	39.6	4.6	245	9	DN237176	DN237176 EST00301	613	39.4	4.5	306	2	BI945447	BI945447 eb86g12.y
541	39.6	4.6	258	7	AW598484	AW598484 BJ44D05.y	614	39.4	4.5	306	3	BUS42579	BUS42579 AGENCOURT
542	39.6	4.6	289	10	DM866666	DM866666 CRP6398.C	615	39.4	4.5	308	3	BUS30904	BUS30904 AGENCOURT
543	39.6	4.6	301	3	BM880539	BM880539 r2b3e02.y	616	39.4	4.5	316	2	BM286318	BM286318 526323.MA
544	39.6	4.6	302	3	BQ453074	BQ453074 s8o95e07.y	C 617	39.4	4.5	321	5	CF330989	CF330989 NACL--06-
545	39.6	4.6	311	1	AI965701	AI965701 sc77c09.y	618	39.4	4.5	325	5	CK151023	CK151023 CsmgEST02
C 546	39.6	4.6	313	3	BQ012596	BQ012596 UT-1-BC1p	619	39.4	4.5	390	1	AL120526	AL120526 DKP2p7610
C 547	39.6	4.6	313	4	CA444611	CA444611 UT-H-DTL	620	39.4	4.5	392	7	AW569872	AW569872 8182f06.y
C 548	39.6	4.6	319	8	CO774070	CO774070 ILLUMIGEN	C 621	39.4	4.5	416	8	CK190001	CK190001 70-E01341
C 549	39.6	4.6	324	8	CN478726	CN478726 UT-CF-FNO	622	39.4	4.5	423	2	BJ366859	BJ366859 BJ366859
C 550	39.6	4.6	332	5	CF314491	CF314491 HD--03-A1	C 623	39.4	4.5	446	1	AI253147	AI253147 Qz38b08.x
C 551	39.6	4.6	350	1	AM004320	AM004320 AM004320	624	39.4	4.5	463	8	CK327218	CK327218 JGI_XZT15
552	39.6	4.6	382	5	CK381708	CK381708 l8g99g07.	625	39.4	4.5	470	7	BF117517	BF117517 uz18a05.y
553	39.6	4.6	384	5	CK379579	CK379579 l8i13e03.	626	39.4	4.5	481	12	CC766090	CC766090 CH240.131
554	39.6	4.6	389	3	BM731463	BM731463 s8180c07.	627	39.4	4.5	482	9	CK567911	CK567911 UI-M-HK0-
C 555	39.6	4.6	392	5	CF331891	CF331891 NACL--08-	628	39.4	4.5	486	9	CK393284	CK393284 JGI_XZT40
C 556	39.6	4.6	403	9	DN882833	DN882833 n8f10d09.	629	39.4	4.5	487	10	DR391327	DR391327 USDA-PP.1
557	39.6	4.6	405	5	CF927527	CF927527 l8f54c10.	630	39.4	4.5	488	3	BP381442	BP381442 BP381442
C 558	39.6	4.6	435	3	BQ526909	BQ526909 NISC.no19	631	39.4	4.5	489	7	AW642784	AW642784 cm22e06.w
C 559	39.6	4.6	444	4	CAB03547	CAB03547 ESG011c.E	632	39.4	4.5	491	8	CK041175	CK041175 1354595.N
C 560	39.6	4.6	459	3	BQ476192	BQ476192 curculio1	633	39.4	4.5	495	11	AQ986347	AQ986347 RPC1-23-3
C 561	39.6	4.6	462	7	BF398814	BF398814 UT-R-CAL-	C 634	39.4	4.5	514	5	CF328406	CF328406 NACL--03-
C 562	39.6	4.6	484	7	BX513394	BX513394 BX513394	635	39.4	4.5	522	9	CK572465	CK572465 TTE000363
C 563	39.6	4.6	484	7	AW558854	AW558854 L0300H05-	C 636	39.4	4.5	524	5	CF316197	CF316197 HD--05-G0
C 564	39.6	4.6	496	8	CO776081	CO776081 JH02005D0	637	39.4	4.5	527	2	BI082991	BI082991 602874496
C 565	39.6	4.6	499	5	CF529813	CF529813 UT-1-BC1p	C 638	39.4	4.5	530	9	DN873278	DN873278 nad25e07.
C 566	39.6	4.6	500	9	DN348514	DN348514 L1B3578-0	639	39.4	4.5	555	10	DT458643	DT458643 GH.ON36H1
C 567	39.6	4.6	532	4	CB619869	CB619869 OSIIIBa04L	C 640	39.4	4.5	698	4	BT703217	BT703217 BX703217
C 568	39.6	4.6	545	3	BM734127	BM734127 k11a04.y	C 641	39.4	4.5	728	8	CR421659	CR421659 CR421659
C 569	39.6	4.6	568	4	CA416240	CA416240 UT-H-PEO-	C 642	39.4	4.5	756	8	CR409060	CR409060 CR409060
C 570	39.6	4.6	575	3	BQ775524	BQ775524 UT-H-FHO-	C 643	39.4	4.5	762	4	BT700523	BT700523 BX700523
C 571	39.6	4.6	589	3	BQ013151	BQ013151 UT-1-BC1p	644	39.4	4.5	785	14	AG511813	AG511813 Mus.muscu
C 572	39.6	4.6	591	4	CA421998	CA421998 UT-H-FGO-	C 645	39.4	4.5	796	14	AG542918	AG542918 Mus.muscu
573	39.6	4.6	606	9	CX442823	CX442823 JGI_XZG84	646	39.4	4.5	808	12	CG499135	CG499135 CH240.336
574	39.6	4.6	611	10	DM171893	DM171893 ZM-BFb017	647	39.4	4.5	819	4	BT710613	BT710613 BX710613
575	39.6	4.6	653	5	CK541111	CK541111 rswhb0.00	C 648	39.4	4.5	833	2	BF791937	BF791937 602252308
C 576	39.6	4.6	665	4	CB290025	CB290025 UT-M-F10-	649	39.4	4.5	857	1	AJ923728	AJ923728 AJ923728
C 577	39.6	4.6	671	3	BU676109	BU676109 UT-CF-DUI-	650	39.4	4.5	862	14	AG463906	AG463906 Mus.muscu
C 578	39.6	4.6	683	4	CA505570	CA505570 UT-R-FS1-	651	39.4	4.5	873	14	DU860232	DU860232 66461.Tom
C 579	39.6	4.6	685	3	BM683048	BM683048 UT-E-E01-	C 652	39.4	4.5	889	4	BT700931	BT700931 BX700931
C 580	39.6	4.6	685	3	BQ683109	BQ683109 UT-CF-EN1	653	39.4	4.5	922	14	AG864076	AG864076 Oriza.sac
C 581	39.6	4.6	686	3	BQ045403	BQ045403 UT-CF-EN1	654	39.4	4.5	927	9	DN571108	DN571108 940533919
C 582	39.6	4.6	686	3	BQ575797	BQ575797 UT-H-E21-	C 655	39.4	4.5	928	10	DT782859	DT782859 125636973
C 583	39.6	4.6	708	3	BQ678435	BQ678435 UT-CF-E00	656	39.4	4.5	936	10	DM069480	DM069480 VP01.01.G
C 584	39.6	4.6	713	8	CO894039	CO894039 BovGen.22	657	39.4	4.5	951	10	DM041273	DM041273 DAY10.01
C 585	39.6	4.6	720	4	CA418566	CA418566 UT-H-E21-	658	39.4	4.5	961	7	BE890494	BE890494 601431564
C 586	39.6	4.6	720	4	CB305432	CB305432 UT-CF-EN1	C 659	39.4	4.5	1011	14	CNS005L1	AL059331 Drosophila
C 587	39.6	4.6	721	3	BU681018	BU681018 UT-CF-EC1	660	39.4	4.5	1034	14	CNS016L1	AL106159 Drosophila
C 588	39.6	4.6	732	4	CA944758	CA944758 UT-CF-FNO	661	39.4	4.5	1035	14	CNS00ZD5	AL097523 Drosophila
C 589	39.6	4.6	754	1	AJ410647	AJ410647 AJ410647	C 662	39.4	4.5	1049	2	BG393206	BG393206 602411629
C 590	39.6	4.6	762	9	DR128525	DR128525 49025125	663	39.4	4.5	1100	14	CNS00G3S	AL071398 Drosophila
C 591	39.6	4.6	768	4	CA417824	CA417824 UT-H-PEO-	C 664	39.4	4.5	1101	14	CNS00FXE	AL071370 Drosophila
C 592	39.6	4.6	789	9	DR125270	DR125270 49113031	665	39.4	4.5	215	8	CK058264	CK058264 PDUta2022
C 593	39.6	4.6	790	9	DR126699	DR126699 49306621	666	39.2	4.5	216	7	BF613033	BF613033 6829902.y
C 594	39.6	4.6	886	4	BM748883	BM748883 BX748883	667	39.2	4.5	222	2	BG945637	BG945637 CW4-KN001
C 595	39.6	4.6	888	8	CO763934	CO763934 brain.EST	668	39.2	4.5	233	2	BI843156	BI843156 ft58a03.x
C 596	39.6	4.6	898	5	CD305481	CD305481 StrpA691.	C 669	39.2	4.5	241	1	AI340570	AI340570 t888h08.x
C 597	39.6	4.6	906	14	AG396436	AG396436 Mus.muscu	670	39.2	4.5	242	1	AL036146	AL036146 DKF29564D
C 598	39.6	4.6	928	10	DT785774	DT785774 126368860	671	39.2	4.5	242	1	AL036146	AL036146 DKF29564D
C 599	39.6	4.6	939	10	DM050388	DM050388 DAY35S.09	C 672	39.2	4.5	256	1	AI570164	AI570164 t075f07.x
600	39.6	4.6	962	10	DT793540	DT793540 126552469	C 673	39.2	4.5	258	7	AW268744	AW268744 X1296004.x
601	39.6	4.6	969	4	CA971584	CA971584 AGENCOURT	C 674	39.2	4.5	266	9	DN274839	DN274839 1153884.M
602	39.6	4.6	1073	3	BQ930284	BQ930284 AGENCOURT	675	39.2	4.5	308	1	AL037521	AL037521 DKF29564E
603	39.6	4.6	1156	13	CL640910	CL640910 CH213-1B1	676	39.2	4.5	310	8	CR557379	CR557379 DKF294690

C 677	39.2	4.5	311	4	CB264177	750	39	4.5	340	5	CF621600	CF621600 lae62b07.
C 678	39.2	4.5	341	2	BG629030	C 751	39	4.5	371	7	AW189482	AW189482 xl07c04.x
C 679	39.2	4.5	348	9	DN896823	C 752	39	4.5	372	7	BE097001	BE097001 UI-R-B0-
C 680	39.2	4.5	375	5	CF803697	C 753	39	4.5	377	5	CF326815	CF326815 NACL--01-
C 681	39.2	4.5	378	2	BW319775	C 754	39	4.5	398	1	UA999157	UA999157 UI-R-C0-h
C 682	39.2	4.5	398	1	AJ499453	C 755	39	4.5	411	9	DN885393	DN885393 naf29c12.
C 683	39.2	4.5	416	9	CV600093	C 756	39	4.5	428	5	CF545395	CF545395 lae78g01.
C 684	39.2	4.5	419	4	CB345973	C 757	39	4.5	445	7	BE105623	BE105623 UI-R-BX0-
C 685	39.2	4.5	442	7	AW597567	C 758	39	4.5	453	1	AI096778	AI096778 qb56e07.x
C 686	39.2	4.5	443	5	CK418085	C 759	39	4.5	457	7	AW529488	AW529488 UI-R-BT1-
C 687	39.2	4.5	453	8	CK062681	C 760	39	4.5	474	8	AX294096	AX294096 C0501A09
C 688	39.2	4.5	455	12	BI490319	C 761	39	4.5	489	1	AL892912	AL892912 AL892912
C 689	39.2	4.5	462	2	CF359777	C 762	39	4.5	499	4	AX779765	AX779765 BX779765
C 690	39.2	4.5	462	3	BQ770924	C 763	39	4.5	499	4	AX779765	AX779765 BX779765
C 691	39.2	4.5	518	1	AM016574	C 764	39	4.5	503	5	BE111550	BE111550 lah98f03.
C 692	39.2	4.5	532	10	DF833093	C 765	39	4.5	511	7	BE111550	BE111550 lah98f03.
C 693	39.2	4.5	533	8	CF321773	C 766	39	4.5	512	9	DN366000	DN366000 LI36629-0
C 694	39.2	4.5	539	5	CF308013	C 767	39	4.5	514	3	BQ389814	BQ389814 NISC mg09
C 695	39.2	4.5	544	3	BQ398892	C 768	39	4.5	530	9	AX770039	AX770039 JGI_XZT55
C 696	39.2	4.5	545	8	CO753692	C 769	39	4.5	536	5	CK815132	CK815132 Ra89gc614
C 697	39.2	4.5	548	4	CB964126	C 770	39	4.5	539	4	CA318931	CA318931 UI-M-FV0-
C 698	39.2	4.5	549	7	BE648293	C 771	39	4.5	548	9	DN366887	DN366887 LI36629-0
C 699	39.2	4.5	549	8	CN727743	C 772	39	4.5	557	9	DN365974	DN365974 LI36629-0
C 700	39.2	4.5	565	2	BJ929052	C 773	39	4.5	571	7	BE105735	BE105735 UI-R-B01-
C 701	39.2	4.5	568	10	DF833077	C 774	39	4.5	576	9	AX775149	AX775149 JGI_XZT58
C 702	39.2	4.5	586	10	DF651269	C 775	39	4.5	579	12	CC961073	CC961073 BO1BQ65TR
C 703	39.2	4.5	592	10	DS539846	C 776	39	4.5	596	10	DR976032	DR976032 Skin-13.H
C 704	39.2	4.5	592	10	DM287773	C 777	39	4.5	647	7	BF399390	BF399390 UI-R-CA1-
C 705	39.2	4.5	594	4	CB288148	C 778	39	4.5	649	1	AL881138	AL881138 AL881138
C 706	39.2	4.5	603	3	BUI39582	C 779	39	4.5	659	8	CO117171	CO117171 GR_Eb019
C 707	39.2	4.5	627	10	DF833785	C 780	39	4.5	677	4	AX726217	AX726217 BX726217
C 708	39.2	4.5	650	14	CR836996	C 781	39	4.5	684	11	BZ061492	BZ061492 lkg92f04.
C 709	39.2	4.5	659	8	CV905600	C 782	39	4.5	687	8	CO042482	CO042482 UI-N-FC0-
C 710	39.2	4.5	679	1	DR039981	C 783	39	4.5	692	2	BI289100	BI289100 UI-R-DK0-
C 711	39.2	4.5	680	9	AL884087	C 784	39	4.5	699	4	AX750709	AX750709 BX750709
C 712	39.2	4.5	680	3	BW724975	C 785	39	4.5	716	1	AV702427	AV702427 AV702427
C 713	39.2	4.5	685	13	CH633535	C 786	39	4.5	737	14	AG240450	AG240450 Mus muscu
C 714	39.2	4.5	688	4	CA419138	C 787	39	4.5	739	10	DR476428	DR476428 WS00967.C
C 715	39.2	4.5	688	10	DR712787	C 788	39	4.5	749	8	CV469923	CV469923 42688.1.C
C 716	39.2	4.5	707	8	CV472320	C 789	39	4.5	749	9	AX454181	AX454181 JGI_XZG55
C 717	39.2	4.5	720	10	DR821106	C 790	39	4.5	772	14	CNS02HPA	AL197911 Tetradon
C 718	39.2	4.5	755	8	CV797445	C 791	39	4.5	797	3	BQ145169	BQ145169 NF011B05G
C 719	39.2	4.5	776	3	BW743213	C 792	39	4.5	798	13	DU100472	DU100472 JBNy021M1
C 720	39.2	4.5	780	7	AV733831	C 793	39	4.5	804	8	CO875720	CO875720 BvgGen.04
C 721	39.2	4.5	805	14	CNS009F8	C 794	39	4.5	813	3	BQ145175	BQ145175 NF011B0GG
C 722	39.2	4.5	816	3	BQ781132	C 795	39	4.5	852	11	BZ0766	BZ0766 T13H7-T7.TA
C 723	39.2	4.5	880	5	CK156543	C 796	39	4.5	878	10	DT783805	DT783805 125653678
C 724	39.2	4.5	894	12	CG766346	C 797	39	4.5	885	10	DT783988	DT783988 126368911
C 725	39.2	4.5	921	10	DT068969	C 798	39	4.5	888	4	AX776606	AX776606 BX776606
C 726	39.2	4.5	924	11	BH155735	C 799	39	4.5	890	4	AX752792	AX752792 BX752792
C 727	39.2	4.5	953	9	DN573040	C 800	39	4.5	899	8	CR440269	CR440269 CR440269
C 728	39.2	4.5	957	9	DN562197	C 801	39	4.5	899	10	DT801057	DT801057 1256502055
C 729	39.2	4.5	972	2	BM464785	C 802	39	4.5	902	9	DN576815	DN576815 93829338
C 730	39.2	4.5	994	9	DN565893	C 803	39	4.5	904	12	CL059947	CL059947 CH216-91A
C 731	39.2	4.5	1101	14	CNS0039G	C 804	39	4.5	936	10	DT779129	DT779129 125631697
C 732	39.2	4.5	1873	6	AF119859	C 805	39	4.5	938	9	DN575944	DN575944 93817604
C 733	39.2	4.5	4127	6	CR861348	C 806	39	4.5	948	9	DN574906	DN574906 90160497
C 734	39.2	4.5	137	10	DN154017	C 807	39	4.5	948	10	DT073220	DT073220 125633868
C 735	39.2	4.5	151	9	AT810589	C 808	39	4.5	959	10	DT773220	DT773220 125633868
C 736	39.2	4.5	164	1	AT810589	C 809	39	4.5	966	10	DT074671	DT074671 VP01_19.N
C 737	39.2	4.5	170	5	CK617891	C 810	39	4.5	978	10	DT054796	DT054796 DL0P01_12
C 738	39.2	4.5	234	1	AW502406	C 811	39	4.5	984	9	DN566597	DN566597 90181003
C 739	39.2	4.5	242	7	AW656503	C 812	39	4.5	984	9	DN566597	DN566597 90181003
C 740	39.2	4.5	257	7	AW656503	C 813	39	4.5	997	10	DT074672	DT074672 VP01_19.N
C 741	39.2	4.5	283	10	CR395426	C 814	39	4.5	1001	10	DT055332	DT055332 DL0P01_13
C 742	39.2	4.5	298	5	CK395426	C 815	39	4.5	1011	10	DNV04755	DNV04755 DAY20_17
C 743	39.2	4.5	312	1	AA909381	C 816	39	4.5	1085	14	CNS0124K	AL101102 Drosophi1
C 744	39.2	4.5	314	2	BI846999	C 817	39	4.5	1094	10	DT054798	DT054798 DL0P01_12
C 745	39.2	4.5	319	10	DR558190	C 818	39	4.5	1101	14	CNS00781	AL067048 Drosophi1
C 746	39.2	4.5	321	5	CF228076	C 819	39	4.5	1275	14	AG333055	AG333055 Mus muscu
C 747	39.2	4.5	324	5	CF423986	C 820	39	4.5	1275	14	AG333055	AG333055 Mus muscu
C 748	39.2	4.5	329	5	CK404969	C 821	39	4.5	225	4	CR858066	CR858066 Pongo pyg
C 749	39.2	4.5	329	8	CN628030	C 822	39	4.5	226	9	DN887238	DN887238 nag03c02.
									292	2	BM033265	BM033265 kh53d01.Y

823	38.8	4.5	293	2	BI502720	BB170002A	BI502720	BB170002A	C 896	38.6	4.4	477	3	BP120207	BP120207	BP120207	BP120207
824	38.8	4.5	328	5	CD512549	AGENCYCOURT	CD512549	AGENCYCOURT	C 897	38.6	4.4	501	9	AW137427	AW137427	AW137427	AW137427
C 825	38.8	4.5	348	12	CE477600	tiqr-q98-	CE477600	tiqr-q98-	C 898	38.6	4.4	507	7	AX135217	AX135217	AX135217	AX135217
C 826	38.8	4.5	373	1	AI253178	q238h10.x	AI253178	q238h10.x	C 899	38.6	4.4	507	9	CX338017	CX338017	CX338017	CX338017
C 827	38.8	4.5	377	1	AJ846519	AJ846519	AJ846519	AJ846519	C 900	38.6	4.4	510	9	CX805458	CX805458	CX805458	CX805458
C 828	38.8	4.5	400	5	CJ127494	CJ127494	CJ127494	CJ127494	C 901	38.6	4.4	519	14	DE064043	DE064043	DE064043	DE064043
C 829	38.8	4.5	413	8	CX330080	JGI_XZT68	CX330080	JGI_XZT68	C 902	38.6	4.4	530	5	CK034703	CK034703	CK034703	CK034703
C 830	38.8	4.5	432	4	CB559646	AGENCYCOURT	CB559646	AGENCYCOURT	C 903	38.6	4.4	543	5	CK414853	CK414853	CK414853	CK414853
C 831	38.8	4.5	434	4	CB793407	AGENCYCOURT	CB793407	AGENCYCOURT	C 904	38.6	4.4	561	8	CN051395	CN051395	CN051395	CN051395
C 832	38.8	4.5	451	5	CK454293	911581.WA	CK454293	911581.WA	C 905	38.6	4.4	581	3	BP375614	BP375614	BP375614	BP375614
C 833	38.8	4.5	453	4	CB046243	NISC_gf03	CB046243	NISC_gf03	C 906	38.6	4.4	585	3	BQ393240	BQ393240	BQ393240	BQ393240
C 834	38.8	4.5	516	2	BI183348	UNL-F-FN-	BI183348	UNL-F-FN-	C 907	38.6	4.4	601	3	BQ396673	BQ396673	BQ396673	BQ396673
C 835	38.8	4.5	521	4	CB257020	51-E01084	CB257020	51-E01084	C 908	38.6	4.4	606	4	CA325540	CA325540	CA325540	CA325540
C 836	38.8	4.5	524	3	BU056256	UT-M-FP0-	BU056256	UT-M-FP0-	C 909	38.6	4.4	620	7	BE965577	BE965577	BE965577	BE965577
C 837	38.8	4.5	531	7	AW632760	92879.MAR	AW632760	92879.MAR	C 910	38.6	4.4	628	4	BX731709	BX731709	BX731709	BX731709
C 838	38.8	4.5	542	5	CK429916	0142812.y	CK429916	0142812.y	C 911	38.6	4.4	629	9	CB827282	CB827282	CB827282	CB827282
C 839	38.8	4.5	558	8	CV659314	tk33905.	CV659314	tk33905.	C 912	38.6	4.4	647	2	BI382924	BI382924	BI382924	BI382924
C 840	38.8	4.5	559	3	BU171114	AGENCYCOURT	BU171114	AGENCYCOURT	C 913	38.6	4.4	663	3	BQ523745	BQ523745	BQ523745	BQ523745
C 841	38.8	4.5	594	5	CK935661	CGF100455	CK935661	CGF100455	C 914	38.6	4.4	676	11	AZ642505	AZ642505	AZ642505	AZ642505
C 842	38.8	4.5	595	4	CA804091	EG0112a.	CA804091	EG0112a.	C 915	38.6	4.4	681	10	DM254197	DM254197	DM254197	DM254197
C 843	38.8	4.5	618	14	CNS008A0	AL055149	CNS008A0	AL055149	C 916	38.6	4.4	682	8	CN159561	CN159561	CN159561	CN159561
C 844	38.8	4.5	630	8	CO043563	UT-M-H00-	CO043563	UT-M-H00-	C 917	38.6	4.4	687	9	DN118164	DN118164	DN118164	DN118164
C 845	38.8	4.5	632	9	AX133255	JGI_XZT29	AX133255	JGI_XZT29	C 918	38.6	4.4	706	8	CN097844	CN097844	CN097844	CN097844
C 846	38.8	4.5	644	10	DM271858	UI-S-GS1-	DM271858	UI-S-GS1-	C 919	38.6	4.4	723	13	DU459833	DU459833	DU459833	DU459833
C 847	38.8	4.5	657	8	CN460959	UT-M-HB0-	CN460959	UT-M-HB0-	C 920	38.6	4.4	733	10	DT482392	DT482392	DT482392	DT482392
C 848	38.8	4.5	672	9	CX763526	AGENCYCOURT	CX763526	AGENCYCOURT	C 921	38.6	4.4	745	14	CT418301	CT418301	CT418301	CT418301
C 849	38.8	4.5	699	9	DN888084	rag11b06.	DN888084	rag11b06.	C 922	38.6	4.4	777	14	AG600118	AG600118	AG600118	AG600118
C 850	38.8	4.5	702	8	CV200323	km02c10.y	CV200323	km02c10.y	C 923	38.6	4.4	827	14	CNS02NEE	CNS02NEE	CNS02NEE	CNS02NEE
C 851	38.8	4.5	719	14	CT120890	Sus scrofa	CT120890	Sus scrofa	C 924	38.6	4.4	835	1	AJ818009	AJ818009	AJ818009	AJ818009
C 852	38.8	4.5	752	4	EX834633	EX834633	EX834633	EX834633	C 925	38.6	4.4	866	14	CT222143	CT222143	CT222143	CT222143
C 853	38.8	4.5	766	1	AJ949219	AJ949219	AJ949219	AJ949219	C 926	38.6	4.4	891	1	AM098436	AM098436	AM098436	AM098436
C 854	38.8	4.5	770	7	AV757293	AV757293	AV757293	AV757293	C 927	38.6	4.4	904	13	DU082930	DU082930	DU082930	DU082930
C 855	38.8	4.5	772	14	CNS03NNT	Tetraodon	CNS03NNT	Tetraodon	C 928	38.6	4.4	910	10	DT772698	DT772698	DT772698	DT772698
C 856	38.8	4.5	790	13	CT305220	ZMRF0084	CT305220	ZMRF0084	C 929	38.6	4.4	942	10	DT778615	DT778615	DT778615	DT778615
C 857	38.8	4.5	795	10	DM280534	UI-S-GU0-	DM280534	UI-S-GU0-	C 930	38.6	4.4	961	10	DM074647	DM074647	DM074647	DM074647
C 858	38.8	4.5	802	12	CC548502	CH240.432	CC548502	CH240.432	C 931	38.6	4.4	1077	2	BM473293	BM473293	BM473293	BM473293
C 859	38.8	4.5	817	4	EX747554	EX747554	EX747554	EX747554	C 932	38.6	4.4	1101	14	CNS00528	CNS00528	CNS00528	CNS00528
C 860	38.8	4.5	823	4	CB315012	AGENCYCOURT	CB315012	AGENCYCOURT	C 933	38.6	4.4	1101	14	CNS010CR	CNS010CR	CNS010CR	CNS010CR
C 861	38.8	4.5	857	5	CD171720	AGENCYCOURT	CD171720	AGENCYCOURT	C 934	38.6	4.4	1201	14	CNS015ZZ	CNS015ZZ	CNS015ZZ	CNS015ZZ
C 862	38.8	4.5	867	12	CG302596	CG0F168TH	CG302596	CG0F168TH	C 935	38.6	4.4	1332	7	BE875442	BE875442	BE875442	BE875442
C 863	38.8	4.5	905	9	CO882398	BovGen.10	CO882398	BovGen.10	C 936	38.6	4.4	1338	14	AG396401	AG396401	AG396401	AG396401
C 864	38.8	4.5	906	8	DN568518	93882112	DN568518	93882112	C 937	38.6	4.4	1403	10	DM775099	DM775099	DM775099	DM775099
C 865	38.8	4.5	933	12	CG302606	CG0F168TV	CG302606	CG0F168TV	C 938	38.6	4.4	2409	6	CR858670	CR858670	CR858670	CR858670
C 866	38.8	4.5	953	3	BU159214	AGENCYCOURT	BU159214	AGENCYCOURT	C 939	38.6	4.4	5664	6	BC036757	BC036757	BC036757	BC036757
C 867	38.8	4.5	965	3	BQ276670	AGENCYCOURT	BQ276670	AGENCYCOURT	C 940	38.4	4.4	106	8	CN797438	CN797438	CN797438	CN797438
C 868	38.8	4.5	1007	12	CL139171	ISB1-112A	CL139171	ISB1-112A	C 941	38.4	4.4	107	8	CN797432	CN797432	CN797432	CN797432
C 869	38.8	4.5	1015	2	BI490178	603031949	BI490178	603031949	C 942	38.4	4.4	117	8	CN800596	CN800596	CN800596	CN800596
C 870	38.8	4.5	1021	14	CNS016E1	Drosophila	CNS016E1	Drosophila	C 943	38.4	4.4	119	8	CN797074	CN797074	CN797074	CN797074
C 871	38.8	4.5	1101	14	CNS0100X	Drosophila	CNS0100X	Drosophila	C 944	38.4	4.4	125	8	CN799579	CN799579	CN799579	CN799579
C 872	38.8	4.5	1267	8	CV861738	gonad.EST	CV861738	gonad.EST	C 945	38.4	4.4	127	8	CN800517	CN800517	CN800517	CN800517
C 873	38.8	4.5	1406	10	DM779642	Hw-Fat.37	DM779642	Hw-Fat.37	C 946	38.4	4.4	130	8	CN796573	CN796573	CN796573	CN796573
C 874	38.8	4.5	1556	6	BC029685	Homo sapi	BC029685	Homo sapi	C 947	38.4	4.4	131	8	CN796329	CN796329	CN796329	CN796329
C 875	38.8	4.5	1591	9	DN688368	COX58-E02	DN688368	COX58-E02	C 948	38.4	4.4	132	1	AI251272	AI251272	AI251272	AI251272
C 876	38.8	4.5	1836	6	HSN802705	HSN802705	HSN802705	HSN802705	C 949	38.4	4.4	132	8	CN797071	CN797071	CN797071	CN797071
C 877	38.6	4.4	112	2	BJ387232	BJ387232	BJ387232	BJ387232	C 950	38.4	4.4	132	8	CN797135	CN797135	CN797135	CN797135
C 878	38.6	4.4	152	4	C94134	Diet	C94134	Diet	C 951	38.4	4.4	135	8	CN800043	CN800043	CN800043	CN800043
C 879	38.6	4.4	227	4	CB066266	PVBE12A02	CB066266	PVBE12A02	C 952	38.4	4.4	136	8	CN796446	CN796446	CN796446	CN796446
C 880	38.6	4.4	299	3	BP704131	BP704131	BP704131	BP704131	C 953	38.4	4.4	138	8	CN796743	CN796743	CN796743	CN796743
C 881	38.6	4.4	301	5	CF384267	Iac04h02.	CF384267	Iac04h02.	C 954	38.4	4.4	140	8	CN797047	CN797047	CN797047	CN797047
C 882	38.6	4.4	330	3	BU760820	8as59a04.	BU760820	8as59a04.	C 955	38.4	4.4	141	8	CN796590	CN796590	CN796590	CN796590
C 883	38.6	4.4	332	1	AL036923	DKFP2564B	AL036923	DKFP2564B	C 956	38.4	4.4	141	8	CN797055	CN797055	CN797055	CN797055
C 884	38.6	4.4	334	8	CO184654	EC28424.5	CO184654	EC28424.5	C 957	38.4	4.4	143	8	CN797147	CN797147	CN797147	CN797147
C 885	38.6	4.4	338	2	BM484670	fV70h10.y	BM484670	fV70h10.y	C 958	38.4	4.4	149	8	CN796719	CN796719	CN796719	CN796719
C 886	38.6	4.4	343	10	DR874327	JGI_CABH9	DR874327	JGI_CABH9	C 959	38.4	4.4	150	8	CN797091	CN797091	CN797091	CN797091
C 887	38.6	4.4	347	8	CO895657	BovGen.23	CO895657	BovGen.23	C 960	38.4	4.4	152	8	CN797334	CN797334	CN797334	CN797334
C 888	38.6	4.4	350	4	CA528397	8072-62.M	CA528397	8072-62.M	C 961	38.4	4.4	152	8	CN801150	CN801150	CN801150	CN801150
C 889	38.6	4.4	353	9	CX363136	JGI_XZT42	CX363136	JGI_XZT42	C 962	38.4	4.4	155	1	AI252692	AI252692	AI252692	AI252692
C 890	38.6	4.4	370	7	AW156431	822b02.y	AW156431	822b02.y	C 963	38.4	4.4	162	1	AA690006	AA690006	AA690006	AA690006
C 891	38.6	4.4	383	14	AG372801	Mus muscu	AG372801	Mus muscu	C 964	38.4	4.4	165					

c 969	38.4	4.4	222	9	DN919564	MCFTRNAL2	1042	38.4	4.4	617	9	CX395364	CX395364 JGI_XZT27
970	38.4	4.4	235	7	BE058624	anl8e10.y	1043	38.4	4.4	621	8	CX318264	CX318264 JGI_XZT59
c 971	38.4	4.4	248	5	FP044537	QCJ30c09.	c1044	38.4	4.4	626	10	DM280243	DM280243 UI-S-GU0-
c 972	38.4	4.4	255	3	BQ090910	ku21h10.y	c1045	38.4	4.4	637	13	CZ098494	CZ098494 OM_Ba010
973	38.4	4.4	267	4	CA802854	sa43b09.	1046	38.4	4.4	639	9	CX394824	CX394824 JGI_XZT27
974	38.4	4.4	271	1	AL837252	AL837252	c1047	38.4	4.4	640	12	CE417423	CE417423 tigr-g88-
975	38.4	4.4	273	2	BG359352	sac23all.	c1048	38.4	4.4	642	10	DM255031	DM255031 UI-S-GB1-
c 976	38.4	4.4	279	7	AW533068	UI-R-BU0-	c1049	38.4	4.4	644	13	CZ056024	CZ056024 OM_Ba004
977	38.4	4.4	280	5	CK378353	lah95c02.	c1050	38.4	4.4	653	1	A1559640	A1559640 tq58f07.x
978	38.4	4.4	281	7	BF452999	ma464b11.	c1051	38.4	4.4	655	9	DN867232	DN867232 nac26e06.
979	38.4	4.4	284	1	AL837227	AL837227	c1052	38.4	4.4	662	8	CR443717	CR443717 CR43717
980	38.4	4.4	299	2	BI501913	rm06g03.y	1053	38.4	4.4	685	10	DT842869	DT842869 LB00466.C
981	38.4	4.4	299	4	CB701265	AMGNNUC.M	c1054	38.4	4.4	693	3	BM974205	BM974205 UI-CF-EC1
982	38.4	4.4	308	9	DN878787	nae22910.	1055	38.4	4.4	696	8	CN155261	CN155261 942544 MA
983	38.4	4.4	314	4	CA793832	AGENCOURT	c1056	38.4	4.4	703	10	DM272325	DM272325 UI-S-GS1-
984	38.4	4.4	318	3	BU716755	SJM2AWG09	c1057	38.4	4.4	708	5	CD741850	CD741850 UI-M-AO0-
c 985	38.4	4.4	324	1	AI842671	UI-M-AO1-	1058	38.4	4.4	709	9	DM237210	DM237210 EST00335
986	38.4	4.4	329	3	BM774043	ra89g10.y	c1059	38.4	4.4	710	10	DM278574	DM278574 UI-S-RH0-
987	38.4	4.4	330	8	CO891122	BovGen_19	c1060	38.4	4.4	714	10	DM257784	DM257784 UI-S-GG0-
c 988	38.4	4.4	341	2	BG869806	602789319	c1061	38.4	4.4	715	13	CZ598794	CZ598794 OM_Ba005
989	38.4	4.4	342	1	AA271298	vb73a07.r	c1062	38.4	4.4	752	12	CC311266	CC311266 TAN32-21P
990	38.4	4.4	347	5	CF968439	lag14h11.	1063	38.4	4.4	777	14	CNS025WB	ALU82612 Tetraodon
c 991	38.4	4.4	349	9	CX456503	JGI_XZG53	1064	38.4	4.4	791	3	BU554551	BU554551 AGENCOURT
c 992	38.4	4.4	352	10	DM279413	UI-S-GU0-	1065	38.4	4.4	802	5	CF288806	CF288806 AGENCOURT
993	38.4	4.4	356	7	AW739766	BR100279	1066	38.4	4.4	802	5	CF288806	CF288806 AGENCOURT
994	38.4	4.4	360	2	BJ680998	BJ680998	1067	38.4	4.4	812	7	BF168820	BF168820 601775145
995	38.4	4.4	363	2	BI383870	BFLG2_002	c1068	38.4	4.4	813	13	DU468889	DU468889 10282920
996	38.4	4.4	364	5	CD812384	BN10_020P	c1069	38.4	4.4	825	4	DX722920	DX722920 BX722920
c 997	38.4	4.4	365	11	AQ043325	CIT-HGP-2	1070	38.4	4.4	845	10	AGV869523	AGV869523 Oryza sat
998	38.4	4.4	369	5	CD811971	BN10_019J	1071	38.4	4.4	860	14	DM308977	DM308977 BalbC11g1
c 999	38.4	4.4	379	1	AI975082	EST269676	1072	38.4	4.4	882	10	DT776163	DT776163 124584470
c1000	38.4	4.4	389	7	AW090103	xc91b07.x	c1073	38.4	4.4	884	8	CV069454	CV069454 WPAEhux15
1001	38.4	4.4	390	5	CK594109	lah03d01.	1074	38.4	4.4	890	11	BH159661	BH159661 ENT2D45TF
1002	38.4	4.4	402	4	CB768951	AMGNNUC.N	c1075	38.4	4.4	893	10	DT771306	DT771306 125590156
1003	38.4	4.4	417	8	CN7979495	DK8P02236	c1076	38.4	4.4	900	3	BU956349	BU956349 AGENCOURT
1004	38.4	4.4	418	5	CD315172	StrPu621.	1077	38.4	4.4	903	10	DM051009	DM051009 DAY35_02
1005	38.4	4.4	421	5	CK422600	AUF_Ipspn	c1078	38.4	4.4	909	2	BM415521	BM415521 Op20597 M-
c1006	38.4	4.4	423	2	BF940879	hu60f02.x	c1079	38.4	4.4	914	9	DN575199	DN575199 90166530
1007	38.4	4.4	425	5	CF804574	lad75f06.	1080	38.4	4.4	918	10	DM072003	DM072003 BX0111.G
1008	38.4	4.4	426	3	BQ107045	A	1081	38.4	4.4	929	4	BA461864	BA461864 VPA1864
1009	38.4	4.4	430	9	CX842735	JGI_CAAK1	c1082	38.4	4.4	944	9	DN584995	DN584995 93006597
c1010	38.4	4.4	447	4	BY716746	BY716746	c1083	38.4	4.4	957	9	DN570114	DN570114 91545629
1011	38.4	4.4	449	9	CX362375	JGI_XZT42	1084	38.4	4.4	970	10	DM070757	DM070757 VP01_07.P
c1012	38.4	4.4	455	9	DN480155	np13_a206	1085	38.4	4.4	975	4	CA460956	CA460956 AGENCOURT
1013	38.4	4.4	461	5	CD812243	BN10_020I	1086	38.4	4.4	981	10	DM056387	DM056387 DL001_18-
1014	38.4	4.4	461	5	CD814226	BN15_022G	1087	38.4	4.4	982	10	DM056386	DM056386 DL001_18-
1015	38.4	4.4	461	5	CD816351	BN15_029F	1088	38.4	4.4	996	10	DT776671	DT776671 125644169
1016	38.4	4.4	462	5	CD811870	BN10_019D	1089	38.4	4.4	1042	5	CD512912	CD512912 AGENCOURT
1017	38.4	4.4	463	5	CD816145	BN15_028L	1090	38.4	4.4	1093	6	CR859867	CR859867 Pongo pyg
1018	38.4	4.4	464	8	CX217408	MNS31478	c1091	38.4	4.4	1101	14	CNS00FR3	ALU071143 Drosoephil
1019	38.4	4.4	465	5	CD812111	BN10_020B	c1092	38.4	4.4	1101	14	CNS016L1	ALU08896 Drosoephil
1020	38.4	4.4	467	5	CD811978	BN10_019J	c1093	38.4	4.4	1101	14	CNS017Y1	ALU08676 Drosoephil
1021	38.4	4.4	469	10	DR403848	CSAH-PNP1	c1094	38.4	4.4	1200	1	AJ928743	AJ928743 AJ928743
c1022	38.4	4.4	478	2	BI289170	UI-R-DK0-	c1095	38.4	4.4	1238	14	AG390565	AG390565 Mus muscu
c1023	38.4	4.4	502	7	AW019444	AW019444	1096	38.4	4.4	2247	6	BC089895	BC089895 Rattus no
1024	38.4	4.4	504	4	CA369462	fe11f09.x	1097	38.4	4.4	3900	6	CR860111	CR860111 Pongo pyg
1025	38.4	4.4	505	12	CE358394	CE358394	1098	38.2	4.4	118	8	DT776677	DT776677 17006001
c1026	38.4	4.4	507	5	DF322068	HD--13-11	c1099	38.2	4.4	169	8	CV933359	CV933359 Pmpcn_107
1027	38.4	4.4	507	10	DF323071	DF323071	1100	38.2	4.4	187	4	CB376955	CB376955 Hb02B04.L
1028	38.4	4.4	512	9	CX389925	JGI_XZT37	1101	38.2	4.4	207	1	AU053554	AU053554 AU053554
1029	38.4	4.4	514	8	CN334881	AGENCOURT	1102	38.2	4.4	222	10	DM125365	DM125365 CV03042A1
1030	38.4	4.4	517	10	DR835849	LB00432.C	c1103	38.2	4.4	230	5	CF336189	CF336189 JMT--06-C
1031	38.4	4.4	518	9	CX382565	JGI_XZT53	c1104	38.2	4.4	251	1	AJ441590	AJ441590 AJ41590
1032	38.4	4.4	526	9	CA409613	CX409613	1105	38.2	4.4	251	4	CA782248	CA782248 sau22n08.
1033	38.4	4.4	533	3	BU523128	AGENCOURT	1106	38.2	4.4	258	1	ALU183717	ALU183717 AU183717
1034	38.4	4.4	553	4	CA374326	648669 NC	1107	38.2	4.4	261	4	CB218062	CB218062 NISC nb06
c1035	38.4	4.4	564	1	AA817900	UI-R-AO-a	1108	38.2	4.4	267	3	BU800887	BU800887 SJF2CX07
c1036	38.4	4.4	567	8	CO875846	BovGen_04	1109	38.2	4.4	270	3	CB219030	CB219030 NISC nb12
1037	38.4	4.4	574	8	CO891009	BovGen_19	1110	38.2	4.4	289	2	BI866594	BI866594 ft58g03.y
1038	38.4	4.4	578	10	DR840068	LB00453.C	1111	38.2	4.4	295	7	BB719628	BB719628 BB719628
c1039	38.4	4.4	581	9	CX883466	JGI_CAA12	1112	38.2	4.4	302	9	DN468775	DN468775 USDA-FP-1
1040	38.4	4.4	596	8	CO880543	BovGen_08	c1113	38.2	4.4	305	1	AA740964	AA740964 ob23909.8
c1041	38.4	4.4	616	4	BY782118	BY782118	1114	38.2	4.4	320	7	BE808228	BE808228 213382 MA



1115	38.2	4.4	320	7	BE808230	213384 MA	1188	38.2	4.4	949	13	CL493875	CL493875 SAIL 587
1116	38.2	4.4	328	1	AU261705	AU261705	1189	38.2	4.4	954	11	BH162327	BH162327 ENTRJ37TR
1117	38.2	4.4	337	1	AJ701136	AJ701136	1190	38.2	4.4	973	10	DT781666	DT781666 126398522
1118	38.2	4.4	353	9	DN904454	OR0907.Y	1191	38.2	4.4	998	10	DT783865	DT783865 127410649
1119	38.2	4.4	358	4	CB931550	CB931550	1192	38.2	4.4	1006	14	CNS07A0G	AL436838 T7 end of
1120	38.2	4.4	359	4	CA488793	CA488793	1193	38.2	4.4	1073	10	DV778378	DV778378 Hw Fat 56
1121	38.2	4.4	359	5	CK421307	AUF Ipspn	1194	38.2	4.4	1113	10	DV795359	DV795359 HW LoIn 1
1122	38.2	4.4	365	7	BE682194	180129 MA	1195	38.2	4.4	1396	13	CL641292	CL641292 CH213-8P2
1123	38.2	4.4	369	2	BI343623	BI343623	1196	38.2	4.4	1396	13	CL641292	CL641292 CH213-8P2
1124	38.2	4.4	376	2	EG05496	EG05496	1197	38.2	4.4	118	10	DV077449	DV077449 DLSFmidgu
1125	38.2	4.4	385	7	BF410618	BF410618	1198	38.2	4.4	124	8	CK996016	CK996016 ip45C10.B
1126	38.2	4.4	390	9	DN950902	OST2T 670	1199	38.2	4.4	161	2	BI426118	BI426118 sat07005.
1127	38.2	4.4	401	4	CB409793	CB409793	1200	38.2	4.4	162	2	BM544151	BM544151 AGENCOURT
1128	38.2	4.4	405	10	DT456585	GH ON3380	1201	38.2	4.4	182	1	AU095033	AU095033 AU095033
1129	38.2	4.4	407	2	BM534766	BM534766	1202	38.2	4.4	186	8	CO722729	CO722729 MdfEr30180
1130	38.2	4.4	414	9	DN483742	DN483742	1203	38.2	4.4	220	7	BE023934	BE023934 sm94d01.Y
1131	38.2	4.4	417	9	DN883249	DN883249	1204	38.2	4.4	221	2	BI898852	BI898852 480638 MA
1132	38.2	4.4	422	2	BI834392	BI834392	1205	38.2	4.4	221	9	CK733504	CK733504 AC45C12.Y
1133	38.2	4.4	422	4	CA957581	CA957581	1206	38.2	4.4	240	5	CF303535	CF303535 ABF1--02-
1134	38.2	4.4	423	5	CJ317620	CJ317620	1207	38.2	4.4	243	3	BU842760	BU842760 AGENCOURT
1135	38.2	4.4	424	8	CK066361	CK066361	1208	38.2	4.4	265	7	AW432196	AW432196 sh70C09.Y
1136	38.2	4.4	426	8	CN990444	CN990444	1209	38.2	4.4	267	8	CO875936	CO875936 BoyGen 04
1137	38.2	4.4	426	8	CN992046	CN992046	1210	38.2	4.4	270	5	CK050931	CK050931 50043Fdic
1138	38.2	4.4	426	10	DT470273	DT470273	1211	38.2	4.4	295	2	BU340235	BU340235 BU340235
1139	38.2	4.4	428	3	BU04457	BU04457	1212	38.2	4.4	298	1	AI249966	AI249966 qx47D01.X
1140	38.2	4.4	439	8	CK033400	CK033400	1213	38.2	4.4	303	2	BM030182	BM030182 488728 MA
1141	38.2	4.4	447	4	BY383776	BY383776	1214	38.2	4.4	306	4	C99456	C99456 C99456 Rice
1142	38.2	4.4	448	10	DV860783	DV860783	1215	38.2	4.4	307	5	CK400031	CK400031 AGENCOURT
1143	38.2	4.4	449	3	BM566470	BM566470	1216	38.2	4.4	310	9	DN135975	DN135975 tam63B05.
1144	38.2	4.4	451	3	BQ432030	BQ432030	1217	38.2	4.4	313	9	DN902820	DN902820 naq39R06.
1145	38.2	4.4	453	3	BQ475957	platvatom	1218	38.2	4.4	315	9	CK733603	CK733603 oc46f03.Y
1146	38.2	4.4	455	4	BE699159	BE699159	1219	38.2	4.4	321	4	CA803028	CA803028 sau46C03.
1147	38.2	4.4	456	5	CF315893	CF315893	1220	38.2	4.4	322	1	AI302128	AI302128 qn19f10.X
1148	38.2	4.4	477	4	C93690	C93690	1221	38.2	4.4	328	7	BU564312	BU564312 AGENCOURT
1149	38.2	4.4	479	9	DN885984	DN885984	1222	38.2	4.4	328	7	BF076909	BF076909 226675 MA
1150	38.2	4.4	481	4	CA515631	CA515631	1223	38.2	4.4	328	12	CC809305	CC809305 ZMMB8C04B
1151	38.2	4.4	486	8	CO923606	CO923606	1224	38.2	4.4	329	4	BF702082	BF702082 BX702082
1152	38.2	4.4	497	10	DM010461	DM010461	1225	38.2	4.4	332	5	CF382719	CF382719 lac90G05.
1153	38.2	4.4	503	9	CK410043	CK410043	1226	38.2	4.4	335	7	AW945168	AW945168 ETSF61361
1154	38.2	4.4	527	4	BX524738	BX524738	1227	38.2	4.4	335	9	AW945168	AW945168 ETSF61361
1155	38.2	4.4	546	9	CK749807	CK749807	1228	38.2	4.4	352	3	BQ424539	BQ424539 AGENCOURT
1156	38.2	4.4	563	3	BM734291	BM734291	1229	38.2	4.4	360	8	CO204707	CO204707 WS0061.B2
1157	38.2	4.4	571	5	CD727102	CD727102	1230	38.2	4.4	369	5	CF926795	CF926795 laf41h01.
1158	38.2	4.4	574	1	AM137799	AM137799	1231	38.2	4.4	375	9	DN114045	DN114045 1113377 M
1159	38.2	4.4	586	1	AI462326	AI462326	1232	38.2	4.4	376	9	DN113691	DN113691 1112993 M
1160	38.2	4.4	603	9	DR901150	DR901150	1233	38.2	4.4	379	9	DN585645	DN585645 93869372
1161	38.2	4.4	622	10	DR901150	DR901150	1234	38.2	4.4	384	8	CO894344	CO894344 BoyGen 22
1162	38.2	4.4	634	9	CK439952	CK439952	1235	38.2	4.4	402	3	BM933517	BM933517 UI-M-B21-
1163	38.2	4.4	639	8	CN985806	CN985806	1236	38.2	4.4	402	5	CF329852	CF329852 NACL--05-
1164	38.2	4.4	644	1	AJ813744	AJ813744	1237	38.2	4.4	411	4	CB802438	CB802438 AMGNNUC:M
1165	38.2	4.4	649	10	DT783479	DT783479	1238	38.2	4.4	412	8	CK123933	CK123933 1323838 N
1166	38.2	4.4	660	2	BM078411	BM078411	1239	38.2	4.4	416	1	AL387990	AL387990 MEBC48A02
1167	38.2	4.4	682	3	BQ200171	BQ200171	1240	38.2	4.4	420	5	CF357670	CF357670 rm94C01.Y
1168	38.2	4.4	682	3	BQ538199	BQ538199	1241	38.2	4.4	429	8	CNS76973	CNS76973 r553g11.X
1169	38.2	4.4	692	10	DT494336	DT494336	1242	38.2	4.4	433	5	CK144522	CK144522 3530 1.11
1170	38.2	4.4	698	8	CV259339	CV259339	1243	38.2	4.4	442	5	CF319079	CF319079 CJ319079
1171	38.2	4.4	699	9	DR132934	DR132934	1244	38.2	4.4	444	5	CF357686	CF357686 rm94d06.Y
1172	38.2	4.4	713	1	AU030034	AU030034	1245	38.2	4.4	454	8	CN194447	CN194447 r994f06.Y
1173	38.2	4.4	722	9	DR025415	DR025415	1246	38.2	4.4	458	8	BM164935	BM164935 995320 MA
1174	38.2	4.4	727	9	DN211025	DN211025	1247	38.2	4.4	462	3	BP214064	BP214064 BP681334
1175	38.2	4.4	761	14	AG303406	AG303406	1248	38.2	4.4	471	3	BP681334	BP681334 BP681334
1176	38.2	4.4	784	14	AG537625	AG537625	1249	38.2	4.4	489	1	AJ701118	AJ701118 AJ701118
1177	38.2	4.4	804	3	BU937914	BU937914	1250	38.2	4.4	495	7	AW294744	AW294744 UI-H-BW0-
1178	38.2	4.4	807	3	BU958859	BU958859	1251	38.2	4.4	495	9	CK512934	CK512934 JGI XZG57
1179	38.2	4.4	842	10	DM259657	DM259657	1252	38.2	4.4	496	10	DT722280	DT722280 LB0133.CR
1180	38.2	4.4	856	7	BE964493	BE964493	1253	38.2	4.4	504	3	BP764256	BP764256 BP764256
1181	38.2	4.4	862	5	CF934053	CF934053	1254	38.2	4.4	511	11	AQ207505	AQ207505 HS 3249 B
1182	38.2	4.4	868	14	CNS07DOU	CNS07DOU	1255	38.2	4.4	512	5	CK421152	CK421152 AUF Ipspn
1183	38.2	4.4	886	4	BX759012	BX759012	1256	38.2	4.4	517	6	AV609838	AV609838 Sus_acroF
1184	38.2	4.4	888	10	DR732583	DR732583	1257	38.2	4.4	520	8	CV549922	CV549922 T9EST2yr3
1185	38.2	4.4	900	10	DM020631	DM020631	1258	38.2	4.4	521	8	CN798395	CN798395 D14P01587
1186	38.2	4.4	926	14	AG399219	AG399219	1259	38.2	4.4	523	10	DT851769	DT851769 LB00493.C
1187	38.2	4.4	948	7	BF141360	BF141360	1260	38.2	4.4	527	9	CK485896	CK485896 JGI XZG35
										529	10	DV947787	DV947787 SB03009A1

1261	38	4.4	530	3	BM942318	UI-M-BZ1-	1334	37.8	4.3	229	8	CV492424
1262	38	4.4	536	5	CF801537	rfj60e11.y	1335	37.8	4.3	234	8	CV492424
1263	38	4.4	543	5	BP935210	BP935210	1336	37.8	4.3	238	8	CX158892
1264	38	4.4	547	10	DT849094	LB00485.C	1337	37.8	4.3	239	3	C0895257
1265	38	4.4	567	8	C0804992	AGENCOURT	1338	37.8	4.3	240	1	BU851712
1266	38	4.4	573	5	CX618908	mk17b09.y	1339	37.8	4.3	254	5	AI678857
1267	38	4.4	579	8	CX037547	1350462.N	1340	37.8	4.3	254	5	tu70a05.x
1268	38	4.4	582	9	DN873497	nad26910.	1341	37.8	4.3	261	10	CF330391
1269	38	4.4	631	3	BU063494	Fgr_3.D01	1342	37.8	4.3	263	1	NACL--06-
1270	38	4.4	632	5	CX461066	1314022.A	1343	37.8	4.3	261	10	CRP6976.C
1271	38	4.4	634	10	DT836009	LB00433.C	1344	37.8	4.3	263	1	AA711043
1272	38	4.4	635	9	DN146170	4842.A10	1345	37.8	4.3	261	10	vt54h03.x
1273	38	4.4	636	9	CX391240	JGI_XZT38	1346	37.8	4.3	263	1	CV546249
1274	38	4.4	640	11	BH186548	025_H16-	1347	37.8	4.3	261	10	ad81e01.
1275	38	4.4	640	14	CNS07R05	AL623495.T2	1348	37.8	4.3	261	10	ad81e01.
1276	38	4.4	641	3	BQ266512	NISC_endof	1349	37.8	4.3	296	1	AD033171
1277	38	4.4	652	1	AV692691	AV692691	1350	37.8	4.3	296	1	AD033171
1278	38	4.4	653	9	CX868726	HESCA_30	1351	37.8	4.3	302	2	BI021679
1279	38	4.4	660	2	BU684084	BJ684084-	1352	37.8	4.3	302	2	sm83f112.y
1280	38	4.4	663	5	CF728119	UI-M-HB0-	1353	37.8	4.3	305	7	BE022424
1281	38	4.4	674	3	BP762184	BP762184	1354	37.8	4.3	305	7	BE022424
1282	38	4.4	679	9	DN883796	DN883796	1355	37.8	4.3	335	4	CB930816
1283	38	4.4	679	10	DR556850	WS0329.C2	1356	37.8	4.3	335	4	CB930816
1284	38	4.4	697	3	BO602834	MI-P-NA-a	1357	37.8	4.3	339	7	AW705520
1285	38	4.4	704	5	CF8552827	67-102016	1358	37.8	4.3	339	7	AW705520
1286	38	4.4	712	1	AV713580	AV713580	1359	37.8	4.3	341	3	BO932932
1287	38	4.4	715	14	AG371878	Mus_muscu	1360	37.8	4.3	341	3	BO932932
1288	38	4.4	716	3	BU620283	UI-H-FH1-	1361	37.8	4.3	343	5	CF317206
1289	38	4.4	717	14	DX064627	KB-B072C1	1362	37.8	4.3	350	5	CF546249
1290	38	4.4	728	4	BX745710	BX745710	1363	37.8	4.3	350	5	CF546249
1291	38	4.4	733	14	AG415916	Mus_muscu	1364	37.8	4.3	359	1	AA270231
1292	38	4.4	737	2	BG288558	602388025	1365	37.8	4.3	359	1	AA270231
1293	38	4.4	741	9	CX579485	TTE000224	1366	37.8	4.3	360	1	AL726038
1294	38	4.4	750	4	CA502810	UI-CF-FN0	1367	37.8	4.3	360	1	AL726038
1295	38	4.4	766	8	CR567068	CR567068	1368	37.8	4.3	382	8	CV999881
1296	38	4.4	776	9	CX584960	TTE000353	1369	37.8	4.3	382	8	CV999881
1297	38	4.4	795	9	DR138548	DR138548	1370	37.8	4.3	392	5	CK380619
1298	38	4.4	828	5	CD356330	AGENCOURT	1371	37.8	4.3	392	5	CK380619
1299	38	4.4	853	13	DU023910	DU023910	1372	37.8	4.3	403	1	AU261558
1300	38	4.4	855	10	DT773495	DT773495	1373	37.8	4.3	403	1	AU261558
1301	38	4.4	864	8	CO763353	brain_EST	1374	37.8	4.3	429	5	CJ315106
1302	38	4.4	865	5	CK198814	FGAS00730	1375	37.8	4.3	429	5	CJ315106
1303	38	4.4	878	3	BU850652	AGENCOURT	1376	37.8	4.3	436	9	CX369376
1304	38	4.4	880	7	BU850652	AGENCOURT	1377	37.8	4.3	436	9	CX369376
1305	38	4.4	888	7	BU900885	BU900885	1378	37.8	4.3	439	9	CX369376
1306	38	4.4	892	4	CB230927	AGENCOURT	1379	37.8	4.3	439	9	CX369376
1307	38	4.4	903	5	CK160110	FGAS04165	1380	37.8	4.3	445	8	CN540860
1308	38	4.4	909	14	CNS00JTL	AL076720	1381	37.8	4.3	445	8	CN540860
1309	38	4.4	931	13	C2999128	188689.To	1382	37.8	4.3	455	10	DR898845
1310	38	4.4	934	3	BU588245	AGENCOURT	1383	37.8	4.3	455	10	DR898845
1311	38	4.4	940	9	DN570209	DN570209	1384	37.8	4.3	473	1	AL041562
1312	38	4.4	944	8	CO766179	spleen_ES	1385	37.8	4.3	473	1	AL041562
1313	38	4.4	951	10	DT771303	CL508148	1386	37.8	4.3	487	5	CD415292
1314	38	4.4	958	13	CL508148	SAIL_792	1387	37.8	4.3	487	5	CD415292
1315	38	4.4	966	4	CB204438	AGENCOURT-	1388	37.8	4.3	493	4	CB969776
1316	38	4.4	970	8	CO762897	brain_EST	1389	37.8	4.3	493	4	CB969776
1317	38	4.4	975	3	BQ718516	AGENCOURT	1390	37.8	4.3	508	9	CX373566
1318	38	4.4	979	10	DT782503	126455302	1391	37.8	4.3	508	9	CX373566
1319	38	4.4	987	10	DT782503	126455302	1392	37.8	4.3	510	8	CV8955245
1320	38	4.4	991	14	CNS00JTB	AL077118	1393	37.8	4.3	510	8	CV8955245
1321	38	4.4	995	4	CB194716	AGENCOURT	1394	37.8	4.3	512	8	CX318063
1322	38	4.4	998	14	AG388659	Mus_muscu	1395	37.8	4.3	512	8	CX318063
1323	38	4.4	1014	1	AU284724	AU284724	1396	37.8	4.3	514	7	AW568434
1324	38	4.4	1019	10	DT784648	VP01_19.N	1397	37.8	4.3	514	7	AW568434
1325	38	4.4	1096	13	CL472179	SAIL_173b	1398	37.8	4.3	529	5	CF518389
1326	38	4.4	1109	12	CC933402	CC933402	1399	37.8	4.3	529	5	CF518389
1327	38	4.4	1160	9	DR151047	49259351	1400	37.8	4.3	538	4	C92760
1328	38	4.4	1345	10	DV781218	Hw_FAT_29	1401	37.8	4.3	538	4	C92760
1329	38	4.4	1345	10	DV781218	Hw_FAT_29	1402	37.8	4.3	545	8	CX030448
1330	37.8	4.3	165	2	BI941711	sc86f03.y	1403	37.8	4.3	545	8	CX030448
1331	37.8	4.3	184	8	CX025427	Md1v4-404	1404	37.8	4.3	561	8	CO810335
1332	37.8	4.3	211	1	AL697999	DKF7p686M	1405	37.8	4.3	566	4	CB202696
1333	37.8	4.3	211	8	CX124919	1324772.N	1406	37.8	4.3	576	7	AW644204

C1407	37.8	37.8	4.3	742	10	DW252250	DW252250 UI-S-GBO-
1408	37.8	37.8	4.3	745	2	BG289608	BG289608 602381575
C1409	37.8	37.8	4.3	747	10	DW278851	DW278851 UI-S-HHO-
C1410	37.8	37.8	4.3	753	3	CA808961	CA808961 CA12L1051
1411	37.8	37.8	4.3	757	3	BM918328	BM918328 AGENCOURT
1412	37.8	37.8	4.3	761	9	CX376482	CX376482 JGI_XZT33
1413	37.8	37.8	4.3	770	9	DN866938	DN866938 nac24908
C1414	37.8	37.8	4.3	783	4	BX730524	BX730524 BX730524
C1415	37.8	37.8	4.3	797	4	BK779860	BK779860 BX779860
C1416	37.8	37.8	4.3	806	5	CJ474328	CJ474328 CJ474328
1417	37.8	37.8	4.3	807	14	CNS0128R	AL101253 Drosophila
1418	37.8	37.8	4.3	811	9	CX390775	CX390775 JGI_XZT38
1419	37.8	37.8	4.3	818	9	CX412492	CX412492 JGI_XZT29
C1420	37.8	37.8	4.3	818	10	DT066980	DT066980 AGENCOURT
1421	37.8	37.8	4.3	824	8	NI157340	NI157340 946039 MA
1422	37.8	37.8	4.3	832	3	BUS58775	BUS58775 AGENCOURT
1423	37.8	37.8	4.3	832	3	BUS962311	BUS962311 AGENCOURT
1424	37.8	37.8	4.3	854	14	AG484151	AG484151 Mus muscu
1425	37.8	37.8	4.3	865	14	CNS02087	AL175264 Tetraodon
C1426	37.8	37.8	4.3	885	10	DT771624	DT771624 125654981
1427	37.8	37.8	4.3	894	14	CNS0188G	AL109126 Drosophila
1428	37.8	37.8	4.3	902	14	AG420319	AG420319 Mus muscu
1429	37.8	37.8	4.3	905	14	CNS008KH	AL077798 Drosophila
1430	37.8	37.8	4.3	908	10	DV616838	DV616838 EST121983
1431	37.8	37.8	4.3	909	5	CK404318	CK404318 AUF Ifhdk
C1432	37.8	37.8	4.3	913	10	DT801869	DT801869 126509595
1433	37.8	37.8	4.3	917	14	CNS00D7X	AL060339 Drosophila
1434	37.8	37.8	4.3	952	12	CC865964	CC865964 NDL109D4
C1435	37.8	37.8	4.3	970	9	DN565766	DN565766 9078393
1436	37.8	37.8	4.3	977	10	DV071505	DV071505 VP01_09 K
1437	37.8	37.8	4.3	996	12	CL078587	CL078587 CH216-151
1438	37.8	37.8	4.3	1024	3	BU907570	BU907570 AGENCOURT
1439	37.8	37.8	4.3	1076	2	BM460792	BM460792 AGENCOURT
C1440	37.8	37.8	4.3	1082	9	DR151016	DR151016 42529339
1441	37.8	37.8	4.3	1101	14	CNS002M0	AL062875 Drosophila
C1442	37.8	37.8	4.3	1102	14	CNS02KTL	AL201954 Tetraodon
C1443	37.8	37.8	4.3	1116	1	AM096949	AM096949 AM096949
1444	37.8	37.8	4.3	1170	9	DR123591	DR123591 49154507
C1445	37.8	37.8	4.3	1182	1	AM091394	AM091394 AM091394
C1446	37.8	37.8	4.3	1257	10	DR957073	DR957073 CFW149-B0
1447	37.8	37.8	4.3	1277	10	DV77879	DV77879 Hw_Fat_21
1448	37.8	37.8	4.3	1361	10	DV782421	DV782421 Hw_liver
1449	37.8	37.8	4.3	1507	10	DR954131	DR954131 CFW131-D0
C1450	37.8	37.8	4.3	1528	14	AG355512	AG355512 Mus muscu
1451	37.8	37.8	4.3	2036	6	BC041059	BC041059 Homo sapi
1452	37.8	37.8	4.3	5007	6	CR936632	CR936632 Homo sapi
C1453	37.6	37.6	4.3	119	7	AW433790	AW433790 UI-R-BJOp
C1454	37.6	37.6	4.3	136	10	DV077658	DV077658 P138Fmidg
1455	37.6	37.6	4.3	188	9	DR066413	DR066413 TP18585 N
1456	37.6	37.6	4.3	211	7	BE057398	BE057398 en02f09.Y
1457	37.6	37.6	4.3	221	8	CX059639	CX059639 PDUt2037
1458	37.6	37.6	4.3	228	2	BI814123	BI814123 PESToal
1459	37.6	37.6	4.3	237	8	CV496004	CV496004 73678.1 C
1460	37.6	37.6	4.3	248	1	AI252008	AI252008 qv39a03.x
1461	37.6	37.6	4.3	251	1	AL725539	AL725539 AL725539
1462	37.6	37.6	4.3	253	1	AI343038	AI343038 tb02b04.x
1463	37.6	37.6	4.3	255	1	AU262602	AU262602 AU262602
1464	37.6	37.6	4.3	257	5	CD679743	CD679743 lab08H12
C1465	37.6	37.6	4.3	258	7	AW205032	AW205032 UI-H-B11
C1466	37.6	37.6	4.3	260	7	BB215975	BB215975 BB215975
1467	37.6	37.6	4.3	268	7	AW302662	AW302662 xr55c08.x
1468	37.6	37.6	4.3	269	1	AI336506	AI336506 ta93g07.x
1469	37.6	37.6	4.3	269	1	AU038592	AU038592 AU038592
1470	37.6	37.6	4.3	271	1	AI254251	AI254251 qv33601.x
1471	37.6	37.6	4.3	274	7	AW273962	AW273962 x871c03.x
1472	37.6	37.6	4.3	274	7	AW303238	AW303238 xr90a12.x
C1473	37.6	37.6	4.3	275	8	CR430362	CR430362 CR430362
1474	37.6	37.6	4.3	276	7	BF186481	BF186481 JAVH0676
1475	37.6	37.6	4.3	278	1	AA250004	AA250004 mx59a10.r
1476	37.6	37.6	4.3	281	7	AW568588	AW568588 g178f08.y
1477	37.6	37.6	4.3	285	7	BF054886	BF054886 7172f08.y
1478	37.6	37.6	4.3	286	7	AW268290	AW268290 xr95b11.x
1479	37.6	37.6	4.3	287	9	DN340369	DN340369 LTB3523-0

## ALIGNMENTS

RESULT 1	748 bp	mRNA	linear	EST 12-FEB-2003
CB242167/c	CB242167	UI-CF-FNO-aggd-f-19-0-UI-s1	UI-CF-FNO Homo sapiens	cdna clone
LOCUS	CB242167	UI-CF-FNO-aggd-f-19-0-UI 3'	mRNA sequence.	
DEFINITION	ACCESSION	VERSION	EST.	
	CB242167.1	GI:28363811	Homo sapiens (human)	
KEYWORDS	SOURCE	ORGANISM		
	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
	Hominidae; Homo.			
REFERENCE	1 (bases 1 to 748)			
AUTHORS	Bonaldi,M.F., Lennon,G. and Soares,M.B.			
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery			
JOURNAL	Genome Res. 6 (9), 791-806 (1996)			
PUBMED	8889548			
COMMENT	Contact: McCray, PB			
	University of Iowa			
	2024 University of Iowa Med Labs, Iowa City, IA 52242, USA			
	Tel: 319 356 4866			
	Fax: 319 356 7171			
	Email: paul-mccray@uiowa.edu			
	Tissue Procurement: Dr. M. J. Welsh, University of Iowa			
	cDNA Library preparation: Dr. M. Bento Soares, University of Iowa			
	cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa			
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa			
	Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).			
	The following repetitive elements were found in this cDNA sequence: 1-38, >AT rich#Low_complexity (matched complement)			
	Seq primer: M13 FORWARD			
	POLYA=Yes			
FEATURES	Location/Qualifiers			
source	1..748			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/clone="UI-CF-FNO-aggd-f-19-0-UI"			
	/tissue_type="Human Lung Epithelial cells"			
	/lab_host="DH10B (Life Technologies)"			
	/clone_lib="UI-CF-FNO"			
	/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a			

modified polylinker; Site.1: EcoR I; Site.2: Not I; UI-CF-FNO is a subtracted cDNA library derived from two non-normalized Human lung epithelial cell libraries (EN1 and DUI). The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@uiowa.edu  
TAG\_TISSUE=Human Lung Epithelial Cell Lines untreated LPS  
6hr to LPS 24h  
TAG\_LIB=UI-CF-FNO  
TAG\_SEQ=CTGCTCAGCT"

Query Match	83.3%	Score 725;	DB 4;	Length 748;
Best Local Similarity	99.6%;	Pred. No. 2.3e-185;		
Matches 747;	Conservative 0;	Mismatches 1;	Indels 2;	Gaps 2;
Qy	121	TCAGCAACATTACAGCTGCACCGCAGCAGTTGGATGAAAGTTCTAATCTCTTCCCTCCCTCC	180	
Db	748	TCAGCAACATTACAGCTGCACCGCAGCAGTTGGATGAAAG-TCTAATCTCTTCCCTCCCTCC	690	
Qy	181	TGTTGCTGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCGCA	240	
Db	689	TGTTGCTGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCA-GGGTGCGCA	631	
Qy	241	GAGGCCACAGGACCGAGGCCAGCGCTTCTAGGAGATGGCTCCAGGAGGGCGGCCCAAGAT	300	
Db	630	GAGGCCACAGGACCGAGGCCAGCGCTTNTAGGAGATGGCTCCAGGAGGGCGGCCCAAGAT	571	
Qy	301	GTGAGTGCAAAGATTGGTTCTTGAGAGCCCCGAGAGAAAATTCATGACAGTGTCTGGGC	360	
Db	570	GTGAGTGCNAAGATTGGTTCTTGAGAGCCCCGAGAGAAAATTCATGACAGTGTCTGGGC	511	
Qy	361	TGCCAAAGAGCAGTGGCCCTGTGATCAATTTCAAAGGCAATGTGAAGAAAACAAGACACC	420	
Db	510	TGCCAAAGAGCAGTGGCCCTGTGATCATTTCAAAGGCAATGTGAAGAAAACAAGACACC	451	
Qy	421	AAAGGCCACACAGAAAGCCAAACAAAGCAATCCAGAGCCTGCAGCAATTTCTCAAAACAAT	480	
Db	450	AAAGGCCACACAGAAAGCCAAACAAAGCAATCCAGAGCCTGCAGCAATTTCTCAAAACAAT	391	
Qy	481	GTACGCTAAGAAAGCTTTTGCTCTGGCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAAATTA	540	
Db	390	GTACGCTAAGAAAGCTTTTGCTCTGGCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAAATTA	331	
Qy	541	AACATTTCTCAGCCAAAGAAAGACAGTGAAGCAACCTTACAGACACTCTTCTTCTCCACCTC	600	
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Qy	601	ACTCTCCACCTGTACCACCCCTTAATCATTTCCAGTGTCTTCAAAAAGCATGTTTTTCAA	660	
Db	270	ACTCTCCACCTGTACCACCCCTTAATCATTTCCAGTGTCTTCAAAAAGCATGTTTTTCAA	211	
Qy	661	GATCAATTTTGTGTGTGCTCTCTAGTGTCTTCTTCTCGTCAGTCTTAGCCTGTGCCC	720	
Db	210	GATCAATTTTGTGTGTGCTCTCTAGTGTCTTCTTCTCGTCAGTCTTAGCCTGTGCCC	151	
Qy	721	CTCCCTTACCAGGCTTAGCGTTAATTACCTGAAAGATTCAGGAAACTGTAGCTTCTCT	780	
Db	150	CTCCCTTACCAGGCTTAGCGTTAATTACCTGAAAGATTCAGGAAACTGTAGCTTCTCT	91	
Qy	781	AGCTAGTGTCAATTTAACTTAATGCAATCAGGAAAGTAGCAAAACAGAAAGTCAATAAATA	840	
Db	90	AGCTAGTGTCAATTTAACTTAATGCAATCAGGAAAGTAGCAAAACAGAAAGTCAATAAATA	31	
Qy	841	TTTTTAAATGTCAAAAAAATAAAAAAATA 870		
Db	30	TTTTTAAATGTCAAAAAAATAAAAAAATA 1		

RESULT 2  
BM982101/c

DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	PUBMED	COMMENT
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## FEATURES

Query Match	Best Local Match
Qy	db

UI-CF-EN1-acr-i-08-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone  
 UI-CF-EN1-acr-i-08-0-UI 3', mRNA sequence.  
 BM982101  
 BM982101.1 GI:19605360  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 1 (bases 1 to 715)  
 Ronaldo,M.F., Lennon,G. and Soares,M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)  
 8889548  
 Contact: McCray, PB  
 McCray Lab  
 University of Iowa  
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
 Tel: 319 356 4866  
 Fax: 319 356 7171  
 Email: paul-mccray@uiowa.edu  
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics ([www.resgen.com](http://www.resgen.com)) or from Open Biosystems  
 ([www.openbiosystems.com](http://www.openbiosystems.com)).  
 The following repetitive elements were found in this cDNA  
 sequence: 1-38, >AT-rich#Low\_complexity (matched complement)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

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Location/Qualifiers
1. .715
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/db_xref="taxon:9606"
/clone="UI-CF-EN1-acr-i-08-0-UI"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial
Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EN1"
/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
UI-CF-EN1 is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an Ecor I adaptor, digested with Not
I, and cloned directionally into p773-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CTGCTCAGGT.
TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG LIB=UI-CF-EN1
TAG_SEQ=CTGCTCAGGT"

```

	78.8%;	Score 685.8;	DB 3;	Length 715;
	1 Similarity 99.3%;	Pred. No. 1e-174;	3;	
	1709; Conservative	0; Mismatches	2; Indels	2; Gaps
57	AAGTCTAATCTCTTCCCTCCTCTCTTGCTGGCCACTAATGCTGATGTCCTCTCTTA	216		
12	AAAGTCTAATCTCTTCCCTCCTCTCTGCTGGCCACTAATGCTGAT-TCCAAAGTCTCTTA	655		





PUBMED  
COMMENT

16341674  
Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 22 row: H column: 10  
High quality sequence stop: 677.  
Location/Qualifiers

FEATURES  
source

1. 677  
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/clone="S14K402-22-H10"  
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/clone\_lib="S14K402"  
/note="Organ: Stomach; Vector: pTZ19Rpl; Site 1: EcoRI;  
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with  
bacterial alkaline phosphatase (BAP) and then decapped  
with tobacco acid pyrophosphatase (TAP). The decapped  
intact mRNA was ligated with DNA-RNA linker including BcoR  
I site by treatment of T4 RNA ligase and the first strand  
cDNA was synthesized from oligo dT-selected mRNA by  
priming with dr-tailed vector. The dT-tailed vector was  
adjusted to have about 60nt. The cDNA vector was  
circularized with E. coli DNA ligase after digestion of  
EcoRI which site is also included in vector. An RNA strand  
converted to a DNA strand by Okayama-Berg method. The  
obtained cDNA vectors were used for transfection of  
competent cells E. coli Top10F' by electroporation method.  
The cDNA libraries constructed by this method are  
full-length enriched cDNA library."

## ORIGIN

Query Match 77.8%; Score 677; DB 3; Length 677;  
Best Local Similarity 100.0%; Pred. No. 2.5e-172;  
Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTGACCTGAGTCATCCCGAGGATCAGGAGCTCCAGCAGGGAACCTTCCATTATATCT 60  
QY 121 TCAAGCACTTACAGTCGACCGACAGTTCGATGAAGTTCTATCTCTCTCTCTCTCC 180  
DB 61 TCAAGCACTTACAGTCGACCGACAGTTCGATGAAGTTCTATCTCTCTCTCTCTCC 120  
QY 181 TGTTCGTCCTATGCTGATGTCCATGCTCTAGCAGCCTGATCCAGGGTCCGCA 240  
DB 121 TGTTCGTCCTATGCTGATGTCCATGCTCTAGCAGCCTGATCCAGGGTCCGCA 180  
QY 241 GAGGCCACAGGACCCAGGCTCTTAGAGATGGCTCCAGGAAGCGCGCAAGAT 300  
DB 181 GAGGCCACAGGACCCAGGCTCTTAGAGATGGCTCCAGGAAGCGCGCAAGAT 240  
QY 301 GTGAGTGAAGATTTGGTCTTAGAGCCCGAGAGAAAATTCATGACAGTGTCTGGGC 360  
DB 241 GTGAGTGAAGATTTGGTCTTAGAGCCCGAGAGAAAATTCATGACAGTGTCTGGGC 300  
QY 361 TGCCAAAGACGATGCTGATCATTTCAAGGGCAATGTGAAGAAACAGACACC 420  
DB 301 TGCCAAAGACGATGCTGATCATTTCAAGGGCAATGTGAAGAAACAGACACC 360  
QY 421 AAAGGCCACACAGAAAGCCAAACAGCATTCAGAGCCTGCCAGCAATTTCTCAAAAT 480  
DB 361 AAAGGCCACACAGAAAGCCAAACAGCATTCAGAGCCTGCCAGCAATTTCTCAAAAT 420  
QY 481 GTCAGCTAAGAAAGCTTTGCTCTGCTTTGTAGAGCTCTGAGCGGCCACTCTTCCAAATTA 540  
DB 421 GTCAGCTAAGAAAGCTTTGCTCTGCTTTGTAGAGCTCTGAGCGGCCACTCTTCCAAATTA 480

QY 541 AACATTCTCAGCCCAAGAGACAGTGAAGACACCTACACAGACACTCTTCTTCTCCACCTC 600  
DB 481 AACATTCTCAGCCCAAGAGACAGTGAAGACACCTACACAGACACTCTTCTTCTCCACCTC 540  
QY 601 ACTCTCCCACTGTACCCACCCCTTAATCATTCAGTGTCTTCAAAAGCATGTTTTTCAA 660  
DB 541 ACTCTCCCACTGTACCCACCCCTTAATCATTCAGTGTCTTCAAAAGCATGTTTTTCAA 600  
QY 661 GATCATTTTGTGTTGTCTCTCTAGTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720  
DB 601 GATCATTTTGTGTTGTCTCTCTAGTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660  
QY 721 CTCCTCTTACCCAGGCT 737  
DB 661 CTCCTCTTACCCAGGCT 677

RESULT 6  
BI770944

LOCUS BI770944 820 bp mRNA linear EST 25-SBP-2001  
DEFINITION 603059769F1 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:5209073 5',  
mRNA sequence.

ACCESSION BI770944

VERSION BI770944.1 GI:15762522

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.

REFERENCE 1 (bases 1 to 820)

AUTHORS NIH-MGC <http://mgi.nhl.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11524 row: j column: 18

High quality sequence stop: 772.

FEATURES  
source

1. 820  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5209073"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_122"  
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;  
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source  
anonymous pool of 24 week female lung, 16 week female  
spleen, and 20-22 week male spleens. Library is oligo-dT  
primed and directionally cloned (EcoRV site is destroyed  
upon cloning). Average insert size 1.4 kb, insert size  
range 1-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 026. Note:  
this is a NIH\_MGC Library."

## ORIGIN

Query Match 77.7%; Score 675.6; DB 2; Length 820;  
Best Local Similarity 94.2%; Pred. No. 6.2e-172;  
Matches 769; Conservative 0; Mismatches 34; Indels 13; Gaps 6;

QY 65 CTGAGTCAATCCCGAGGATCAGGAGCTCCAGAGGGAACCTTCCATTATATTTCTTCAA 124  
DB 1 CTTGAGTCAATCCCGAGGATCAGGAGCTCCAGAGGGAACCTTCCATTATATTTCTTCAA 59

QY 125 GCAACTTACAGCTGCACCGACAGTTGGCATGAAAGTTCTTAATCTCTTCCCTCCTCTGTT 184  
Db 60 GCAACTTACAGCTGCACCGACAGTTGGCATGAAAGTTCTTAATCTCTTCCCTCCTCTGTT 119  
QY 185 GCTGCCACTTAATGCTGATGTCATGCTCTCTAGCAGCCTGGAATCCAGGSGTCCGACAGG 244  
Db 120 GCTGCCACTTAATGCTGATGTCATGCTCTCTAGCAGCCTGGAATCCA-GGGTCCGACAGG 178  
QY 245 CCACAGGACCGAGCCAGGCTTCTAGGAGATGGCTCCAGGAAGCGCGCAAGATGTGA 304  
Db 179 CCACAGGACCGAGCCAGGCTTCTAGGAGATGGCTCCAGGAAGCGCGCAAGATGTGA 238  
QY 305 GTGCAAGATTGTTCTCTG-AGAGCCCGCAGAGAAAATTCATGACAGTGTCTGGGCTGC 363  
Db 239 GTGCAAGATTGTTCTCTGCTCGGCCCGCCCAAGAAAATTCATGACAGTGTCTGGGCTGC 298  
QY 364 CAAGAAGCAGTGCCTCTGATCATTTTCAGGGCAATGTGAAGAAAACAAGACACCAA 423  
Db 299 CAAGAAGCAGTGCCTCTGATCATTTTCAGGGCAATGTGAAGAAAACAAGACACCAA 358  
QY 424 GGCACACAGAAAGCAACAGCAATTCAGAGCCTGCCAGCAATTTCTCAAAACAATGTC 483  
Db 359 GGCACACAGAAAGCAACAGCAATTCAGAGCCTGCCAGCAATTTCTCAAAACAATGTC 418  
QY 484 AGCTAAGAAGCTTGTCTGCTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAAC 543  
Db 419 AGCTAAGAAGCTTGTCTGCTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAAC 478  
QY 544 ATTCTCAGCAAGAGACAGTGCACACCTACAGACACTCTTCTTCCACCTCACT 603  
Db 479 ATTCTCAGCAAGAGACAGTGCACACCTACAGACACTCTTCTTCCACCTCACT 538  
QY 604 CTCCCACTGTACCCACCTCTAAATCATTCAGTGTCTCAAAAGCATGTTTTCAAGAT 663  
Db 539 CTCCCACTGTACCCACCTCTAAATCATTCAGTGTCTCAAAAGCATGTTTTCAAGAT 598  
QY 664 CATTTTGTGTTGCTCTCTCTAGTGTCTTCTCTCTGTCAGTCTTACGCTGTGCGCTC 723  
Db 599 CA-TTTGTTGTTGCTCTCTCTAGTGTCTTCTCTCTGTCAGTCTTAGCCTGTGCGCTC 657  
QY 724 CCTTACCCAGCTTAGCTTAATTAACCTGAAAGATTCAGGAATCTAGCTTCTTCTAGC 783  
Db 658 CCTTACCCAGCTTAGCTTAATTAACCTGAAAGATTCAGGAATCTTAGCTTCTTCTAGC 717  
QY 784 TAGTGTCAAT-----TAACCTTAAATGCAATCAGGAAGTAGCAACAGAGTCAA- 834  
Db 718 TAGTGTCAATTTAAGCCCTTAAATTTGCCACTCAGGAACAGCTAGGCAACAGAGTCAAT 777  
QY 835 TAAATATTTTAAATGTCAAAAAAAMAAAAA 870  
Db 778 TAAATATTTTAAATGTCAACCAACCAACACGAA 813

RESULT 7  
BX102380  
LOCUS BX102380 Soares ovary tumor NbHOT Homo sapiens cdna clone  
DEFINITION IMAGp998H051817 ; IMAGE:740020, mRNA sequence.  
ACCESSION BX102380  
VERSION BX102380.1 GI:27831743  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 671)  
Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,  
Radelof,U., Schneider,D. and Korn,B.  
TITLE Human Unigeneset - RZPD3  
JOURNAL Unpublished (2003)  
COMMENT Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD; IMAGp998H051817.  
RZPDLIB; I.M.A.G.E. cdna Clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No.972)  
http://www.rzpd.de/CloneCards/cgi-  
bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
www.rzpd.de

This clone is available royalty-free from RZPD;  
contact RZPD (clone@rzpd.de) for further information. Seq primer:  
M13r, Primer sequence: TTTCACACAGAAACAGCTATGAC.  
Location/Qualifiers

FEATURES

source

1..671  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGp998H051817 ; IMAGE:740020"  
/sex="Female"  
/tissue\_type="ovarian tumor"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares ovary tumor NbHOT"  
/note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a  
modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cdna was primed with a Not I - oligo(dT) primer (5'  
TGTTACCAATCTGAATGGAGCGCGCGGTTTTTTTTTTTTTTT 3'),  
double-stranded cdna was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7T3 vector  
(Pharmacia). Library constructed by Bento Soares and  
M.Fatima Bonaldo. "

ORIGIN

Query Match 77.1%; Score 671; DB 4; Length 671;  
Best Local Similarity 100.0%; Pred. No. 1e-170;  
Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTCGCCCTCAAAATGGGAACGCTGGCGCTGGGACTAAAGCATAGACACAGGCTGAGTATC 60  
Db 1 CTCGCCCTCAAAATGGGAACGCTGGCGCTGGGACTAAAGCATAGACACAGGCTGAGTATC 60  
QY 61 CTGACCTGAGTCATCCCAGGGATCAGGAGCCTCAGCAGGGAACCTTCCATTATATCT 120  
Db 61 CTGACCTGAGTCATCCCAGGGATCAGGAGCCTCAGCAGGGAACCTTCCATTATATCT 120  
QY 121 TCAAGCAACTTACAGCTGCACCGCAGTTGGGATGAAAGTTCTTAATCTCTTCCCTCCTCC 180  
Db 121 TCAAGCAACTTACAGCTGCACCGCAGTTGGGATGAAAGTTCTTAATCTCTTCCCTCCTCC 180  
QY 181 TGTTCCTGCCACTAATGCTGATGTCATGTCCTTAGCAGCCTGAATCCAGGGTTCGCCA 240  
Db 181 TGTTCCTGCCACTAATGCTGATGTCATGTCCTTAGCAGCCTGAATCCAGGGTTCGCCA 240  
QY 241 GAGGCCACAGGACCGAGGCCAGGCTTCTAGAGATGCTCCAGGAAGCGCGCCCAAGAT 300  
Db 241 GAGGCCACAGGACCGAGGCCAGGCTTCTAGAGATGCTCCAGGAAGCGCGCCCAAGAT 300  
QY 301 GTGAGTCCAAAGATTGGTTCTCTGAGAGCCCGCAGAGAAAATTCATGACAGTGTCTGGGC 360  
Db 301 GTGAGTCCAAAGATTGGTTCTCTGAGAGCCCGCAGAGAAAATTCATGACAGTGTCTGGGC 360  
QY 361 TGCCAAAGAAGCAGTGGCCCTGTGATCATTTTCAAGGGCAATGTGAAGAAAACAAGACACC 420  
Db 361 TGCCAAAGAAGCAGTGGCCCTGTGATCATTTTCAAGGGCAATGTGAAGAAAACAAGACACC 420  
QY 421 AAAGGCACCAAGAAAGCAACCAAGCAATTCAGAGCCTGCCAGCAATTTCTCAACCAAT 480  
Db 421 AAAGGCACCAAGAAAGCAACCAAGCAATTCAGAGCCTGCCAGCAATTTCTCAACCAAT 480  
QY 481 GTCAGCTAAGAAGCTTTGCTCTGCTTGTAGGAGCTCTGAGCGCCCACTCTTCCCAATTA 540



Db 481 GTCAGCTAAGAAGCTTTGGCTCTGCTCTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTA 540  
Qy 541 AACATTCTCAGCCCAAGAAGACAGTGTAGCAGACCTACAGACACTCTTCTTCTCCCACTTC 600  
Db 541 AACATTCTCAGCCCAAGAAGACAGTGTAGCAGACCTACAGACACTCTTCTTCTCCCACTTC 600  
Qy 601 ACTCTCCCACTGTACCCACCCCTTAATCATTTCCAGTGTCTCAAAAGCATGTTTTTCAA 660  
Db 601 ACTCTCCCACTGTACCCACCCCTTAATCATTTCCAGTGTCTCAAAAGCATGTTTTTCAA 660  
Qy 661 GATCATTGTTGT 671  
Db 661 GATCATTGTTGT 671

RESULT 8  
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LOCUS K-EST0104808 S14K402s1 Homo sapiens cDNA clone S14K402s1-18-A11 5',  
DEFINITION mRNA sequence.  
ACCESSION BM831028  
VERSION BM831028.1 GI:19187437  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 666)  
Oh, J. H., Yang, J. O., Hahn, Y., Kim, M. R., Byun, S. S., Jeon, Y. J.,  
Kim, J. M., Song, K. S., Noh, S. M., Kim, S., Yoo, H. S., Kim, Y. S. and  
Kim, N. S.  
Transcriptome analysis of human gastric cancer  
Mamm. Genome 16 (12), 942-954 (2005)  
16341674  
Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yusong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsaung@mail.kribb.re.kr  
Plate: 18 row: A column: 11  
High quality sequence stop: 666.  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="S14K402s1-18-A11"  
/cell\_line="K402"  
/lab\_host="Top10f"  
/clone\_lib="S14K402s1"  
/notes="Organ: Stomach; Vector: pTZ19RP1; Site 1: EcoRI;  
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with  
bacterial alkaline phosphatase (BAP) and then decapped  
with tobacco acid pyrophosphatase (TAP). The decapped  
intact mRNA was ligated with DNA-RNA linker including EcoR  
I site by treatment of T4 RNA ligase and the first strand  
cDNA was synthesized from oligo dt-selected mRNA by  
priming with dt-tailed vector. The dt-tailed vector was  
adjusted to have about 60nt. The cDNA vector was  
circularized with E. coli DNA ligase after digestion of  
EcoRI which site is also included in vector. An RNA strand  
converted to a DNA strand by Okayama-Berg method. The  
obtained cDNA vectors were used for transformation of  
competent cells E. coli Top10f' by electroporation method.  
The cDNA libraries constructed by this method are  
full-length enriched cDNA library. After analyzing and  
sequencing about 2,000 ~ 3,000 colonies in original cDNA  
library, the abundant cDNAs were selected and amplified by  
PCR reaction using vector region primer including T7  
promotor as 5' primer and N(dt)14 as 3' primer. The PCR

TITLE Transcriptome analysis of human gastric cancer

JOURNAL Mamm. Genome 16 (12), 942-954 (2005)

PUBLISHED 16341674

COMMENT Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Boeun-dong Yusong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsaung@mail.kribb.re.kr

Plate: 18 row: A column: 11

High quality sequence stop: 666.

Location/Qualifiers

1. 666

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="S14K402s1-18-A11"

/cell\_line="K402"

/lab\_host="Top10f"

/clone\_lib="S14K402s1"

products were used as template for synthesis of  
biotinylated single stranded RNA by in vitro transcription  
reaction. The synthesized RNA probes were hybridized with  
antisense single stranded cDNAs prepared from original  
library and incubated with avidin-gel. After removing  
DNA-RNA hybrids by centrifuge, the subtracted cDNA  
libraries were constructed by transformation of the  
remaining DNA into competent cells E. coli Top10f' with  
electroporation method."

ORIGIN

Query Match 76.6%; Score 666; DB 3; Length 666;  
Best Local Similarity 100.0%; Pred. No. 2.4e-169;  
Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 CTGACCTGAGTCATCCCCAGGGATCAGGAGCTCCAGCAGGGAACCTTCCATTATATTTCT 120  
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Qy 121 TCAAGCAACTTACAGCTGCACCGACAGTTCGATGAAGTTCTAAATCTCTTCCCTCTCC 180  
Db 61 TCAAGCAACTTACAGCTGCACCGACAGTTCGATGAAGTTCTAAATCTCTTCCCTCTCC 120  
Qy 181 TGTGCTGCCACTTAATGCTGTGATGTCATGCTCTTAGCAGCTTGAATCCAGGGGTGCCCA 240  
Db 121 TGTGCTGCCACTTAATGCTGTGATGTCATGCTCTTAGCAGCTTGAATCCAGGGGTGCCCA 180  
Qy 241 GAGGCCACAGGACCGAGCGCCAGGCTTCTAGGAGATGGCTCCAGGAGGCGGCAAGAAT 300  
Db 181 GAGGCCACAGGACCGAGCGCCAGGCTTCTAGGAGATGGCTCCAGGAGGCGGCAAGAAT 240  
Qy 301 GTGAGTGCAAGATTTGGTTCTTGAGAGCCCGAGAGAAAATTCATGACAGTGTCTGGGC 360  
Db 241 GTGAGTGCAAGATTTGGTTCTTGAGAGCCCGAGAGAAAATTCATGACAGTGTCTGGGC 300  
Qy 361 TGCCAAAGAACAGTGTGCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACC 420  
Db 301 TGCCAAAGAACAGTGTGCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACC 360  
Qy 421 AAAGGCCACACAGAAAGCCAAACAGCCTCCAGGCGCTCCAGCAATTTCTCAACAAT 480  
Db 361 AAAGGCCACACAGAAAGCCAAACAGCCTCCAGGAGCTTCCAGAGCAATTTCTCAACAAT 420  
Qy 481 GTCAGCTAAGAAGCTTTGCTCTGCTCTGTAGAGCTCTGAGCGCCCACTTCTCCAATTA 540  
Db 421 GTCAGCTAAGAAGCTTTGCTCTGCTCTGTAGAGCTCTGAGCGCCCACTTCTCCAATTA 480  
Qy 541 AACATTCTCAGCCCAAGAAGACAGTGTAGCAGACCTACAGACACTTCTTCTCCCACTTC 600  
Db 481 AACATTCTCAGCCCAAGAAGACAGTGTAGCAGACCTACAGACACTTCTTCTCCCACTTC 540  
Qy 601 ACTCTCCCACTGTACCCACCCCTTAATCATTTCCAGTGTCTCAAAAGCATGTTTTTCAA 660  
Db 541 ACTCTCCCACTGTACCCACCCCTTAATCATTTCCAGTGTCTCAAAAGCATGTTTTTCAA 600  
Qy 661 GATCATTGTTGTTGCTCTCTCTAGTGTCTTCTCTCTCGTCAGTCTTAGCTGTGCC 720  
Db 601 GATCATTGTTGTTGCTCTCTCTAGTGTCTTCTCTCTCGTCAGTCTTAGCTGTGCC 660  
Qy 721 CTCCCC 726  
Db 661 CTCCCC 666

RESULT 9  
BM854000  
LOCUS K-EST0136291 S14K402 Homo sapiens cDNA clone S14K402-37-E04 5',  
DEFINITION mRNA sequence.  
ACCESSION BM854000  
VERSION BM854000.1 GI:19210399  
KEYWORDS EST.  
SOURCE Homo sapiens (human)



expression library"  
/note="Organ: Mammary gland (cancer tissue); Vector:  
pCMV6-XL5; Site 1: EcoRI; Site 2: XhoI/Sall compatible end  
ligatio; Oligo-dT primed reverse transcription optimized  
for large and GC rich mRNA transcripts, cDNA size  
selection, optimized ligation for large inserts into  
mammalian expression vector, random clones selected for  
end sequence verification of full-length genes"

## ORIGIN

Query Match 71.5%; Score 622; DB 9; Length 628;  
Best Local Similarity 100.0%; Pred. No. 2.1e-157;  
Matches 622; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GGACTAAGCATAGACACACAGCTGAGTATCTGACCTGAGTCATCCCGAGGATCAGG 88  
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QY 89 AGCCTCCAGCAGGAAACCTTCCATTATATTTCTTCAAGCAACTTACAGCTGCACCGACAGT 148  
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QY 149 TGGATGAAGATTTCTAATCTTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 208  
Db 127 TGGATGAAGATTTCTAATCTTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 186  
QY 209 GGTCTTAGCAGCTGAATCCAGGGTTCGCGAGGCGCCAGAGGCGGAGGCGGAGGCTTC 268  
Db 187 GGTCTTAGCAGCTGAATCCAGGGTTCGCGAGGCGCCAGAGGCGGAGGCGGAGGCTTC 246  
QY 269 TAGGAGATGGCTCTCAGGAAGCGCGCAAGAAATGTGAGTGCAAGAGATTTGGTTCTTGAGAGC 328  
Db 247 TAGGAGATGGCTCTCAGGAAGCGCGCAAGAAATGTGAGTGCAAGAGATTTGGTTCTTGAGAGC 306  
QY 329 CCCGAGAAGAAATTCATGACAGTGTCTGGGCTGCCAAGAGAGAGAGTGCCTCTGTATCA 388  
Db 307 CCCGAGAAGAAATTCATGACAGTGTCTGGGCTGCCAAGAGAGAGAGTGCCTCTGTATCA 366  
QY 389 TTTCAGGGCAATGTGAAGAAACACACACACAGGCGCCAGAGGCGGAGGCGGAGGCGGAGGCA 448  
Db 367 TTTCAGGGCAATGTGAAGAAACACACACACAGGCGCCAGAGGCGGAGGCGGAGGCGGAGGCA 426  
QY 449 TTCCAGAGCTGCGCAGCAATTTCTCAAAACAATGTCAAGTAAAGAGTCTTGCTCTGCTTT 508  
Db 427 TTCCAGAGCTGCGCAGCAATTTCTCAAAACAATGTCAAGTAAAGAGTCTTGCTCTGCTTT 486  
QY 509 GTAGAGCTCTGAGCGCCCACTCTTCCAAATTAACAATTTTCAGCCCAAGAGAGAGTGAAGC 568  
Db 487 GTAGAGCTCTGAGCGCCCACTCTTCCAAATTAACAATTTTCAGCCCAAGAGAGAGTGAAGC 546  
QY 569 ACACCTACAGACACTTCTTCTCCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 628  
Db 547 ACACCTACAGACACTTCTTCTCTCCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 606  
QY 629 ATTCCAGTGTCTCAAAAAGCA 650  
Db 607 ATTCCAGTGTCTCAAAAAGCA 628

## RESULT 11

DN998245  
LOCUS  
DEFINITION  
TC124609 Human breast cancer tissue, large insert, pCMV expression  
library Homo sapiens cDNA clone TC124609 5', similar to Homo sapiens  
DMC (U0473), mRNA sequence.  
DN998245  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
DN998245 628 bp mRNA linear EST 17-MAY-2005  
TC124609 Human breast cancer tissue, large insert, pCMV expression  
library Homo sapiens cDNA clone TC124609 5', similar to Homo sapiens  
DMC (U0473), mRNA sequence.  
DN998245.1 GI:66258072  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.

REFERENCE  
AUTHORS

1 (bases 1 to 628)  
Birkett, C., Cho, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, L.,  
Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M.,  
Zhang, X., Jay, G. and He, W.  
High-throughput cloning of full-length human cDNAs directly from  
cDNA libraries optimized for large and rare transcripts  
Unpublished (2005)

## TITLE

## JOURNAL

## COMMENT

Contact: Kovacs, KF  
High Throughput cDNA Cloning  
Origene Technologies, Inc. (www.origene.com)  
6 Taft Court, Suite 100, Rockville, MD 20850, USA  
Tel: 301 340 3188  
Fax: 301 340 8606  
Email: cDNA@origene.com

This EST submission is part of an on-going human full-length  
cloning project at Origene Technologies, Inc.  
Please contact Origene for access.  
Origene Technologies, Inc.  
6 Taft Ct. Suite 100  
Rockville, MD 20850  
Tel: (301) 340-3188  
http://www.origene.com

Seq primer: pCMV6 5prime forward vector primer, Origene  
Technologies Inc.

Location/Qualifiers

FEATURES  
source

1..628  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="TC124609"  
/tissue type="Breast cancer"  
/clone lib="Human breast cancer tissue, large insert, pCMV  
expression library"  
/notes="Organ: Mammary gland (cancer tissue); Vector:  
pCMV6-XL5; Site 1: EcoRI; Site 2: XhoI/Sall compatible end  
ligatio; Oligo-dT primed reverse transcription optimized  
for large and GC rich mRNA transcripts, cDNA size  
selection, optimized ligation for large inserts into  
mammalian expression vector, random clones selected for  
end sequence verification of full-length genes"

## ORIGIN

Query Match 71.4%; Score 621.4; DB 9; Length 628;  
Best Local Similarity 99.8%; Pred. No. 3.1e-157;  
Matches 622; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 AGCATAGACACAGCTGAGTATCTGACCTGAGTCATCCCGAGGATCAGAGGCTCC 95  
Db 6 AGCATAGACACAGCTGAGTATCTGACCTGAGTCATCCCGAGGATCAGAGGCTCC 65  
QY 96 AGCAGGGACCTTCCATTATTTCTTCAAGCAACTTACAGCTGCACCGACAGTTGGATG 155  
Db 66 AGCAGGGACCTTCCATTATTTCTTCAAGCAACTTACAGCTGCACCGACAGTTGGATG 125  
QY 156 AAAGTTCTAATCTTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 215  
Db 126 AAAGTTCTAATCTTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 185  
QY 216 AGCAGCTGAATCCAGGGTTCGCGAGGCGCCAGAGGCGGAGGCGGAGGCGGAGG 275  
Db 186 AGCAGCTGAATCCAGGGTTCGCGAGGCGCCAGAGGCGGAGGCGGAGGCGGAGG 245  
QY 276 TGGCTCCAGAGAGGCGGCGCAAGATGTGAGTGCAGAGATTTGGTTCTGAGAGCCCCGAGA 335  
Db 246 TGGCTCCAGAGAGGCGGCGCAAGATGTGAGTGCAGAGATTTGGTTCTGAGAGCCCCGAGA 305  
QY 336 AGAAATTCATGACAGTGTCTGGGCTGCCAAGAGACAGTGCCTCTGTATCATTTCAAG 395  
Db 306 AGAAATTCATGACAGTGTCTGGGCTGCCAAGAGACAGTGCCTCTGTATCATTTCAAG 365  
QY 396 GGCATGTGAAGAAACCAAGACACCAAGAGGCGCCAGAGAGGCGGAGGCGGAGGCGGAGG 455  
Db 366 GGCATGTGAAGAAACCAAGACACCAAGAGGCGCCAGAGAGGCGGAGGCGGAGGCGGAGG 425

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QY 456 GCCTGCCAGCAATTTCTCAAAACAATGTGAGTCAAGAGCTTTGCTCTGCTTTGTAGGAG 515
Db 426 GCCTGCCAGCAATTTCTCAAAACAATGTGAGTCAAGAGCTTTGCTCTGCTTTGTAGGAG 485
QY 516 CTCTGAGCGCCACATCTTCCCAATTAACAATCTCAGCCCAAGAGACAGTGAGCACACCTA 575
Db 486 CTCTGAGCGCCACATCTTCCCAATTAACAATCTCAGCCCAAGAGACAGTGAGCACACCTA 545
QY 576 CCAGACATCTTCTTCTCCACCTCACTCTCCACTGTACCCACCCCTAAATCATTTCCAG 635
Db 546 CCAGACATCTTCTTCTCCACCTCACTCTCCACTGTACCCACCCCTAAATCATTTCCAG 605
QY 636 TGCTCTCAAAAAGCATGTTTTTC 658
Db 606 TGCTCTCAAAAAGCATGTTTTTC 628

RESULT 12
CD688783 631 bp mRNA linear EST 25-JUN-2003
LOCUS EST5305 human nasopharynx Homo sapiens cDNA, mRNA sequence.
DEFINITION CD688783
ACCESSION CD688783
VERSION CD688783.1 GI:32207896
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 631)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
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Tel: 86-1380-9770-743
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Email: yxzeng@zsuums.edu.cn.

FEATURES
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library from southern Chinese"

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Best Local Similarity 99.7%; Pred. No. 1.5e-153;
Matches 609; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 637 GCTCTCAAAA 647
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RESULT 13
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ACCESSION BM746867
VERSION BM746867.1 GI:19076451
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 628)
AUTHORS Oh,J.H., Yang,J.O., Hahn,Y., Kim,M.R., Byun,S.S., Jeon,Y.J.,
Kim,J.M., Song,K.S., Noh,S.M., Kim,S., Yoo,H.S., Kim,Y.S. and
Kim,N.S.
TITLE Transcriptome analysis of human gastric cancer
JOURNAL Mamm. Genome 16 (12), 942-954 (2005)
PUBMED 16341674
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 4 row: A column: 11
High quality sequence stop: 628.
Location/Qualifiers
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Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deapped
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with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10<sup>+</sup> by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10<sup>+</sup> with electroporation method."

ORIGIN

Query Match		69.8%;	Score 607.2;	DB 3;	Length 628;
Best Local Similarity		98.6%;	Pred. No. 2.2e-153;		
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QY	216	AGCAGCTGAAATCCAGGGTGCAGAGGCGCACAGGACCGAGGCGAGGCTTCAGGAGA	275		
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QY	276	TGGCTCCAGAGGCGGCGCAAGATCTGAGTGCAAGATTGGTTCTGAGGCGCCGAGA	335		
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QY	456	GCTGCGAGCAATTTCTCAACATGTCAGCTAAGAGCTTTGCTCTGCTTTGTAGGAG	515		
DB	421	GCTGCGAGCAATTTCTCAACATGTCAGCTAAGAGCTTTGCTCTGCTTTGTAGGAG	480		
QY	516	CTCTGAGCGCCACTCTTCCAAATTAACATTTCTCAGCCAGAGAGACAGTGAGCACACCTA	575		
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DEFINITION					
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VERSION					
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;					
Hominidae; Homo.					
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AUTHORS					
TITLE					
JOURNAL					
PUBMED					
COMMENT					
Genome Res. 6 (9), 791-806 (1996)					
8889548					
Contact: McCray, PB					
McCray Lab					
University of Iowa					
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA					
Tel: 319 356 4866					
Fax: 319 356 7171					
Email: paul-mccray@uiowa.edu					
Tissue Procurement: Dr. M. J. Welsh, University of Iowa					
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa					
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa					
Clone Distribution: Researchers may obtain clones from Research					
Genetics (www.resgen.com) or from Open Biosystems					
(www.openbiosystems.com).					
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day 64, day 87, week 19 and week 42. The library was					
constructed according to Bonaldo, Lennon and Soares,					
Genome Research, 6:791-806, 1996. First strand cDNA					
synthesis was primed with an oligo-dT primer containing a					
Not I site. Double stranded cDNA was ligated to an EcoR I					
adaptor, digested with Not I, and cloned directionally					
into pT7T3-Pac vector. The oligonucleotide used to prime					
the synthesis of first-strand cDNA contains a library tag					
sequence that is located between the Not I site and the					
(dT)18 tail. The sequence tag for this library is					
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and 380-383					
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ORIGIN					
Query Match					
Best Local Similarity					
Matches 591; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
67.9%; Score 590.4; DB 3; Length 592;					
99.8%; Pred. No. 8e-149;					

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QY	699	CTCGTCAGTCTTAGCGCTGTGCCCTCCCTTACCAGGCTTAGGCTTAATTTACCTGAAAGA	758
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AUTHORS	Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yoneyama, T., Oteuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Sugano, S., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.				
TITLE	Diversification of Transcriptional Modulation: large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes				
JOURNAL	Genome Res. 16 (1), 55-65 (2006)				
PUBMED	16344560				
COMMENT	Contact: Takao Isogai FLJ Project (HRI Team) Helix Research Institute 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986				

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Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
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## ORIGIN

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C 849	40.6	4.7	2619	16	US-11-091-883-478	Sequence 478, App	C 924	38.2	4.4	1389	9	US-10-425-115-50365	Sequence 50365, A
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C 881	39	4.5	2211	16	US-11-232-440-36	Sequence 36, Appl	C 956	37.8	4.3	654	12	US-10-301-480-1181593	Sequence 1181593,
C 882	39	4.5	2249	9	US-10-723-860-6384	Sequence 6384, Ap	C 957	37.8	4.3	654	12	US-10-301-480-1181596	Sequence 1181596,
C 883	39	4.5	413	3	US-09-918-995-17652	Sequence 17652, A	C 958	37.6	4.3	654	12	US-10-357-930-56482	Sequence 56482, A
C 885	38.8	4.5	546	8	US-10-021-323-4518	Sequence 4518, Ap	C 960	37.6	4.3	450	8	US-10-425-115-60121	Sequence 60121, A
C 886	38.8	4.5	551	8	US-10-424-599-123498	Sequence 123498,	C 961	37.6	4.3	506	9	US-10-424-599-50022	Sequence 50022, A
C 887	38.8	4.5	862	7	US-10-264-043-359	Sequence 359, App	C 962	37.6	4.3	521	8	US-10-021-323-3016	Sequence 3016, Ap
C 888	38.8	4.5	1042	10	US-10-750-185-57597	Sequence 57597, A	C 963	37.6	4.3	560	8	US-10-021-323-6397	Sequence 6397, Ap
C 889	38.8	4.5	1042	10	US-10-750-623-57597	Sequence 57597, A	C 964	37.6	4.3	579	8	US-10-021-323-6397	Sequence 117, App
C 890	38.8	4.5	2814	4	US-09-925-065A-58402	Sequence 58402, A	C 965	37.6	4.3	8649	8	US-10-221-613-117	Sequence 51, Appl
C 891	38.8	4.5	2814	5	US-09-925-065A-58402	Sequence 58402, A	C 966	37.6	4.3	8649	8	US-10-504-601-21	Sequence 21, Appl
C 892	38.8	4.5	2814	12	US-10-301-480-159640	Sequence 159640,	C 967	37.6	4.3	16132	10	US-09-768-827-50	Sequence 50, Appl
C 893	38.8	4.5	2814	12	US-10-301-480-773049	Sequence 773049,	C 968	37.6	4.3	158	3	US-09-918-995-17909	Sequence 17909, A
C 894	38.6	4.4	332	9	US-10-723-860-353	Sequence 353, App	C 969	37.4	4.3	416	3	US-09-764-831-1336	Sequence 1336, Ap
C 895	38.6	4.4	332	9	US-10-756-149-379	Sequence 379, App	C 970	37.4	4.3	439	3	US-09-960-352-13817	Sequence 13817, A
C 896	38.6	4.4	1083	9	US-10-723-860-5056	Sequence 5056, Ap	C 971	37.4	4.3	500	9	US-10-425-115-5045	Sequence 5045, Ap
C 897	38.6	4.4	2125	3	US-09-880-107-2412	Sequence 2412, Ap	C 972	37.4	4.3	579	9	US-10-425-115-140518	Sequence 140518,
C 898	38.6	4.4	2125	8	US-10-706-791-20	Sequence 20, Appl	C 973	37.4	4.3	638	9	US-10-425-115-94457	Sequence 94457, A
C 899	38.6	4.4	6609	7	US-10-311-455-1856	Sequence 1856, Ap	C 974	37.4	4.3	932	9	US-10-425-115-105074	Sequence 105074,
C 900	38.4	4.4	417	9	US-10-425-115-209	Sequence 209, App	C 975	37.4	4.3	8111	6	US-10-172-086-55	Sequence 55, Appl
C 901	38.4	4.4	424	6	US-10-198-846-2329	Sequence 2329, Ap	C 976	37.4	4.3	8111	6	US-10-311-507-85	Sequence 85, Appl
C 902	38.4	4.4	488	9	US-10-425-115-108291	Sequence 108291,	C 977	37.4	4.3	8111	9	US-10-480-846-55	Sequence 55, Appl
C 903	38.4	4.4	499	8	US-10-021-323-1716	Sequence 1716, Ap	C 978	37.4	4.3	14950	7	US-10-311-455-1230	Sequence 1230, Ap
C 904	38.4	4.4	565	4	US-09-925-065A-500019	Sequence 500019,	C 979	37.4	4.3	80226	13	US-11-097-143-25216	Sequence 25216, A
C 905	38.4	4.4	565	4	US-09-925-065A-500020	Sequence 500020,	C 980	37.4	4.3	111836	8	US-10-322-281-51	Sequence 51, Appl
C 906	38.4	4.4	565	5	US-09-925-065A-500019	Sequence 500019,	C 981	37.2	4.3	426	3	US-09-960-352-13817	Sequence 13817, A
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C 911	38.4	4.4	1954	9	US-10-723-860-7576	Sequence 7576, Ap	C 986	37.2	4.3	2274	9	US-10-425-115-169213	Sequence 169213,
C 912	38.4	4.4	2890	10	US-10-487-078-147	Sequence 147, App	C 987	37.2	4.3	2549	3	US-09-764-898-82	Sequence 82, Appl
C 913	38.4	4.4	5195	7	US-10-311-455-1570	Sequence 1570, Ap	C 988	37.2	4.3	2911	7	US-10-264-049-283	Sequence 283, Appl
C 914	38.4	4.4	15743	4	US-10-240-453-269	Sequence 269, App	C 989	37.2	4.3	6577	8	US-10-311-455-1329	Sequence 1329, Ap
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C 916	38.2	4.4	277	3	US-09-764-877-22	Sequence 22, Appl	C 991	37.2	4.3	240825	3	US-09-790-289-1	Sequence 1, Appli
C 917	38.2	4.4	277	7	US-10-242-515-22	Sequence 22, Appl	C 992	37.2	4.3	240825	8	US-10-468-582-1	Sequence 1, Appli



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c 1001	37	4.3	580	8	US-10-424-599-111106	Sequence 111106, A	c1074	36.4	4.2	261	8	US-10-085-783A-8796	Sequence 8796, Ap
c 1002	37	4.3	619	12	US-10-301-480-33171	Sequence 33171, A	c1075	36.4	4.2	286	9	US-10-425-115-13235	Sequence 13235, A
c 1003	37	4.3	619	12	US-10-301-480-645580	Sequence 645580, A	c1076	36.4	4.2	395	9	US-10-425-115-134040	Sequence 134040, A
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c 1023	36.8	4.2	391	9	US-10-723-860-3748	Sequence 3748, Ap	c1096	36.4	4.2	662	12	US-10-301-480-534274	Sequence 534274, A
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c 1027	36.8	4.2	483	8	US-10-021-323-13466	Sequence 13466, A	c1100	36.4	4.2	826	10	US-10-878-523-35	Sequence 35, Appl
c 1028	36.8	4.2	598	8	US-10-767-701-24993	Sequence 24993, A	c1101	36.4	4.2	880	9	US-10-425-115-161875	Sequence 161875, A
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c 1049	36.8	4.2	5511	7	US-10-311-455-1844	Sequence 1844, Ap	c1122	36.2	4.2	282	8	US-10-021-323-14775	Sequence 14775, A
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4	870	100.0	870	3	US-09-992-598-164
5	870	100.0	870	4	US-09-989-735-164
6	870	100.0	870	5	US-09-989-726-164
7	870	100.0	870	5	US-09-997-514-164
8	870	100.0	870	5	US-09-989-728-164
9	870	100.0	870	5	US-09-997-349-164
10	870	100.0	870	5	US-09-989-293A-164
11	870	100.0	870	5	US-09-997-653-164
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13	525.8	60.4	533	3	US-09-736-457-113
14	525.8	60.4	533	3	US-09-614-124B-113
15	525.8	60.4	533	3	US-09-671-325-113
16	525.8	60.4	533	3	US-09-589-184-113
17	525.8	60.4	533	3	US-09-658-824-113
18	525.8	60.4	533	3	US-10-017-754-113
19	525.8	60.4	533	3	US-09-551-563-113
20	525.8	60.4	533	3	US-09-519-642-113
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22	443	50.9	29907	3	US-09-949-016-13395
23	443	50.9	29913	3	US-09-949-016-12481

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312	35.9	312	3	US-09-668-097A-21	Sequence 21, Appl
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312	35.9	312	3	US-09-270-767-13424	Sequence 13424, A
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312	35.9	312	3	US-10-011-893A-377	Sequence 377, App
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98	35.2	4.0	496	5	US-10-006-485A-377	Sequence 377, App	171	34.2	3.9	2017	5	US-10-062-831-45	Sequence 45, Appl
99	35.2	4.0	496	5	US-10-006-746A-377	Sequence 377, App	172	34.2	3.9	8100	3	US-09-554-337-4	Sequence 1, Appl
100	35.2	4.0	496	5	US-10-013-752A-377	Sequence 377, App	173	34.2	3.9	11517	2	US-07-920-281C-1	Sequence 1, Appl
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105	35.2	4.0	1066	2	US-08-1007-236A-377	Sequence 377, App	c 178	34.2	3.9	112508	3	US-09-949-016-12420	Sequence 12420, A
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111	35	4.0	2350	3	US-09-292-036-1	Sequence 1, Appl	c 184	34	3.9	787	3	US-09-621-976-1878	Sequence 1878, Ap
112	35	4.0	2350	3	US-09-398-395A-55	Sequence 55, Appl	c 185	34	3.9	832	3	US-09-621-976-2813	Sequence 2813, Ap
113	35	4.0	2861	3	US-09-887-586A-55	Sequence 55, Appl	c 186	34	3.9	2349	3	US-10-104-047-1148	Sequence 1148, Ap
114	35	4.0	2861	3	US-09-895-752-55	Sequence 55, Appl	c 187	34	3.9	2438	3	US-09-393-634-4	Sequence 4, Appl
115	35	4.0	2861	3	US-09-903-012B-55	Sequence 55, Appl	c 188	34	3.9	2438	5	US-10-770-127-80	Sequence 80, Appl
116	35	4.0	2861	3	US-09-900-797-55	Sequence 55, Appl	c 189	34	3.9	612327	3	US-09-949-016-16809	Sequence 16809, A
117	35	4.0	2861	3	US-09-893-820-55	Sequence 55, Appl	c 190	34	3.9	109974	4	US-09-531-120-204	Sequence 204, App
118	35	4.0	2861	3	US-10-041-007-3	Sequence 3, Appl	c 191	33.8	3.9	289	3	US-09-007-005-17	Sequence 17, Appl
119	35	4.0	11209	3	US-09-949-016-17514	Sequence 17514, A	c 192	33.8	3.9	289	3	US-09-244-796-17	Sequence 17, Appl
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123	34.8	4.0	612	3	US-09-385-982A-280	Sequence 280, App	c 196	33.8	3.9	552	3	US-09-270-767-24063	Sequence 24063, A
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125	34.8	4.0	977	3	US-09-484-970B-137	Sequence 137, App	c 198	33.8	3.9	837	4	US-09-297-648-4026	Sequence 4026, Ap
126	34.8	4.0	2066	3	US-09-205-258-105	Sequence 105, App	c 199	33.8	3.9	943	3	US-09-149-476-35	Sequence 35, Appl
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128	34.6	4.0	601	3	US-09-621-976-16246	Sequence 16246, A	c 201	33.8	3.9	1925	3	US-09-621-011-128	Sequence 128, App
129	34.6	4.0	601	3	US-09-949-016-146956	Sequence 146956, A	c 202	33.8	3.9	2379	4	US-10-036-041-71	Sequence 71, Appl
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131	34.6	4.0	997	3	US-09-905-125A-376	Sequence 376, App	c 204	33.8	3.9	3060	3	US-09-990-444-504	Sequence 504, App
132	34.6	4.0	997	3	US-09-902-775A-376	Sequence 376, App	c 205	33.8	3.9	3060	3	US-09-997-333-504	Sequence 504, App
133	34.6	4.0	997	3	US-09-902-775A-376	Sequence 376, App	c 206	33.8	3.9	3060	3	US-09-992-598-504	Sequence 504, App
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136	34.6	4.0	997	3	US-09-909-064-376	Sequence 376, App	c 209	33.8	3.9	3060	5	US-09-997-514-504	Sequence 504, App
137	34.6	4.0	997	3	US-09-905-381A-376	Sequence 376, App	c 210	33.8	3.9	3060	5	US-09-989-728-504	Sequence 504, App
138	34.6	4.0	997	3	US-09-906-618-376	Sequence 376, App	c 211	33.8	3.9	3060	5	US-09-997-349-504	Sequence 504, App
139	34.6	4.0	997	3	US-09-906-646-376	Sequence 376, App	c 212	33.8	3.9	3060	5	US-09-997-653-504	Sequence 504, App
140	34.6	4.0	997	3	US-09-904-462-376	Sequence 376, App	c 213	33.8	3.9	3060	5	US-09-989-232A-504	Sequence 504, App
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145	34.6	4.0	997	4	US-09-906-679A-376	Sequence 376, App	c 218	33.8	3.9	9058	3	US-09-653-285-9	Sequence 9, Appl
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160	34.4	4.0	1792	3	US-08-747-221B-18	Sequence 18, Appl	c 233	33.6	3.9	611	3	US-10-004-860-109	Sequence 109, App
161	34.4	4.0	1792	3	US-08-747-221B-20	Sequence 20, Appl	c 234	33.6	3.9	931	3	US-09-482-273-31	Sequence 31, Appl
162	34.4	4.0	1792	3	US-09-005-051-18	Sequence 18, Appl	c 235	33.6	3.9	1191	2	US-08-671-320-14	Sequence 14, Appl
163	34.4	4.0	1792	3	US-09-005-051-20	Sequence 20, Appl	c 236	33.6	3.9	1191	2	US-08-868-577-14	Sequence 14, Appl
164	34.4	4.0	1792	3	US-09-403-943F-18	Sequence 18, Appl	c 237	33.6	3.9	1191	3	US-09-207-914-14	Sequence 14, Appl
165	34.4	4.0	1792	3	US-09-403-943F-20	Sequence 20, Appl	c 238	33.6	3.9	1196	3	US-09-065-040-2	Sequence 2, Appl
166	34.4	4.0	2668	3	US-09-370-838-156	Sequence 156, App	c 239	33.6	3.9	1230	3	US-09-244-805-45	Sequence 45, Appl
167	34.4	4.0	2668	3	US-09-854-133-156	Sequence 156, App	c 240	33.6	3.9	1230	3	US-09-244-805-6	Sequence 6, Appl
168	34.2	3.9	619	3	US-09-328-111-415	Sequence 415, App	c 241	33.6	3.9	2002	3	US-09-819-993-1	Sequence 1, Appl
169	34.2	3.9	990	3	US-09-800-729-79	Sequence 79, Appl	c 242	33.6	3.9	2002	3	US-10-193-295-1	Sequence 1, Appl

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246	33.6	3.9	2498	2	US-08-347-003-3	Sequence 3, Appl	c 319	33.2	3.8	42053	3	US-09-949-016-15924	Sequence 15924, A
247	33.6	3.9	2504	2	US-08-946-412-1	Sequence 1, Appl	c 320	33.2	3.8	69263	3	US-09-949-016-12594	Sequence 12594, A
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c 251	33.6	3.9	6896	3	US-09-573-080A-422	Sequence 422, App	c 324	33.2	3.8	151256	3	US-09-949-016-12674	Sequence 12674, A
c 252	33.6	3.9	6896	5	US-09-854-867-422	Sequence 422, App	c 325	33.2	3.8	151261	3	US-09-949-016-13242	Sequence 13242, A
253	33.6	3.9	8220	2	US-08-568-459A-11	Sequence 11, Appl	c 326	33.2	3.8	235064	3	US-09-949-016-15390	Sequence 15390, A
254	33.6	3.9	8220	2	US-08-487-826B-11	Sequence 11, Appl	c 327	33	3.8	194	3	US-09-621-976-9596	Sequence 9596, Ap
255	33.6	3.9	8220	3	US-09-210-288-11	Sequence 11, Appl	c 328	33	3.8	247	2	US-08-691-641-4	Sequence 4, Appl
256	33.6	3.9	8220	3	US-10-153-273-11	Sequence 11, Appl	c 329	33	3.8	275	3	US-09-328-111-385	Sequence 385, App
c 257	33.6	3.9	54945	3	US-09-967-669-10	Sequence 10, Appl	c 330	33	3.8	300	3	US-09-621-976-16227	Sequence 16227, A
c 258	33.6	3.9	65485	3	US-09-949-016-13757	Sequence 13757, A	c 331	33	3.8	323	3	US-09-621-976-10374	Sequence 10374, A
c 259	33.6	3.9	65552	3	US-09-949-016-12303	Sequence 12303, A	c 332	33	3.8	347	3	US-09-621-976-16136	Sequence 16136, A
c 260	33.6	3.9	83938	3	US-09-949-016-16068	Sequence 16068, A	c 333	33	3.8	444	3	US-08-688-988-44	Sequence 44, Appl
c 261	33.6	3.9	219964	3	US-09-949-016-15086	Sequence 15086, A	c 334	33	3.8	457	3	US-09-385-982-15	Sequence 15, Appl
c 262	33.6	3.9	227750	3	US-09-949-016-17175	Sequence 17175, A	c 335	33	3.8	601	3	US-09-621-976-15639	Sequence 15639, A
263	33.4	3.8	140	2	US-08-628-417-5	Sequence 5, Appl	c 336	33	3.8	601	3	US-09-949-016-20341	Sequence 20341, A
264	33.4	3.8	147	3	US-09-621-976-10383	Sequence 10383, A	c 337	33	3.8	601	3	US-09-949-016-20341	Sequence 20341, A
265	33.4	3.8	191	3	US-09-621-976-10184	Sequence 10184, A	c 338	33	3.8	601	3	US-09-949-016-20342	Sequence 20342, A
266	33.4	3.8	240	2	US-08-628-417-6	Sequence 6, Appl	c 339	33	3.8	607	3	US-09-809-545A-19	Sequence 19, Appl
267	33.4	3.8	348	3	US-09-621-976-16137	Sequence 16137, A	c 340	33	3.8	700	3	US-09-735-271-1096	Sequence 1096, Ap
268	33.4	3.8	601	3	US-09-949-016-58445	Sequence 58445, A	c 341	33	3.8	1049	3	US-09-800-729-67	Sequence 67, Appl
269	33.4	3.8	1074	3	US-09-248-335-67	Sequence 67, Appl	c 342	33	3.8	1249	3	US-09-461-325-128	Sequence 128, App
270	33.4	3.8	1100	3	US-07-861-458C-4	Sequence 4, Appl	c 343	33	3.8	1249	3	US-10-012-543-128	Sequence 128, App
271	33.4	3.8	1114	3	US-09-152-060-4	Sequence 4, Appl	c 344	33	3.8	1249	3	US-10-115-123-128	Sequence 128, App
272	33.4	3.8	1114	3	US-09-852-797-41	Sequence 41, Appl	c 345	33	3.8	1260	3	US-09-461-323-93	Sequence 93, Appl
273	33.4	3.8	1114	3	US-09-853-161-41	Sequence 41, Appl	c 346	33	3.8	1260	3	US-10-012-543-93	Sequence 93, Appl
274	33.4	3.8	1114	3	US-10-058-993-41	Sequence 41, Appl	c 347	33	3.8	1260	3	US-10-115-123-93	Sequence 93, Appl
275	33.4	3.8	1129	3	US-09-227-357-40	Sequence 40, Appl	c 348	33	3.8	1401	4	US-09-605-703B-543	Sequence 543, App
276	33.4	3.8	1129	3	US-09-973-278-80	Sequence 80, Appl	c 349	33	3.8	1738	2	US-08-379-482A-2	Sequence 2, Appl
c 277	33.4	3.8	1141	3	US-09-806-708B-22	Sequence 22, Appl	c 350	33	3.8	2158	2	US-07-602-608-1	Sequence 1, Appl
278	33.4	3.8	1461	3	US-08-722-126A-4	Sequence 4, Appl	c 351	33	3.8	2158	2	US-08-261-578-1	Sequence 1, Appl
279	33.4	3.8	1461	7	PCT-US95-04258-4	Sequence 4, Appl	c 352	33	3.8	3299	3	US-09-800-729-68	Sequence 68, Appl
280	33.4	3.8	1468	3	US-10-205-258-142	Sequence 142, App	c 353	33	3.8	3581	2	US-08-738-349-1	Sequence 1, Appl
281	33.4	3.8	1468	3	US-10-004-860-142	Sequence 142, App	c 354	33	3.8	50217	3	US-09-949-016-16067	Sequence 16067, A
282	33.4	3.8	1840	3	US-08-977-001-2	Sequence 2, Appl	c 355	33	3.8	76962	3	US-09-949-016-17482	Sequence 17482, A
283	33.4	3.8	1806	3	US-09-820-004-1	Sequence 1, Appl	c 356	33	3.8	390416	3	US-09-949-016-16923	Sequence 16923, A
284	33.4	3.8	2043	3	US-09-614-912-171	Sequence 171, App	c 357	32.8	3.8	250	3	US-09-621-976-18363	Sequence 18363, A
285	33.4	3.8	3593	3	US-09-645-069-22	Sequence 22, Appl	c 358	32.8	3.8	386	3	US-10-131-831-8646	Sequence 8646, Ap
286	33.4	3.8	3593	3	US-09-644-934-10	Sequence 10, Appl	c 359	32.8	3.8	386	5	US-10-131-831-8646	Sequence 8646, Ap
287	33.4	3.8	3593	5	US-10-115-609-22	Sequence 22, Appl	c 360	32.8	3.8	445	3	US-09-247-153-53	Sequence 53, Appl
c 288	33.4	3.8	18999	3	US-09-949-002-703	Sequence 703, App	c 361	32.8	3.8	445	3	US-09-903-190-53	Sequence 53, Appl
c 289	33.4	3.8	26225	5	US-09-984-429-448	Sequence 448, App	c 362	32.8	3.8	601	3	US-09-949-016-27649	Sequence 27649, A
c 290	33.4	3.8	27271	3	US-09-949-002-622	Sequence 622, App	c 363	32.8	3.8	601	3	US-09-949-016-158180	Sequence 158180, A
291	33.4	3.8	130724	3	US-09-949-016-13753	Sequence 13753, A	c 364	32.8	3.8	601	3	US-09-949-016-199729	Sequence 199729, A
292	33.4	3.8	580073	3	US-08-545-528D-1	Sequence 1, Appl	c 365	32.8	3.8	903	7	PCT-US95-06406A-21	Sequence 21, Appl
293	33.2	3.8	364	3	US-09-621-976-17202	Sequence 17202, A	c 366	32.8	3.8	963	3	US-09-328-352-400	Sequence 400, App
294	33.2	3.8	601	3	US-09-949-016-27650	Sequence 27650, A	c 367	32.8	3.8	1117	3	US-09-247-373B-33	Sequence 33, Appl
295	33.2	3.8	601	3	US-09-949-016-34608	Sequence 34608, A	c 368	32.8	3.8	1189	3	US-09-716-123-46	Sequence 46, Appl
c 296	33.2	3.8	601	3	US-09-949-016-70844	Sequence 70844, A	c 369	32.8	3.8	1212	3	US-09-182-145-34	Sequence 34, Appl
c 297	33.2	3.8	601	3	US-09-949-016-70845	Sequence 70845, A	c 370	32.8	3.8	1212	3	US-09-182-145-35	Sequence 35, Appl
c 298	33.2	3.8	601	3	US-09-949-016-70846	Sequence 70846, A	c 371	32.8	3.8	1333	5	US-09-537-654-5	Sequence 5, Appl
c 299	33.2	3.8	601	3	US-09-949-016-120218	Sequence 120218, A	c 372	32.8	3.8	1333	5	US-10-818-809-5	Sequence 5, Appl
300	33.2	3.8	601	3	US-09-949-016-148785	Sequence 148785, A	c 373	32.8	3.8	1733	3	US-09-073-569-1	Sequence 1, Appl
301	33.2	3.8	601	3	US-09-949-016-152844	Sequence 152844, A	c 374	32.8	3.8	1872	3	US-09-801-052-1	Sequence 1, Appl
302	33.2	3.8	601	3	US-09-949-016-158181	Sequence 158181, A	c 375	32.8	3.8	1872	3	US-10-020-121-1	Sequence 1, Appl
303	33.2	3.8	611	3	US-09-385-983-66	Sequence 66, Appl	c 376	32.8	3.8	1872	3	US-10-636-579-1	Sequence 1, Appl
304	33.2	3.8	1195	4	US-09-297-648-3131	Sequence 3131, Ap	c 377	32.8	3.8	1895	3	US-09-444-336-7	Sequence 7, Appl
305	33.2	3.8	1195	4	US-09-297-648-3132	Sequence 3132, Ap	c 378	32.8	3.8	1895	3	US-10-093-045-7	Sequence 7, Appl
306	33.2	3.8	1419	3	US-09-270-767-30857	Sequence 30857, A	c 379	32.8	3.8	1895	3	US-10-093-246-7	Sequence 7, Appl
c 307	33.2	3.8	1467	3	US-09-949-016-2761	Sequence 2761, Ap	c 380	32.8	3.8	1914	3	US-09-690-454-34	Sequence 34, Appl
308	33.2	3.8	1738	3	US-09-918-909A-27	Sequence 27, Appl	c 381	32.8	3.8	1914	5	US-10-062-831-34	Sequence 34, Appl
309	33.2	3.8	2005	2	US-07-916-901-5	Sequence 5, Appl	c 382	32.8	3.8	1986	3	US-08-687-590-57	Sequence 57, Appl
310	33.2	3.8	2311	3	US-09-800-729-66	Sequence 66, Appl	c 383	32.8	3.8	2625	3	US-09-270-767-10080	Sequence 10080, A
311	33.2	3.8	2394	3	US-09-800-729-33	Sequence 33, Appl	c 384	32.8	3.8	2686	3	US-09-228-986-3	Sequence 3, Appl
312	33.2	3.8	3585	3	US-09-270-767-14479	Sequence 14479, A	c 385	32.8	3.8	2886	3	US-10-101-464A-3	Sequence 3, Appl
313	33.2	3.8	3701	3	US-09-220-132-57	Sequence 57, Appl	c 386	32.8	3.8	3275	3	US-09-370-838-151	Sequence 151, App
c 314	33.2	3.8	16506	3	US-09-949-016-11962	Sequence 11962, A	c 387	32.8	3.8	3275	3	US-09-854-133-151	Sequence 151, App
c 315	33.2	3.8	16506	3	US-09-949-016-13836	Sequence 13836, A	c 388	32.8	3.8	4086	3	US-09-702-705-1801	Sequence 1801, Ap

389	32.8	3.8	4086	3	US-09-736-457-1801	Sequence 1801, App	462	32.6	3.7	1878	3	US-09-465-558-39	Sequence 39, Appl
390	32.8	3.8	4086	3	US-09-671-325-1801	Sequence 1801, App	463	32.6	3.7	1883	3	US-10-012-231A-145	Sequence 145, App
391	32.8	3.8	4086	3	US-10-017-754-1801	Sequence 1801, App	464	32.6	3.7	1883	3	US-10-015-389A-145	Sequence 145, App
392	32.8	3.8	12001	2	US-08-458-568A-11	Sequence 11, Appl	465	32.6	3.7	1883	3	US-10-006-768A-145	Sequence 145, App
393	32.8	3.8	152331	3	US-09-128-135-16	Sequence 16, Appl	466	32.6	3.7	1883	3	US-10-015-671A-145	Sequence 145, App
394	32.8	3.8	183202	3	US-09-949-016-13614	Sequence 13614, A	467	32.6	3.7	1883	3	US-10-015-393A-145	Sequence 145, App
395	32.8	3.8	371182	3	US-09-949-016-17371	Sequence 17371, A	468	32.6	3.7	1883	3	US-10-011-833A-145	Sequence 145, App
396	32.8	3.8	373694	3	US-09-949-016-12062	Sequence 12062, A	469	32.6	3.7	1883	3	US-10-006-041A-145	Sequence 145, App
397	32.8	3.8	393753	3	US-09-949-016-14573	Sequence 14573, A	470	32.6	3.7	1883	3	US-10-012-064A-145	Sequence 145, App
398	32.8	3.8	393753	3	US-09-949-016-14573	Sequence 14574, A	471	32.6	3.7	1883	4	US-10-015-392A-145	Sequence 145, App
399	32.8	3.8	818128	3	US-09-949-016-14546	Sequence 14546, A	472	32.6	3.7	1883	5	US-10-011-795B-145	Sequence 145, App
400	32.8	3.8	818128	3	US-09-949-016-14547	Sequence 14547, A	473	32.6	3.7	1883	5	US-10-015-386A-145	Sequence 145, App
401	32.8	3.8	818128	3	US-09-949-016-14548	Sequence 14548, A	474	32.6	3.7	1883	5	US-10-012-121A-145	Sequence 145, App
402	32.8	3.8	818128	3	US-09-949-016-14549	Sequence 14549, A	475	32.6	3.7	1883	5	US-10-006-485A-145	Sequence 145, App
403	32.8	3.8	818128	3	US-09-949-016-14550	Sequence 14550, A	476	32.6	3.7	1883	5	US-10-006-746A-145	Sequence 145, App
404	32.8	3.8	818128	3	US-09-949-016-14551	Sequence 14551, A	477	32.6	3.7	1883	5	US-10-012-752A-145	Sequence 145, App
405	32.8	3.8	818128	3	US-09-949-016-14552	Sequence 14552, A	478	32.6	3.7	1883	5	US-10-017-253A-145	Sequence 145, App
406	32.8	3.8	818128	3	US-09-949-016-14553	Sequence 14553, A	479	32.6	3.7	1883	5	US-10-015-519A-145	Sequence 145, App
407	32.8	3.8	818128	3	US-09-949-016-14554	Sequence 14554, A	480	32.6	3.7	1883	5	US-10-015-715A-145	Sequence 145, App
408	32.8	3.8	818128	3	US-09-949-016-14555	Sequence 14555, A	481	32.6	3.7	1883	5	US-10-007-236A-145	Sequence 145, App
409	32.8	3.8	818128	3	US-09-949-016-14556	Sequence 14556, A	482	32.6	3.7	1920	3	US-10-214-269-17	Sequence 17, Appl
410	32.8	3.8	818128	3	US-09-949-016-14557	Sequence 14557, A	483	32.6	3.7	2026	3	US-09-690-454-30	Sequence 30, Appl
411	32.8	3.8	818128	3	US-09-949-016-14558	Sequence 14558, A	484	32.6	3.7	2026	5	US-10-062-831-30	Sequence 30, Appl
412	32.8	3.8	818128	3	US-09-949-016-14559	Sequence 14559, A	485	32.6	3.7	2525	3	US-09-239-583A-1	Sequence 1, Appl
413	32.8	3.8	818128	3	US-09-949-016-14560	Sequence 14560, A	486	32.6	3.7	2525	3	US-10-187-904-1	Sequence 1, Appl
414	32.8	3.8	818128	3	US-09-949-016-14561	Sequence 14561, A	487	32.6	3.7	2550	10	5258287-23	Patent No. 5258287
415	32.8	3.8	818128	3	US-09-949-016-14562	Sequence 14562, A	488	32.6	3.7	2671	10	5168051-9	Patent No. 5168051
416	32.8	3.8	818128	3	US-09-949-016-14564	Sequence 14564, A	C 489	32.6	3.7	4946	3	US-10-148-806-1	Sequence 1, Appl
417	32.8	3.8	818128	3	US-09-949-016-14565	Sequence 14565, A	C 490	32.6	3.7	4950	3	US-09-949-016-1805	Sequence 1805, Ap
418	32.8	3.8	818128	3	US-09-949-016-14566	Sequence 14566, A	C 491	32.6	3.7	4950	3	US-09-949-016-1806	Sequence 1806, Ap
419	32.8	3.8	818128	3	US-09-949-016-14567	Sequence 14567, A	C 492	32.6	3.7	6388	3	US-09-573-080A-179	Sequence 179, App
420	32.8	3.8	1082144	4	US-09-531-120-211	Sequence 211, App	C 493	32.6	3.7	6388	5	US-09-854-867-179	Sequence 179, App
421	32.8	3.8	1664976	3	US-08-916-421B-1	Sequence 1, Appl	C 494	32.6	3.7	6877	2	US-08-347-340-1	Sequence 1, Appl
422	32.8	3.7	258	3	US-09-692-570-1	Sequence 1, Appl	C 495	32.6	3.7	20608	3	US-09-949-016-16595	Sequence 16595, A
423	32.6	3.7	271	3	US-09-621-976-15353	Sequence 15353, A	C 496	32.6	3.7	37925	5	US-09-984-429-701	Sequence 701, App
424	32.6	3.7	299	3	US-09-621-976-10380	Sequence 10380, A	C 497	32.6	3.7	111235	3	US-09-949-016-15328	Sequence 15328, A
425	32.6	3.7	384	3	US-09-621-976-10211	Sequence 10211, A	C 498	32.6	3.7	114183	3	US-09-949-002-849	Sequence 849, App
426	32.6	3.7	384	3	US-10-131-827-8187	Sequence 8187, Ap	C 499	32.6	3.7	115814	3	US-09-949-016-16205	Sequence 16205, A
427	32.6	3.7	384	3	US-10-131-831-8187	Sequence 8187, Ap	C 500	32.6	3.7	127546	3	US-09-949-002-624	Sequence 624, App
428	32.6	3.7	412	3	US-09-270-767-2370	Sequence 2370, Ap	C 501	32.6	3.7	636591	3	US-09-949-016-11808	Sequence 11808, A
429	32.6	3.7	412	3	US-09-270-767-18252	Sequence 18252, A	C 502	32.6	3.7	636591	3	US-09-949-016-13388	Sequence 13388, A
430	32.6	3.7	601	3	US-09-949-016-159666	Sequence 159666, A	C 503	32.6	3.7	1230025	3	US-09-198-452A-1	Sequence 1, Appl
431	32.6	3.7	882	2	US-08-908-965C-9	Sequence 9, Appl	C 504	32.6	3.7	1330230	3	US-09-438-185A-1	Sequence 1, Appl
432	32.6	3.7	1172	2	US-07-945-288-9	Sequence 9, Appl	C 505	32.4	3.7	132	3	US-09-621-976-13468	Sequence 13468, A
433	32.6	3.7	1172	2	US-08-462-831-9	Sequence 9, Appl	C 506	32.4	3.7	188	3	US-09-621-976-10364	Sequence 10364, A
434	32.6	3.7	1172	2	US-08-461-809-9	Sequence 9, Appl	C 507	32.4	3.7	221	3	US-09-621-976-15416	Sequence 15416, A
435	32.6	3.7	1172	2	US-08-461-441-9	Sequence 9, Appl	C 508	32.4	3.7	231	3	US-09-248-796A-12356	Sequence 12356, A
436	32.6	3.7	1172	3	PCT-US93-08518-9	Sequence 9, Appl	C 509	32.4	3.7	250	3	US-09-621-976-17371	Sequence 17371, A
437	32.6	3.7	1273	3	US-09-270-767-14731	Sequence 14731, A	C 510	32.4	3.7	415	4	US-09-880-107-3593	Sequence 3593, Ap
438	32.6	3.7	1412	3	US-09-614-912-197	Sequence 197, App	C 511	32.4	3.7	484	3	US-09-270-767-3048	Sequence 3048, Ap
439	32.6	3.7	1662	3	US-09-668-097A-13	Sequence 13, App	C 512	32.4	3.7	484	3	US-09-270-767-18330	Sequence 18330, A
440	32.6	3.7	1674	3	US-09-991-181-300	Sequence 300, App	C 513	32.4	3.7	572	3	US-09-696-169A-12	Sequence 12, Appl
441	32.6	3.7	1674	3	US-09-990-444-300	Sequence 300, App	C 514	32.4	3.7	601	3	US-09-949-016-70924	Sequence 70924, A
442	32.6	3.7	1674	3	US-09-997-333-300	Sequence 300, App	C 515	32.4	3.7	601	3	US-09-949-016-70925	Sequence 70925, A
443	32.6	3.7	1674	3	US-09-992-598-300	Sequence 300, App	C 516	32.4	3.7	631	3	US-08-817-913-6	Sequence 6, Appl
444	32.6	3.7	1674	4	US-09-989-735-300	Sequence 300, App	C 517	32.4	3.7	674	3	US-08-817-913-7	Sequence 7, Appl
445	32.6	3.7	1674	5	US-09-989-726-300	Sequence 300, App	C 518	32.4	3.7	687	3	US-08-817-913-8	Sequence 8, Appl
446	32.6	3.7	1674	5	US-09-997-514-300	Sequence 300, App	C 519	32.4	3.7	693	3	US-08-817-913-9	Sequence 9, Appl
447	32.6	3.7	1674	5	US-09-989-728-300	Sequence 300, App	C 520	32.4	3.7	758	3	US-08-817-913-10	Sequence 10, Appl
448	32.6	3.7	1674	5	US-09-997-349-300	Sequence 300, App	C 521	32.4	3.7	855	3	US-08-817-913-11	Sequence 11, Appl
449	32.6	3.7	1674	5	US-09-997-653-300	Sequence 300, App	C 522	32.4	3.7	859	3	US-08-817-913-12	Sequence 12, Appl
450	32.6	3.7	1674	5	US-09-989-293A-300	Sequence 300, App	C 523	32.4	3.7	991	3	US-08-924-747-25	Sequence 25, Appl
451	32.6	3.7	1736	3	US-09-182-816-22	Sequence 22, Appl	C 524	32.4	3.7	991	3	US-09-247-373B-25	Sequence 25, Appl
452	32.6	3.7	1736	3	US-09-182-816-22	Sequence 24, Appl	C 525	32.4	3.7	991	3	US-09-256-715-25	Sequence 25, Appl
453	32.6	3.7	1736	3	US-09-471-528-24	Sequence 24, Appl	C 526	32.4	3.7	1151	3	US-09-270-767-12633	Sequence 12633, A
454	32.6	3.7	1736	3	US-09-471-528-24	Sequence 24, Appl	C 527	32.4	3.7	1201	3	US-09-461-325-36	Sequence 36, Appl
455	32.6	3.7	1736	3	US-09-634-530-22	Sequence 22, Appl	C 528	32.4	3.7	1201	3	US-10-012-542-36	Sequence 36, Appl
456	32.6	3.7	1736	3	US-09-634-530-24	Sequence 24, Appl	C 529	32.4	3.7	1201	3	US-10-115-123-36	Sequence 13, Appl
457	32.6	3.7	1740	3	US-09-709-103-45	Sequence 45, Appl	C 530	32.4	3.7	1214	3	US-08-817-913-13	Sequence 14, Appl
458	32.6	3.7	1740	3	US-09-439-410A-45	Sequence 45, Appl	C 531	32.4	3.7	1232	3	US-08-817-913-14	Sequence 15, Appl
459	32.6	3.7	1782	3	US-09-069-023-37	Sequence 37, Appl	C 532	32.4	3.7	1352	3	US-08-817-913-15	Sequence 15, Appl
460	32.6	3.7	1801	3	US-09-709-103-3	Sequence 3, Appl	C 533	32.4	3.7	1411	3	US-09-904-615-38	Sequence 38, Appl
461	32.6	3.7	1801	3	US-09-439-410A-3	Sequence 3, Appl	C 534	32.4	3.7	1411	3	US-10-054-988-38	Sequence 38, Appl



535	32.4	3.7	1641	2	US-08-300-903A-8	Sequence 8, Appli	608	32.2	3.7	6755	3	US-08-931-999-4	Sequence 4, Appli
536	32.4	3.7	1641	3	US-08-988-197-8	Sequence 8, Appli	c 609	32.2	3.7	10053	3	US-09-949-016-17485	Sequence 17485, A
537	32.4	3.7	1641	3	US-10-385-072-8	Sequence 8, Appli	c 610	32.2	3.7	13335	3	US-09-949-016-13162	Sequence 13162, A
538	32.4	3.7	1734	3	US-08-817-913-16	Sequence 16, Appli	c 611	32.2	3.7	32099	3	US-09-949-016-16562	Sequence 16562, A
539	32.4	3.7	1753	3	US-09-870-956-53	Sequence 16, Appli	c 612	32.2	3.7	32099	4	US-09-880-107-2380	Sequence 2380, Ap
540	32.4	3.7	1795	3	US-09-646-561-16	Sequence 16, Appli	c 613	32.2	3.7	33006	3	US-09-662-254B-23	Sequence 23, Appli
541	32.4	3.7	1795	3	US-09-646-561-18	Sequence 18, Appli	614	32.2	3.7	50000	3	US-09-949-016-11900	Sequence 11900, A
542	32.4	3.7	1920	3	US-08-817-913-17	Sequence 17, Appli	615	32.2	3.7	809716	3	US-09-949-016-13766	Sequence 13766, A
543	32.4	3.7	2079	3	US-09-489-847-25	Sequence 25, Appli	c 616	32.2	3.7	100877	3	US-09-949-016-13766	Sequence 13766, A
544	32.4	3.7	2579	3	US-08-949-016-2494	Sequence 24, Appli	c 617	32.2	3.7	114842	3	US-09-949-016-12454	Sequence 12454, A
545	32.4	3.7	2621	3	US-09-949-016-1072	Sequence 1072, Ap	c 618	32.2	3.7	120609	3	US-09-949-016-14933	Sequence 14933, A
546	32.4	3.7	3975	3	US-09-270-767-3	Sequence 3, Appli	c 619	32.2	3.7	120609	3	US-09-949-016-13315	Sequence 13315, A
547	32.4	3.7	4466	3	US-09-410-551B-20	Sequence 20, Appli	c 620	32.2	3.7	135667	3	US-09-949-016-15051	Sequence 15051, A
548	32.4	3.7	4466	3	US-09-940-316B-20	Sequence 20, Appli	621	32.2	3.7	149971	3	US-09-949-016-13590	Sequence 13590, A
549	32.4	3.7	4478	3	US-09-410-551B-16	Sequence 16, Appli	622	32.2	3.7	152486	3	US-09-949-016-12869	Sequence 12869, A
550	32.4	3.7	4478	3	US-09-940-316B-16	Sequence 16, Appli	623	32.2	3.7	172951	3	US-09-949-016-15941	Sequence 15941, A
551	32.4	3.7	4547	3	US-09-410-551B-22	Sequence 22, Appli	c 624	32.2	3.7	256171	3	US-09-949-016-12822	Sequence 12822, A
552	32.4	3.7	4547	3	US-09-940-316B-22	Sequence 22, Appli	625	32.2	3.7	256176	3	US-09-949-016-15524	Sequence 15524, A
553	32.4	3.7	4571	3	US-09-940-316B-18	Sequence 18, Appli	626	32	3.7	260247	3	US-09-949-016-13358	Sequence 13358, A
554	32.4	3.7	4571	3	US-09-940-316B-18	Sequence 18, Appli	627	32	3.7	268	3	US-09-270-767-27621	Sequence 27621, A
555	32.4	3.7	11151	5	US-09-984-429-496	Sequence 496, App	628	32	3.7	81	3	US-09-621-976-73	Sequence 73, Appli
556	32.4	3.7	14176	2	US-08-307-499-1	Sequence 1, Appli	629	32	3.7	405	3	US-09-513-999C-14389	Sequence 14389, A
557	32.4	3.7	14176	2	US-08-307-499-14	Sequence 14, Appli	c 630	32	3.7	424	3	US-09-621-976-11043	Sequence 11043, A
558	32.4	3.7	14176	3	US-09-299-268-1	Sequence 1, Appli	c 631	32	3.7	480	3	US-10-131-827-8192	Sequence 8192, Ap
559	32.4	3.7	14176	3	US-09-299-268-14	Sequence 14, Appli	632	32	3.7	480	5	US-10-131-831-8192	Sequence 8192, Ap
560	32.4	3.7	34185	3	US-09-545-481-3	Sequence 3, Appli	633	32	3.7	552	3	US-09-461-325-111	Sequence 111, App
561	32.4	3.7	77536	3	US-09-410-551B-1	Sequence 1, Appli	634	32	3.7	552	3	US-10-012-542-111	Sequence 111, App
562	32.4	3.7	77536	3	US-09-940-316B-1	Sequence 1, Appli	635	32	3.7	554	3	US-10-115-123-111	Sequence 111, App
563	32.4	3.7	105189	3	US-09-949-016-13029	Sequence 13029, A	636	32	3.7	748	2	US-09-696-169A-14	Sequence 14, Appli
564	32.4	3.7	139049	3	US-09-949-016-17030	Sequence 17030, A	637	32	3.7	748	2	US-08-361-467B-3	Sequence 3, Appli
565	32.4	3.7	276687	3	US-09-949-016-13840	Sequence 13840, A	638	32	3.7	766	3	US-08-484-332C-3	Sequence 3, Appli
566	32.4	3.7	1830121	3	US-09-557-884-1	Sequence 1, Appli	639	32	3.7	824	3	US-10-125-258-1	Sequence 1, Appli
567	32.4	3.7	1830121	3	US-09-643-990A-1	Sequence 1, Appli	640	32	3.7	873	3	US-10-144-929-29	Sequence 29, Appli
568	32.4	3.7	1830121	3	US-10-158-865-1	Sequence 1, Appli	641	32	3.7	873	3	US-09-270-767-6426	Sequence 6426, Ap
569	32.2	3.7	147	3	US-09-621-976-10254	Sequence 10254, A	642	32	3.7	890	3	US-09-270-767-21708	Sequence 21708, A
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571	32.2	3.7	396	3	US-09-713-550-16	Sequence 16, Appli	644	32	3.7	890	3	US-09-853-797-16	Sequence 16, Appli
572	32.2	3.7	396	3	US-09-825-294-16	Sequence 16, Appli	645	32	3.7	890	3	US-09-853-161-16	Sequence 16, Appli
573	32.2	3.7	396	3	US-09-970-966-16	Sequence 16, Appli	646	32	3.7	1016	3	US-10-058-993-16	Sequence 16, Appli
574	32.2	3.7	601	3	US-09-949-016-20883	Sequence 20883, A	647	32	3.7	1016	3	US-09-989-833A-96	Sequence 96, Appli
575	32.2	3.7	601	3	US-09-949-016-55342	Sequence 55342, A	648	32	3.7	1016	3	US-10-020-445A-96	Sequence 96, Appli
576	32.2	3.7	601	3	US-09-949-016-170626	Sequence 170626, A	649	32	3.7	1016	4	US-09-978-189-96	Sequence 96, Appli
577	32.2	3.7	687	3	US-09-907-907A-38	Sequence 38, Appli	650	32	3.7	1016	5	US-10-017-085A-96	Sequence 96, Appli
578	32.2	3.7	695	3	US-10-401-038-2	Sequence 2, Appli	651	32	3.7	1016	5	US-10-145-129A-96	Sequence 96, Appli
579	32.2	3.7	822	2	US-07-644-372-1	Sequence 1, Appli	c 652	32	3.7	1016	5	US-10-013-929A-96	Sequence 96, Appli
580	32.2	3.7	1011	3	US-09-662-254B-74	Sequence 74, Appli	653	32	3.7	1039	3	US-10-013-917A-96	Sequence 96, Appli
581	32.2	3.7	1048	3	US-09-489-847-38	Sequence 38, Appli	654	32	3.7	1051	3	US-09-902-540-1280	Sequence 1280, Ap
582	32.2	3.7	1069	3	US-09-205-258-74	Sequence 74, Appli	655	32	3.7	1104	4	US-09-270-767-11946	Sequence 11946, A
583	32.2	3.7	1069	3	US-10-004-860-74	Sequence 74, Appli	656	32	3.7	1126	4	US-09-297-648-3396	Sequence 3396, Ap
584	32.2	3.7	1315	3	US-09-721-822A-10	Sequence 10, Appli	657	32	3.7	1141	3	US-09-489-847-60	Sequence 60, Appli
585	32.2	3.7	1518	3	US-09-614-912-191	Sequence 191, App	658	32	3.7	1296	3	US-09-806-708B-22	Sequence 22, Appli
586	32.2	3.7	1834	3	US-09-927-738-26	Sequence 26, Appli	659	32	3.7	1296	3	US-09-461-325-29	Sequence 29, Appli
587	32.2	3.7	2114	3	US-09-602-472A-5	Sequence 5, Appli	660	32	3.7	1296	3	US-10-012-542-29	Sequence 29, Appli
588	32.2	3.7	2406	2	US-08-687-702-2	Sequence 2, Appli	661	32	3.7	1400	3	US-10-115-123-29	Sequence 29, Appli
589	32.2	3.7	2525	3	US-09-234-393-39	Sequence 39, Appli	662	32	3.7	1404	4	US-09-774-490-5	Sequence 5, Appli
590	32.2	3.7	2525	3	US-09-865-171-31	Sequence 31, Appli	663	32	3.7	1515	4	US-09-880-107-3399	Sequence 3399, Ap
591	32.2	3.7	2665	3	US-08-971-089-5	Sequence 5, Appli	664	32	3.7	1570	3	US-09-880-107-3396	Sequence 3396, Ap
592	32.2	3.7	2665	3	US-10-117-604A-5	Sequence 5, Appli	665	32	3.7	1570	3	US-10-012-231A-291	Sequence 291, App
593	32.2	3.7	2852	3	US-09-027-137-2	Sequence 2, Appli	666	32	3.7	1570	3	US-10-015-389A-231	Sequence 231, App
594	32.2	3.7	2852	3	US-09-344-441-2	Sequence 2, Appli	667	32	3.7	1570	3	US-10-006-768A-231	Sequence 231, App
595	32.2	3.7	3116	3	US-09-311-021-187	Sequence 187, App	668	32	3.7	1570	3	US-10-015-671A-231	Sequence 231, App
596	32.2	3.7	3124	3	US-09-734-030-1	Sequence 1, Appli	669	32	3.7	1570	3	US-10-015-393A-231	Sequence 231, App
597	32.2	3.7	3124	3	US-10-153-921-1	Sequence 1, Appli	670	32	3.7	1570	3	US-10-011-833A-231	Sequence 231, App
598	32.2	3.7	3134	3	US-10-669-689-1	Sequence 1, Appli	671	32	3.7	1570	3	US-10-006-041A-231	Sequence 231, App
599	32.2	3.7	5275	2	US-08-485-588-1	Sequence 1, Appli	672	32	3.7	1570	3	US-10-012-064A-231	Sequence 231, App
600	32.2	3.7	5275	2	US-08-484-565-1	Sequence 1, Appli	673	32	3.7	1570	5	US-10-015-392A-231	Sequence 231, App
601	32.2	3.7	5275	2	US-08-480-751-1	Sequence 1, Appli	674	32	3.7	1570	5	US-10-011-795B-231	Sequence 231, App
602	32.2	3.7	5275	2	US-08-943-986-1	Sequence 1, Appli	675	32	3.7	1570	5	US-10-015-386A-231	Sequence 231, App
603	32.2	3.7	5275	3	US-08-353-784-1	Sequence 1, Appli	676	32	3.7	1570	5	US-10-012-121A-231	Sequence 231, App
604	32.2	3.7	5275	3	US-08-484-719B-1	Sequence 1, Appli	677	32	3.7	1570	5	US-10-006-485A-231	Sequence 231, App
605	32.2	3.7	5275	3	US-08-484-159-1	Sequence 1, Appli	678	32	3.7	1570	5	US-10-006-746A-231	Sequence 231, App
606	32.2	3.7	6409	3	US-09-967-908A-1	Sequence 1, Appli	679	32	3.7	1570	5	US-10-012-752A-231	Sequence 231, App
607	32.2	3.7	6409	3	US-10-159-151-1	Sequence 1, Appli	680	32	3.7	1570	5	US-10-017-253A-231	Sequence 231, App

681	32	3.7	1570	5	US-10-015-715A-291	Sequence 291, Appl	C 754	31.8	3.7	62327	3	US-09-949-016-16809	Sequence 16809, A
682	32	3.7	1570	5	US-10-007-236A-291	Sequence 291, Appl	C 755	31.8	3.7	67755	3	US-09-949-016-13703	Sequence 13703, A
683	32	3.7	1734	3	US-10-012-231A-51	Sequence 51, Appl	C 756	31.8	3.7	79122	4	US-09-531-120-200	Sequence 200, App
684	32	3.7	1734	3	US-10-015-389A-51	Sequence 51, Appl	C 757	31.8	3.7	130563	3	US-09-949-016-12273	Sequence 12273, A
685	32	3.7	1734	3	US-10-006-768A-51	Sequence 51, Appl	C 758	31.8	3.7	131379	3	US-09-949-016-16050	Sequence 16050, A
686	32	3.7	1734	3	US-10-015-671A-51	Sequence 51, Appl	C 759	31.8	3.7	168104	3	US-09-949-016-12026	Sequence 12026, A
687	32	3.7	1734	3	US-10-015-393A-51	Sequence 51, Appl	C 760	31.8	3.7	168105	3	US-09-949-016-16554	Sequence 16554, A
688	32	3.7	1734	3	US-10-011-833A-51	Sequence 51, Appl	C 761	31.8	3.7	314798	3	US-09-949-016-13539	Sequence 13539, A
689	32	3.7	1734	3	US-10-006-041A-51	Sequence 51, Appl	C 762	31.8	3.7	314798	3	US-09-949-016-13539	Sequence 13539, A
690	32	3.7	1734	3	US-10-012-064A-51	Sequence 51, Appl	C 763	31.8	3.7	390890	3	US-09-949-016-14720	Sequence 14720, A
691	32	3.7	1734	4	US-10-015-392A-51	Sequence 51, Appl	C 764	31.6	3.6	212	3	US-09-621-976-1325	Sequence 1325, Ap
692	32	3.7	1734	5	US-10-011-795B-51	Sequence 51, Appl	C 765	31.6	3.6	215	3	US-09-621-976-15321	Sequence 15321, A
693	32	3.7	1734	5	US-10-015-386A-51	Sequence 51, Appl	C 766	31.6	3.6	253	3	US-08-520-678A-25	Sequence 25, Appl
694	32	3.7	1734	5	US-10-012-121A-51	Sequence 51, Appl	C 767	31.6	3.6	253	3	US-08-897-126-25	Sequence 25, Appl
695	32	3.7	1734	5	US-10-006-485A-51	Sequence 51, Appl	C 768	31.6	3.6	253	3	US-10-158-314B-25	Sequence 25, Appl
696	32	3.7	1734	5	US-10-006-746A-51	Sequence 51, Appl	C 769	31.6	3.6	257	2	US-08-520-678A-24	Sequence 24, Appl
697	32	3.7	1734	5	US-10-013-752A-51	Sequence 51, Appl	C 770	31.6	3.6	257	3	US-08-897-126-24	Sequence 24, Appl
698	32	3.7	1734	5	US-10-017-253A-51	Sequence 51, Appl	C 771	31.6	3.6	257	3	US-10-158-314B-24	Sequence 24, Appl
699	32	3.7	1734	5	US-10-015-519A-51	Sequence 51, Appl	C 772	31.6	3.6	319	2	US-07-593-657-14	Sequence 14, Appl
700	32	3.7	1734	5	US-10-015-715A-51	Sequence 51, Appl	C 773	31.6	3.6	450	3	US-10-111-827-8720	Sequence 8720, Ap
701	32	3.7	1734	5	US-10-007-236A-51	Sequence 51, Appl	C 774	31.6	3.6	450	5	US-10-131-831-8720	Sequence 8720, Ap
702	32	3.7	1936	3	US-09-949-016-716	Sequence 716, Appl	C 775	31.6	3.6	601	3	US-09-949-016-180739	Sequence 180739,
703	32	3.7	2031	3	US-09-417-251A-9	Sequence 9, Appl	C 776	31.6	3.6	614	3	US-09-902-540-1318	Sequence 1318, Ap
704	32	3.7	2031	3	US-09-417-251A-9	Sequence 9, Appl	C 777	31.6	3.6	664	3	US-09-904-615-66	Sequence 66, Appl
705	32	3.7	2065	3	US-09-370-473-5	Sequence 5, Appl	C 778	31.6	3.6	664	3	US-10-054-988-66	Sequence 66, Appl
706	32	3.7	2101	3	US-08-190-204-1	Sequence 1, Appl	C 779	31.6	3.6	801	3	US-10-039-659A-5	Sequence 5, Appl
707	32	3.7	2338	3	US-09-582-337-1	Sequence 1, Appl	C 780	31.6	3.6	850	3	US-09-311-021-167	Sequence 167, App
708	32	3.7	2434	3	US-09-489-847-67	Sequence 67, Appl	C 781	31.6	3.6	1013	3	US-09-322-409-6	Sequence 6, Appl
709	32	3.7	2474	3	US-10-164-230-62	Sequence 62, Appl	C 782	31.6	3.6	1013	3	US-09-322-409-8	Sequence 8, Appl
710	32	3.7	2738	4	US-08-927-939A-80	Sequence 80, Appl	C 783	31.6	3.6	1013	3	US-09-451-527-6	Sequence 6, Appl
711	32	3.7	3824	3	US-09-688-188B-20	Sequence 20, Appl	C 784	31.6	3.6	1013	3	US-09-451-527-8	Sequence 8, Appl
712	32	3.7	3824	3	US-09-291-417D-20	Sequence 20, Appl	C 785	31.6	3.6	1013	3	US-10-262-439-6	Sequence 6, Appl
713	32	3.7	4931	3	US-08-726-320-2	Sequence 2, Appl	C 786	31.6	3.6	1013	5	US-10-262-439-8	Sequence 8, Appl
714	32	3.7	4931	3	US-09-208-716-2	Sequence 2, Appl	C 787	31.6	3.6	1040	3	US-09-589-287B-22	Sequence 22, Appl
715	32	3.7	5000	3	US-08-836-687B-35	Sequence 35, Appl	C 788	31.6	3.6	1040	3	US-09-588-947A-22	Sequence 22, Appl
716	32	3.7	82612	3	US-09-949-016-16823	Sequence 16823, A	C 789	31.6	3.6	1040	3	US-09-589-286A-22	Sequence 22, Appl
717	32	3.7	138993	3	US-09-949-016-16724	Sequence 16724, A	C 790	31.6	3.6	1040	3	US-09-507-968D-22	Sequence 22, Appl
718	32	3.7	152524	3	US-09-949-016-16683	Sequence 12683, A	C 791	31.6	3.6	1040	3	US-09-589-285-22	Sequence 22, Appl
719	32	3.7	152524	3	US-09-949-016-16110	Sequence 13194, A	C 792	31.6	3.6	1117	3	US-09-148-545-54	Sequence 54, Appl
720	32	3.7	162025	3	US-09-834-700-13	Sequence 13, Appl	C 793	31.6	3.6	1146	3	US-09-621-011-54	Sequence 54, Appl
721	32	3.7	162025	3	US-09-834-700-14	Sequence 14, Appl	C 794	31.6	3.6	1146	3	US-09-596-684F-1	Sequence 1, Appl
722	32	3.7	162025	3	US-09-834-700-17	Sequence 17, Appl	C 795	31.6	3.6	1146	3	US-09-949-016-4186	Sequence 4186, Ap
723	32	3.7	162025	3	US-09-834-700-18	Sequence 18, Appl	C 796	31.6	3.6	1279	3	US-09-248-335-25	Sequence 25, Appl
724	32	3.7	200863	3	US-09-949-016-12569	Sequence 12569, A	C 797	31.6	3.6	1308	3	US-10-151-832-1	Sequence 1, Appl
725	32	3.7	203093	3	US-09-949-016-14445	Sequence 14445, A	C 798	31.6	3.6	1398	3	US-09-949-016-1132	Sequence 1132, Ap
726	32	3.7	231129	3	US-09-949-016-16110	Sequence 16110, A	C 799	31.6	3.6	1507	3	US-09-453-323-1	Sequence 1, Appl
727	32	3.7	266293	3	US-09-949-016-11934	Sequence 11934, A	C 800	31.6	3.6	1526	3	US-10-067-443-23	Sequence 23, Appl
728	32	3.7	340380	3	US-09-949-016-14179	Sequence 14179, A	C 801	31.6	3.6	1591	3	US-09-399-913-50	Sequence 50, Appl
729	32	3.7	640681	3	US-09-790-988-1	Sequence 1, Appl	C 802	31.6	3.6	1591	3	US-09-350-614-50	Sequence 50, Appl
730	31.8	3.7	351	3	US-09-621-976-16140	Sequence 16140, A	C 803	31.6	3.6	1636	3	US-09-578-194-6	Sequence 1, Appl
731	31.8	3.7	577	3	US-09-385-982-203	Sequence 203, Appl	C 804	31.6	3.6	1798	3	US-09-797-906-1	Sequence 1, Appl
732	31.8	3.7	601	3	US-09-949-016-66701	Sequence 66701, A	C 805	31.6	3.6	1883	3	US-09-646-561-46	Sequence 46, Appl
733	31.8	3.7	832	3	US-09-621-976-2813	Sequence 2813, Ap	C 806	31.6	3.6	1883	3	US-09-646-561-48	Sequence 48, Appl
734	31.8	3.7	1024	3	US-09-328-475C-50	Sequence 50, Appl	C 807	31.6	3.6	1927	3	US-09-336-536-66	Sequence 66, Appl
735	31.8	3.7	1065	3	US-09-976-594-833	Sequence 833, Appl	C 808	31.6	3.6	2010	2	US-07-864-475A-4	Sequence 4, Appl
736	31.8	3.7	1069	2	US-08-768-964-1	Sequence 1, Appl	C 809	31.6	3.6	2010	2	US-08-468-249A-4	Sequence 4, Appl
737	31.8	3.7	1069	2	US-08-768-964-3	Sequence 3, Appl	C 810	31.6	3.6	2106	3	US-09-856-327-1	Sequence 1, Appl
738	31.8	3.7	1069	3	US-09-005-299-1	Sequence 1, Appl	C 811	31.6	3.6	2197	3	US-10-067-443-1	Sequence 1, Appl
739	31.8	3.7	1069	3	US-09-005-299-3	Sequence 3, Appl	C 812	31.6	3.6	2218	2	US-08-985-090-4	Sequence 4, Appl
740	31.8	3.7	1069	3	US-09-515-431-1	Sequence 1, Appl	C 813	31.6	3.6	2218	3	US-09-165-543-31	Sequence 31, Appl
741	31.8	3.7	1069	3	US-09-515-431-3	Sequence 3, Appl	C 814	31.6	3.6	2285	2	US-08-967-101-136	Sequence 136, App
742	31.8	3.7	1191	3	US-09-459-133-3	Sequence 3, Appl	C 815	31.6	3.6	2285	2	US-08-592-541-136	Sequence 136, App
743	31.8	3.7	1454	3	US-09-372-422A-19	Sequence 19, Appl	C 816	31.6	3.6	2285	3	US-09-124-688-136	Sequence 136, App
744	31.8	3.7	1817	2	US-08-473-981A-5	Sequence 5, Appl	C 817	31.6	3.6	2285	3	US-09-127-480-136	Sequence 136, App
745	31.8	3.7	1817	2	US-08-474-087-5	Sequence 5, Appl	C 818	31.6	3.6	2285	3	US-09-124-523-136	Sequence 136, App
746	31.8	3.7	2038	3	US-09-885-723-6	Sequence 6, Appl	C 819	31.6	3.6	2285	3	US-09-636-796A-136	Sequence 136, App
747	31.8	3.7	2202	3	US-09-465-558-59	Sequence 59, Appl	C 820	31.6	3.6	2285	4	US-09-878-454B-25	Sequence 25, Appl
748	31.8	3.7	2246	3	US-09-363-708-3	Sequence 3, Appl	C 821	31.6	3.6	2413	3	US-09-689-159A-137	Sequence 137, App
749	31.8	3.7	7200	3	US-09-083-587-3	Sequence 3, Appl	C 822	31.6	3.6	2413	3	US-09-399-913-48	Sequence 48, Appl
750	31.8	3.7	7608	3	US-09-853-450-14	Sequence 48, Appl	C 823	31.6	3.6	2583	3	US-09-350-614-48	Sequence 9, Appl
751	31.8	3.7	9196	3	US-09-221-017B-14	Sequence 14, Appl	C 824	31.6	3.6	2628	2	US-09-857-556A-9	Sequence 9, Appl
752	31.8	3.7	9196	3	US-09-971-773-3	Sequence 3, Appl	C 825	31.6	3.6	2628	2	US-08-143-219-1	Sequence 1, Appl
753	31.8	3.7	40493	3	US-09-949-016-15453	Sequence 15453, A	C 826	31.6	3.6	2915	3	US-09-549-872B-4	Sequence 4, Appl

827	31.6	3.6	3244	3	US-09-165-543-4	Sequence 4, Appli	900	31.4	3.6	1969	3	US-10-012-064A-49	Sequence 49, Appl
828	31.6	3.6	5026	3	US-09-549-872B-3	Sequence 3, Appli	901	31.4	3.6	1969	4	US-10-015-392A-49	Sequence 49, Appl
829	31.6	3.6	6344	3	US-08-843-417-1	Sequence 1, Appli	902	31.4	3.6	1969	5	US-10-011-795B-49	Sequence 49, Appl
830	31.6	3.6	6344	3	US-09-527-013-1	Sequence 1, Appli	903	31.4	3.6	1969	5	US-10-015-386A-49	Sequence 49, Appl
831	31.6	3.6	6612	3	US-09-549-872B-5	Sequence 5, Appli	904	31.4	3.6	1969	5	US-10-012-121A-49	Sequence 49, Appl
832	31.6	3.6	8330	5	US-09-347-311A-3	Sequence 3, Appli	905	31.4	3.6	1969	5	US-10-006-485A-49	Sequence 49, Appl
833	31.6	3.6	9772	3	US-09-949-016-17211	Sequence 17211, A	906	31.4	3.6	1969	5	US-10-006-746A-49	Sequence 49, Appl
834	31.6	3.6	11207	3	US-09-549-872B-2	Sequence 2, Appli	907	31.4	3.6	1969	5	US-10-012-752A-49	Sequence 49, Appl
835	31.6	3.6	41578	3	US-09-949-016-15245	Sequence 15245, A	908	31.4	3.6	1969	5	US-10-017-253A-49	Sequence 49, Appl
836	31.6	3.6	45365	3	US-09-949-016-11893	Sequence 11893, A	909	31.4	3.6	1969	5	US-10-015-519A-49	Sequence 49, Appl
837	31.6	3.6	45456	3	US-09-949-016-17007	Sequence 17007, A	910	31.4	3.6	1969	5	US-10-015-715A-49	Sequence 49, Appl
838	31.6	3.6	47110	3	US-09-949-016-17609	Sequence 17609, A	911	31.4	3.6	1969	5	US-10-007-236A-49	Sequence 49, Appl
839	31.6	3.6	70770	3	US-09-949-016-16938	Sequence 16938, A	912	31.4	3.6	2263	3	US-09-399-913-69	Sequence 69, Appl
840	31.6	3.6	71387	3	US-09-949-016-16938	Sequence 16938, A	913	31.4	3.6	2263	3	US-09-350-614-69	Sequence 69, Appl
841	31.6	3.6	79835	3	US-09-949-016-16754	Sequence 16754, A	914	31.4	3.6	2327	3	US-10-066-130-20	Sequence 20, Appl
842	31.6	3.6	79835	3	US-09-949-016-16754	Sequence 16754, A	915	31.4	3.6	2327	3	US-09-463-238-3	Sequence 3, Appli
843	31.6	3.6	84761	3	US-09-949-016-16121	Sequence 16121, A	916	31.4	3.6	2674	3	US-10-066-130-19	Sequence 19, Appl
844	31.6	3.6	84761	3	US-09-949-016-11919	Sequence 11919, A	917	31.4	3.6	2674	3	US-10-066-130-18	Sequence 18, Appl
845	31.6	3.6	86585	4	US-09-531-120-198	Sequence 198, App	918	31.4	3.6	2783	3	US-09-136-282-1	Sequence 1, Appli
846	31.6	3.6	105168	3	US-09-949-016-13296	Sequence 13296, A	919	31.4	3.6	2783	3	US-09-505-744-1	Sequence 1, Appli
847	31.6	3.6	135476	3	US-09-949-016-14113	Sequence 14113, A	920	31.4	3.6	2882	3	US-09-949-016-724	Sequence 724, App
848	31.6	3.6	135476	3	US-09-949-016-14113	Sequence 14113, A	921	31.4	3.6	2882	10	5378464-1	Patent No. 5378464
849	31.6	3.6	135667	3	US-09-949-016-15051	Sequence 15051, A	922	31.4	3.6	3438	3	US-10-164-595-29	Sequence 29, Appl
850	31.6	3.6	142504	3	US-09-949-016-13693	Sequence 13693, A	923	31.4	3.6	3580	3	US-09-081-345-1	Sequence 1, Appli
851	31.6	3.6	142506	3	US-09-949-016-12474	Sequence 12474, A	924	31.4	3.6	3580	3	US-09-822-295-1	Sequence 1, Appli
852	31.6	3.6	143550	3	US-09-949-016-12474	Sequence 12474, A	925	31.4	3.6	4182	3	US-09-667-422-2	Sequence 2, Appli
853	31.6	3.6	152486	3	US-09-949-016-14143	Sequence 14143, A	926	31.4	3.6	4182	3	US-10-246-435-2	Sequence 2, Appli
854	31.6	3.6	260286	3	US-09-949-016-17037	Sequence 17037, A	927	31.4	3.6	5329	3	US-09-949-016-12252	Sequence 12252, A
855	31.6	3.6	260293	3	US-09-949-016-12106	Sequence 12106, A	928	31.4	3.6	5330	3	US-09-949-016-14028	Sequence 14028, A
856	31.4	3.6	141	3	US-09-621-976-8705	Sequence 8705, Ap	929	31.4	3.6	5860	3	US-10-066-130-17	Sequence 17, Appl
857	31.4	3.6	150	3	US-09-621-976-13989	Sequence 13989, A	930	31.4	3.6	9646	3	US-08-811-566-1	Sequence 1, Appli
858	31.4	3.6	169	3	US-09-621-976-11249	Sequence 11249, A	931	31.4	3.6	9646	3	US-09-034-756-1	Sequence 1, Appli
859	31.4	3.6	179	3	US-09-621-976-9575	Sequence 9575, Ap	932	31.4	3.6	12980	3	US-08-811-566-5	Sequence 5, Appli
860	31.4	3.6	179	3	US-09-621-976-18054	Sequence 18054, A	933	31.4	3.6	12980	3	US-09-034-756-5	Sequence 5, Appli
861	31.4	3.6	347	3	US-09-621-976-16026	Sequence 16026, A	934	31.4	3.6	42246	3	US-09-949-016-17008	Sequence 17008, A
862	31.4	3.6	356	2	US-08-520-678A-22	Sequence 22, Appl	935	31.4	3.6	56302	3	US-09-949-016-11892	Sequence 11892, A
863	31.4	3.6	356	2	US-08-520-678A-22	Sequence 22, Appl	936	31.4	3.6	58407	3	US-09-949-016-11892	Sequence 2, Appli
864	31.4	3.6	356	3	US-10-158-314B-22	Sequence 22, Appl	937	31.4	3.6	58407	3	US-09-692-570-2	Sequence 2, Appli
865	31.4	3.6	357	3	US-09-621-976-16058	Sequence 16058, A	938	31.4	3.6	59123	3	US-09-949-016-12177	Sequence 12177, A
866	31.4	3.6	359	3	US-09-621-976-16008	Sequence 16008, A	939	31.4	3.6	59519	3	US-09-949-016-13504	Sequence 13504, A
867	31.4	3.6	362	3	US-09-621-976-16019	Sequence 16019, A	940	31.4	3.6	60376	3	US-09-949-016-15004	Sequence 15004, A
868	31.4	3.6	362	3	US-09-621-976-16010	Sequence 16010, A	941	31.4	3.6	60338	3	US-09-949-016-15694	Sequence 15694, A
869	31.4	3.6	365	3	US-09-621-976-16042	Sequence 16042, A	942	31.4	3.6	64309	3	US-09-949-016-14581	Sequence 14581, A
870	31.4	3.6	449	3	US-09-621-976-15458	Sequence 15458, A	943	31.4	3.6	76264	3	US-09-949-016-15773	Sequence 15773, A
871	31.4	3.6	500	3	US-09-004-730A-126	Sequence 126, App	944	31.4	3.6	77536	3	US-09-410-551B-1	Sequence 1, Appli
872	31.4	3.6	500	3	US-09-004-730A-126	Sequence 126, App	945	31.4	3.6	77536	3	US-09-940-318B-1	Sequence 1, Appli
873	31.4	3.6	500	3	US-08-981-799A-128	Sequence 128, App	946	31.4	3.6	109974	4	US-09-531-120-204	Sequence 204, App
874	31.4	3.6	500	3	US-08-981-799A-128	Sequence 128, App	947	31.4	3.6	114139	3	US-09-949-016-16536	Sequence 16536, A
875	31.4	3.6	566	3	US-09-621-976-14817	Sequence 14817, A	948	31.4	3.6	176006	3	US-09-949-016-16804	Sequence 16804, A
876	31.4	3.6	601	3	US-09-949-016-20694	Sequence 20694, A	949	31.4	3.6	186959	3	US-09-949-016-13125	Sequence 13125, A
877	31.4	3.6	601	3	US-09-949-016-60283	Sequence 60283, A	950	31.4	3.6	235033	5	US-08-852-495C-1	Sequence 1, Appli
878	31.4	3.6	601	3	US-09-949-016-60282	Sequence 60282, A	951	31.4	3.6	237326	5	US-08-852-495C-2	Sequence 2, Appli
879	31.4	3.6	601	3	US-09-949-016-62062	Sequence 62062, A	952	31.4	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
880	31.4	3.6	601	3	US-09-949-016-68093	Sequence 68093, A	953	31.4	3.6	246240	2	US-08-724-394A-21	Sequence 21, Appl
881	31.4	3.6	601	3	US-09-949-016-68093	Sequence 68093, A	954	31.4	3.6	246240	2	US-08-724-394A-22	Sequence 22, Appl
882	31.4	3.6	690	3	US-09-363-970-4	Sequence 4, Appli	955	31.4	3.6	253375	3	US-09-949-016-12849	Sequence 12849, A
883	31.4	3.6	855	3	US-09-270-767-12433	Sequence 12433, A	956	31.4	3.6	255679	3	US-09-949-016-17189	Sequence 17189, A
884	31.4	3.6	882	3	US-09-311-021-107	Sequence 107, App	957	31.2	3.6	244	3	US-09-621-976-484	Sequence 484, App
885	31.4	3.6	1052	3	US-09-489-847-23	Sequence 23, Appl	958	31.2	3.6	250	3	US-09-621-976-18893	Sequence 18893, A
886	31.4	3.6	1190	3	US-09-390-207-1	Sequence 1, Appli	959	31.2	3.6	270	3	US-09-248-796A-2621	Sequence 2621, Ap
887	31.4	3.6	1545	3	US-09-559-023-1	Sequence 1, Appli	960	31.2	3.6	275	3	US-09-270-767-2418	Sequence 2418, Ap
888	31.4	3.6	1579	3	US-09-482-273-71	Sequence 71, Appl	961	31.2	3.6	275	3	US-09-270-767-17700	Sequence 17700, A
889	31.4	3.6	1582	3	US-08-545-196B-10	Sequence 10, Appl	962	31.2	3.6	285	2	US-08-630-822A-85	Sequence 85, Appl
890	31.4	3.6	1582	3	US-08-545-196B-12	Sequence 12, Appl	963	31.2	3.6	285	2	US-09-005-063-85	Sequence 85, Appl
891	31.4	3.6	1582	3	US-09-109-082A-10	Sequence 10, Appl	964	31.2	3.6	285	3	US-09-171-156A-34	Sequence 34, Appl
892	31.4	3.6	1582	5	US-09-109-082A-12	Sequence 12, Appl	965	31.2	3.6	285	3	US-09-004-730A-34	Sequence 34, Appl
893	31.4	3.6	1969	3	US-10-012-231A-49	Sequence 49, Appl	966	31.2	3.6	285	3	US-08-981-799A-34	Sequence 34, Appl
894	31.4	3.6	1969	3	US-10-015-389A-49	Sequence 49, Appl	967	31.2	3.6	321	2	US-08-520-678A-23	Sequence 23, Appl
895	31.4	3.6	1969	3	US-10-006-768A-49	Sequence 49, Appl	968	31.2	3.6	321	3	US-08-897-126-23	Sequence 23, Appl
896	31.4	3.6	1969	3	US-10-015-671A-49	Sequence 49, Appl	969	31.2	3.6	321	3	US-10-158-314B-23	Sequence 23, Appl
897	31.4	3.6	1969	3	US-10-015-393A-49	Sequence 49, Appl	970	31.2	3.6	356	3	US-09-513-999C-578	Sequence 578, App
898	31.4	3.6	1969	3	US-10-011-833A-49	Sequence 49, Appl	971	31.2	3.6	396	3	US-09-640-173-53	Sequence 53, Appl
899	31.4	3.6	1969	3	US-10-006-041A-49	Sequence 49, Appl	972	31.2	3.6	396	3	US-09-713-550-53	Sequence 53, Appl

c 973	31.2	3.6	396	3	US-09-825-294-53	Sequence 53, Appl	1046	31.2	3.6	2406	3	US-09-594-506-37	Sequence 37, Appl
c 974	31.2	3.6	396	3	US-09-970-966-53	Sequence 53, Appl	1047	31.2	3.6	2476	3	US-10-012-231A-131	Sequence 131, App
c 975	31.2	3.6	402	3	US-10-131-827-8426	Sequence 8426, Ap	1048	31.2	3.6	2476	3	US-10-012-231A-131	Sequence 131, App
c 976	31.2	3.6	402	5	US-10-131-831-8426	Sequence 8426, Ap	1049	31.2	3.6	2476	3	US-10-006-768A-131	Sequence 131, App
c 977	31.2	3.6	548	3	US-09-036-335A-1	Sequence 1, Appli	1050	31.2	3.6	2476	3	US-10-015-671A-131	Sequence 131, App
c 978	31.2	3.6	548	3	US-09-702-647A-1	Sequence 1, Appli	1051	31.2	3.6	2476	3	US-10-015-671A-131	Sequence 131, App
c 979	31.2	3.6	548	3	US-10-218-689-1	Sequence 1, Appli	1052	31.2	3.6	2476	3	US-10-011-833A-131	Sequence 131, App
c 980	31.2	3.6	601	3	US-09-943-016-77505	Sequence 77505, A	1053	31.2	3.6	2476	3	US-10-006-041A-131	Sequence 131, App
c 981	31.2	3.6	601	3	US-09-949-016-77506	Sequence 77506, A	1054	31.2	3.6	2476	3	US-10-012-064A-131	Sequence 131, App
c 982	31.2	3.6	601	3	US-09-949-016-77507	Sequence 77507, A	1055	31.2	3.6	2476	4	US-10-015-392A-131	Sequence 131, App
c 983	31.2	3.6	601	3	US-09-949-016-119283	Sequence 119283, A	1056	31.2	3.6	2476	5	US-10-011-795B-131	Sequence 131, App
c 984	31.2	3.6	601	3	US-09-949-016-119284	Sequence 119284, A	1057	31.2	3.6	2476	5	US-10-015-386A-131	Sequence 131, App
c 985	31.2	3.6	601	3	US-09-949-016-168244	Sequence 168244, A	1058	31.2	3.6	2476	5	US-10-012-121A-131	Sequence 131, App
c 986	31.2	3.6	606	3	US-09-004-730A-100	Sequence 100, App	1059	31.2	3.6	2476	5	US-10-006-485A-131	Sequence 131, App
c 987	31.2	3.6	606	3	US-09-004-730A-102	Sequence 102, App	1060	31.2	3.6	2476	5	US-10-006-746A-131	Sequence 131, App
c 988	31.2	3.6	606	3	US-08-981-799A-100	Sequence 100, App	1061	31.2	3.6	2476	5	US-10-012-752A-131	Sequence 131, App
c 989	31.2	3.6	606	3	US-08-981-799A-102	Sequence 102, App	1062	31.2	3.6	2476	5	US-10-017-253A-131	Sequence 131, App
c 990	31.2	3.6	612	3	US-09-902-540-1357	Sequence 1357, Ap	1063	31.2	3.6	2476	5	US-10-015-519A-131	Sequence 131, App
c 991	31.2	3.6	708	4	US-09-297-648-3418	Sequence 3418, Ap	1064	31.2	3.6	2476	5	US-10-015-715A-131	Sequence 131, App
c 992	31.2	3.6	708	4	US-09-297-648-3419	Sequence 3419, Ap	1065	31.2	3.6	2476	5	US-10-007-236A-131	Sequence 131, App
c 993	31.2	3.6	763	3	US-09-743-207-3	Sequence 3, Appli	1066	31.2	3.6	2483	3	US-09-205-258-68	Sequence 68, Appl
c 994	31.2	3.6	789	3	US-09-020-956-32	Sequence 32, Appl	1067	31.2	3.6	2483	3	US-10-004-860-68	Sequence 9, Appl
c 995	31.2	3.6	789	3	US-09-030-607-32	Sequence 32, Appl	1068	31.2	3.6	2485	3	US-09-889-463A-9	Sequence 8, Appl
c 996	31.2	3.6	789	3	US-09-439-313-32	Sequence 32, Appl	1069	31.2	3.6	2608	2	US-08-160-861-1	Sequence 1, Appli
c 997	31.2	3.6	789	3	US-09-352-616A-32	Sequence 32, Appl	1070	31.2	3.6	2771	3	US-09-674-824-1	Sequence 1, Appli
c 998	31.2	3.6	789	3	US-09-232-149A-32	Sequence 32, Appl	1071	31.2	3.6	3055	3	US-10-001-887-57	Sequence 57, Appl
c 1000	31.2	3.6	789	3	US-09-159-812-32	Sequence 32, Appl	1072	31.2	3.6	3152	4	US-09-880-107-3431	Sequence 3431, Ap
c 1001	31.2	3.6	789	3	US-09-636-215-32	Sequence 32, Appl	1073	31.2	3.6	3410	3	US-09-020-956-110	Sequence 110, App
c 1002	31.2	3.6	789	3	US-09-685-166A-32	Sequence 32, Appl	1074	31.2	3.6	3410	3	US-09-030-607-110	Sequence 110, App
c 1003	31.2	3.6	789	3	US-09-115-453-32	Sequence 32, Appl	1075	31.2	3.6	3410	3	US-09-439-313-110	Sequence 110, App
c 1004	31.2	3.6	789	3	US-09-688-489-32	Sequence 32, Appl	1076	31.2	3.6	3410	3	US-09-352-616A-110	Sequence 110, App
c 1005	31.2	3.6	789	3	US-09-678-428-32	Sequence 32, Appl	1077	31.2	3.6	3410	3	US-09-602-877A-100	Sequence 100, App
c 1006	31.2	3.6	789	3	US-09-759-143-32	Sequence 32, Appl	1078	31.2	3.6	3410	3	US-09-232-149A-110	Sequence 110, App
c 1007	31.2	3.6	789	3	US-09-651-236-32	Sequence 32, Appl	1079	31.2	3.6	3410	3	US-09-159-812-110	Sequence 110, App
c 1008	31.2	3.6	789	3	US-09-657-279-32	Sequence 32, Appl	1080	31.2	3.6	3410	3	US-09-636-215-110	Sequence 110, App
c 1009	31.2	3.6	789	3	US-10-012-896-32	Sequence 32, Appl	1081	31.2	3.6	3410	3	US-09-685-166A-110	Sequence 110, App
c 1010	31.2	3.6	789	5	US-09-116-134-32	Sequence 32, Appl	1082	31.2	3.6	3410	3	US-09-115-453-110	Sequence 110, App
c 1011	31.2	3.6	789	5	US-10-144-678A-32	Sequence 32, Appl	1083	31.2	3.6	3410	3	US-09-688-489-110	Sequence 110, App
c 1012	31.2	3.6	796	2	US-08-104-073-2	Sequence 2, Appli	1084	31.2	3.6	3410	3	US-09-679-426-110	Sequence 110, App
c 1013	31.2	3.6	831	3	US-09-118-554-66	Sequence 66, Appl	1085	31.2	3.6	3410	3	US-09-759-143-110	Sequence 110, App
c 1014	31.2	3.6	831	3	US-09-118-627-66	Sequence 66, Appl	1086	31.2	3.6	3410	3	US-09-651-236-110	Sequence 110, App
c 1015	31.2	3.6	831	3	US-09-602-877A-66	Sequence 66, Appl	1087	31.2	3.6	3410	3	US-09-030-606-110	Sequence 110, App
c 1016	31.2	3.6	985	3	US-09-322-409-25	Sequence 25, Appl	1088	31.2	3.6	3410	3	US-09-657-279-110	Sequence 110, App
c 1017	31.2	3.6	985	3	US-09-322-409-27	Sequence 27, Appl	1089	31.2	3.6	3410	3	US-10-012-896-110	Sequence 110, App
c 1018	31.2	3.6	985	3	US-09-451-527-25	Sequence 25, Appl	1090	31.2	3.6	3410	5	US-09-116-134-110	Sequence 110, App
c 1019	31.2	3.6	985	3	US-09-451-527-27	Sequence 27, Appl	1091	31.2	3.6	3410	5	US-10-144-678A-110	Sequence 110, App
c 1020	31.2	3.6	985	5	US-10-262-439-25	Sequence 25, Appl	1092	31.2	3.6	3556	3	US-09-270-767-10439	Sequence 10439, A
c 1021	31.2	3.6	985	5	US-10-262-439-27	Sequence 27, Appl	1093	31.2	3.6	3848	3	US-09-112-096-28	Sequence 28, Appl
c 1022	31.2	3.6	1097	3	US-09-270-767-5246	Sequence 5246, Ap	1094	31.2	3.6	4674	3	US-09-410-551B-26	Sequence 26, Appl
c 1023	31.2	3.6	1097	3	US-09-270-767-20528	Sequence 20528, A	1095	31.2	3.6	4674	3	US-09-940-316B-26	Sequence 26, Appl
c 1024	31.2	3.6	1098	3	US-09-248-335-35	Sequence 35, Appl	1096	31.2	3.6	4725	3	US-09-940-316B-24	Sequence 24, Appl
c 1025	31.2	3.6	1133	3	US-09-916-204-1	Sequence 1, Appli	1097	31.2	3.6	4725	3	US-09-940-316B-24	Sequence 24, Appl
c 1026	31.2	3.6	1133	3	US-10-282-048-1	Sequence 1, Appli	1098	31.2	3.6	4737	3	US-09-410-551B-30	Sequence 30, Appl
c 1027	31.2	3.6	1141	3	US-09-800-729-78	Sequence 78, Appl	1099	31.2	3.6	4737	3	US-09-940-316B-30	Sequence 30, Appl
c 1028	31.2	3.6	1258	3	US-09-208-258-169	Sequence 169, App	1100	31.2	3.6	4767	3	US-09-940-316B-28	Sequence 28, Appl
c 1029	31.2	3.6	1258	3	US-10-004-860-169	Sequence 169, App	1101	31.2	3.6	4767	3	US-09-940-316B-28	Sequence 28, Appl
c 1030	31.2	3.6	1277	3	US-09-270-767-25838	Sequence 25838, A	1102	31.2	3.6	4818	3	US-09-410-551B-32	Sequence 32, Appl
c 1031	31.2	3.6	1297	3	US-09-800-729-80	Sequence 80, Appl	1103	31.2	3.6	4818	3	US-09-940-316B-32	Sequence 32, Appl
c 1032	31.2	3.6	1365	3	US-09-107-532A-1659	Sequence 1659, Ap	1104	31.2	3.6	5668	3	US-09-112-096-14	Sequence 14, Appl
c 1033	31.2	3.6	1493	2	US-08-340-820-24	Sequence 24, Appl	1105	31.2	3.6	5668	3	US-09-636-215-777	Sequence 777, App
c 1034	31.2	3.6	1493	2	US-08-593-535-24	Sequence 24, Appl	1106	31.2	3.6	5668	3	US-09-685-166A-777	Sequence 777, App
c 1035	31.2	3.6	1512	2	US-08-909-965C-8	Sequence 8, Appli	1107	31.2	3.6	5668	3	US-09-679-426-777	Sequence 777, App
c 1036	31.2	3.6	1728	3	US-08-985-950-7	Sequence 7, Appli	1108	31.2	3.6	5668	3	US-09-759-143-777	Sequence 777, App
c 1037	31.2	3.6	1728	3	US-09-546-049-7	Sequence 7, Appli	1109	31.2	3.6	5668	3	US-09-651-236-777	Sequence 777, App
c 1038	31.2	3.6	1788	3	US-09-328-352-306	Sequence 306, App	1110	31.2	3.6	5668	3	US-09-657-279-777	Sequence 777, App
c 1039	31.2	3.6	2239	3	US-09-196-390-1	Sequence 1, Appli	1111	31.2	3.6	5668	5	US-10-012-896-777	Sequence 777, App
c 1040	31.2	3.6	2239	3	US-09-952-677-1	Sequence 1, Appli	1112	31.2	3.6	5668	5	US-10-144-678A-777	Sequence 777, App
c 1041	31.2	3.6	2264	3	US-09-126-109-9	Sequence 9, Appli	1113	31.2	3.6	7286	3	US-09-331-581-3	Sequence 3, Appli
c 1042	31.2	3.6	2271	3	US-10-104-047-155	Sequence 155, App	1114	31.2	3.6	7938	3	US-09-331-581-14	Sequence 14, Appl
c 1043	31.2	3.6	2279	3	US-09-949-016-254	Sequence 254, App	c1115	31.2	3.6	20407	3	US-09-949-002-666	Sequence 666, App
c 1044	31.2	3.6	2279	3	US-09-949-016-2520	Sequence 2520, Ap	c1116	31.2	3.6	25992	3	US-09-949-016-17308	Sequence 17308, A
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cl120	31.2	3.6	50000	3	US-09-146-053-3	Sequence 3, Appli	1193	31	3.6	1701	3	US-09-992-598-114	Sequence 114, App
cl121	31.2	3.6	64024	3	US-09-949-016-17593	Sequence 17593, A	1194	31	3.6	1701	4	US-09-989-735-114	Sequence 114, App
cl122	31.2	3.6	101011	3	US-09-949-016-16333	Sequence 16333, A	1195	31	3.6	1701	5	US-09-989-726-114	Sequence 114, App
cl123	31.2	3.6	105055	3	US-09-949-016-14001	Sequence 14001, A	1196	31	3.6	1701	5	US-09-997-514-114	Sequence 114, App
cl124	31.2	3.6	114842	3	US-09-949-016-14993	Sequence 14993, A	1197	31	3.6	1701	5	US-09-989-728-114	Sequence 114, App
cl125	31.2	3.6	147382	3	US-09-949-016-14624	Sequence 14624, A	1198	31	3.6	1701	5	US-09-997-349-114	Sequence 114, App
cl126	31.2	3.6	169998	3	US-09-676-610B-24	Sequence 24, Appl	1199	31	3.6	1701	5	US-09-997-653-114	Sequence 114, App
cl127	31.2	3.6	176373	3	US-09-128-155-17	Sequence 17, Appl	1200	31	3.6	1701	5	US-09-989-293A-114	Sequence 114, App
cl128	31.2	3.6	197496	3	US-09-877-177A-10	Sequence 10, Appl	1201	31	3.6	1746	3	US-09-485-529-57	Sequence 57, Appl
cl129	31.2	3.6	278866	3	US-09-949-016-13922	Sequence 13922, A	1202	31	3.6	1766	3	US-10-142-835-27	Sequence 27, Appl
cl130	31.2	3.6	278866	3	US-09-949-016-13923	Sequence 13923, A	1203	31	3.6	1768	3	US-09-485-529-13	Sequence 13, Appl
cl131	31.2	3.6	278866	3	US-09-949-016-13924	Sequence 13924, A	1204	31	3.6	1835	3	US-09-485-549-1	Sequence 1, Appli
cl132	31.2	3.6	278866	3	US-09-949-016-13925	Sequence 13925, A	1205	31	3.6	1843	3	US-08-718-738-1	Sequence 1, Appli
cl133	31.2	3.6	278866	3	US-09-949-016-13926	Sequence 13926, A	1206	31	3.6	1843	3	US-09-221-844-1	Sequence 1, Appli
cl134	31.2	3.6	278866	3	US-09-949-016-14699	Sequence 14699, A	1207	31	3.6	1843	3	US-09-843-846-1	Sequence 1, Appli
cl135	31.2	3.6	278866	3	US-09-949-016-14700	Sequence 14700, A	1208	31	3.6	1843	7	PCT-US95-0333A-1	Sequence 1, Appli
cl136	31.2	3.6	278866	3	US-09-949-016-14701	Sequence 14701, A	1209	31	3.6	1844	3	US-09-123-913-88	Sequence 88, Appl
cl137	31.2	3.6	278866	3	US-09-949-016-14702	Sequence 14702, A	1210	31	3.6	1844	3	US-09-643-597-88	Sequence 88, Appl
cl138	31.2	3.6	278866	3	US-09-949-016-14703	Sequence 14703, A	1211	31	3.6	1844	3	US-09-480-884A-88	Sequence 88, Appl
cl139	31.2	3.6	580073	3	US-08-545-5280-1	Sequence 1, Appli	1212	31	3.6	1844	3	US-09-542-615A-88	Sequence 88, Appl
cl140	31.2	3.6	1664976	3	US-08-596-421B-1	Sequence 1, Appli	1213	31	3.6	1844	3	US-09-606-421B-88	Sequence 88, Appl
cl141	31.2	3.6	1664976	3	US-09-692-570-1	Sequence 1, Appli	1214	31	3.6	1844	3	US-09-221-107-88	Sequence 88, Appl
cl142	31	3.6	127	3	US-10-021-338A-29	Sequence 29, Appl	1215	31	3.6	1844	3	US-09-466-396A-88	Sequence 88, Appl
cl143	31	3.6	181	3	US-09-621-976-17313	Sequence 17313, A	1216	31	3.6	1844	3	US-09-476-496A-88	Sequence 88, Appl
cl144	31	3.6	190	3	US-09-621-976-16784	Sequence 16784, A	1217	31	3.6	1844	3	US-09-630-940B-88	Sequence 88, Appl
cl145	31	3.6	191	4	US-09-880-107-525	Sequence 525, App	1218	31	3.6	1844	3	US-09-285-479-88	Sequence 88, Appl
cl146	31	3.6	195	3	US-09-621-976-18062	Sequence 18062, A	1219	31	3.6	1844	3	US-10-007-700-88	Sequence 88, Appl
cl147	31	3.6	226	3	US-10-131-827-8671	Sequence 8671, Ap	1220	31	3.6	1872	3	US-09-291-922-27	Sequence 27, Appl
cl148	31	3.6	226	5	US-10-131-831-8671	Sequence 8671, Ap	1221	31	3.6	1975	3	US-09-910-174B-3	Sequence 3, Appli
cl149	31	3.6	272	3	US-09-621-976-8353	Sequence 8353, Ap	1222	31	3.6	1975	3	US-09-620-461-3	Sequence 3, Appli
cl150	31	3.6	358	3	US-09-621-976-927	Sequence 927, App	1223	31	3.6	1985	3	US-09-907-794A-212	Sequence 212, App
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cl152	31	3.6	414	3	US-09-270-767-6943	Sequence 6943, Ap	1225	31	3.6	1985	3	US-09-902-755A-212	Sequence 212, App
cl153	31	3.6	414	3	US-09-270-767-22225	Sequence 22225, A	1226	31	3.6	1985	3	US-09-906-700-212	Sequence 212, App
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cl155	31	3.6	491	3	US-09-621-976-14374	Sequence 14374, A	1228	31	3.6	1985	3	US-09-904-920A-212	Sequence 212, App
cl156	31	3.6	505	3	US-09-621-976-15639	Sequence 15639, A	1229	31	3.6	1985	3	US-09-909-064-212	Sequence 212, App
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cl158	31	3.6	528	5	US-10-131-831-8186	Sequence 8186, Ap	1231	31	3.6	1985	3	US-09-906-646-212	Sequence 212, App
cl159	31	3.6	546	3	US-09-280-116-48	Sequence 48, Appl	1232	31	3.6	1985	3	US-09-904-462-212	Sequence 212, App
cl160	31	3.6	601	3	US-09-949-016-53615	Sequence 53615, A	1233	31	3.6	1985	3	US-09-902-736A-212	Sequence 212, App
cl161	31	3.6	601	3	US-09-949-016-57438	Sequence 57438, A	1234	31	3.6	1985	3	US-09-906-722A-212	Sequence 212, App
cl162	31	3.6	601	3	US-09-949-016-57438	Sequence 57438, A	1235	31	3.6	1985	4	US-09-905-443-212	Sequence 212, App
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cl164	31	3.6	601	3	US-09-949-016-116679	Sequence 116679, A	1237	31	3.6	1985	4	US-09-906-618-212	Sequence 212, App
cl165	31	3.6	601	3	US-09-949-016-117755	Sequence 117755, A	1238	31	3.6	1985	5	US-09-907-841-212	Sequence 212, App
cl166	31	3.6	601	3	US-09-949-016-131371	Sequence 131371, A	1239	31	3.6	2065	2	US-08-968-751-1	Sequence 1, Appli
cl167	31	3.6	601	3	US-09-949-016-139892	Sequence 139892, A	1240	31	3.6	2198	2	US-08-755-728-2	Sequence 2, Appli
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cl169	31	3.6	601	3	US-09-949-016-159667	Sequence 159667, A	1242	31	3.6	2198	2	US-08-974-653-2	Sequence 2, Appli
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cl171	31	3.6	601	3	US-09-949-016-192607	Sequence 192607, A	1244	31	3.6	2198	3	US-09-012-135A-2	Sequence 2, Appli
cl172	31	3.6	601	3	US-09-949-016-192608	Sequence 192608, A	1245	31	3.6	2198	3	US-09-784-332-2	Sequence 2, Appli
cl173	31	3.6	601	4	US-09-880-107-1421	Sequence 1421, Ap	1246	31	3.6	2218	3	US-09-016-434-1157	Sequence 1157, Ap
cl174	31	3.6	700	3	US-09-832-129-23	Sequence 23, Appl	1247	31	3.6	2218	3	US-10-329-668-7	Sequence 7, Appli
cl175	31	3.6	742	3	US-09-950-933A-35	Sequence 35, Appl	1248	31	3.6	2218	4	US-09-880-107-3411	Sequence 3411, Ap
cl176	31	3.6	774	3	US-09-105-542A-4	Sequence 4, Appli	1249	31	3.6	2229	3	US-09-910-174B-1	Sequence 1, Appli
cl177	31	3.6	840	3	US-09-244-111-5	Sequence 5, Appli	1250	31	3.6	2229	3	US-09-620-461-1	Sequence 1, Appli
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cl179	31	3.6	1008	3	US-09-780-641-1	Sequence 1, Appli	1252	31	3.6	2242	3	US-09-482-273-35	Sequence 35, Appli
cl180	31	3.6	1167	2	US-08-671-320-16	Sequence 16, Appl	1253	31	3.6	2292	5	US-09-430-590B-128	Sequence 128, App
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cl184	31	3.6	1342	3	US-09-489-847-89	Sequence 89, Appl	1257	31	3.6	2407	3	US-09-921-259-7	Sequence 7, Appli
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1268	31	3.6	9711	3	US-10-009-011-3	Sequence 3, Appli	1341	30.8	3.5	1743	3	US-10-012-231A-235	Sequence 235, App
1269	31	3.6	24984	3	US-09-949-016-14950	Sequence 14950, A	1342	30.8	3.5	1743	3	US-10-015-389A-235	Sequence 235, App
1270	31	3.6	26640	3	US-09-949-016-17431	Sequence 17431, A	1343	30.8	3.5	1743	3	US-10-006-768A-235	Sequence 235, App
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## ALIGNMENTS

## RESULT 1

US-09-991-181-164  
; Sequence 164, Application US/09991181  
; Patent No. 6913919  
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; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
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; PRIOR FILING DATE: 1988-07-09

Query Match 100.0%; Score 870; DB 3; Length 870;  
Best Local Similarity 100.0%; Pred. No. 5.2e-265;

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Db	1	CTCGCCCTCAAAATGGGAAACGCTGGCTGGGACTAAAGCATAGACCAACGAGCTGAGTATC	60	
Qy	61	CTGACCTGAGTCATCCCAGGGATCAGGAGCCTCCAGACGGAACTTCCATTATATCTCT	120	
Db	61	CTGACCTGAGTCATCCCAGGGATCAGGAGCCTCCAGACGGAACTTCCATTATATCTCT	120	
Qy	121	TCAAGCAACTTACAGCTGCAACCGACAGTTCGGATGAAAGTTCTAATCTCTTCCCTCCTCC	180	
Db	121	TCAAGCAACTTACAGCTGCAACCGACAGTTCGGATGAAAGTTCTAATCTCTTCCCTCCTCC	180	
Qy	181	TGTTGCTGCCACTAAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGTCGCCA	240	
Db	181	TGTTGCTGCCACTAAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGTCGCCA	240	
Qy	241	GAGGCCACAGGGACCGAGGCGAGGCTTCTAGGAGATGGCTCCAGGAAGCGGGCCAGAAT	300	
Db	241	GAGGCCACAGGGACCGAGGCGAGGCTTCTAGGAGATGGCTCCAGGAAGCGGGCCAGAAT	300	
Qy	301	GTGAGTCAAGAATTTGGTTCTTGAGGCCCGAGAGAAATTCATGACAGTGTCTGGGC	360	
Db	301	GTGAGTCAAGAATTTGGTTCTTGAGGCCCGAGAGAAATTCATGACAGTGTCTGGGC	360	
Qy	361	TGCGAAAGAACAGTCGCCCTGTGATCATTTCAAGGGCAATGTCAAGAAACCAAGACACC	420	
Db	361	TGCGAAAGAACAGTCGCCCTGTGATCATTTCAAGGGCAATGTCAAGAAACCAAGACACC	420	
Qy	421	AAAGGCCACACAGAAAGCCAAAACGACATTTCCAGAGCTTCGACGCAATTTCTCAAA	480	
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Db	481	GTGAGCTTAAGAACTTTGCTTCGCTTTGAGGAGCTCTGAGCGCCACATCTTCCAAATTA	540	
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Db	541	AACATTTCCAGCCAAAGAACAGTGAGCACACCTTACCAGACACTTCTTCTTCCACCTC	600	
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Db	601	ACTCTCCACTGTACCCACCCCTAAATCATTTCCAGTGTCTCTCAAAAAAGCATGTTTTCAA	660	
Qy	661	GATCATTTTGTGTGTGCTCTCTAGTGTCTTCTCTCGTCAGTCTTAGCCTGTGCC	720	
Db	661	GATCATTTTGTGTGTGCTCTCTAGTGTCTTCTCTCGTCAGTCTTAGCCTGTGCC	720	
Qy	721	CTCCCTTACCCAGGCTTAGGCTTAAATTTACTGAAAGATTCAGGAAACTGTAGCTTCCT	780	
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Qy	781	AGCTAGTGTCTATTTAACTTTAAATGCAATCAGGAAAGTAGCAAAACAGAAAGTCAATAATA	840	
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Qy	841	TTTTTAAATGTCAAAAAAATAAAAAA	870	
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## RESULT 2

US-09-990-444-164

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding
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Db 61 CTGACCTGAGTCATCCCGAGGATCAGGAGCTCCAGCAGGGAACCTTCCATTATTTCT 120  
Qy 121 TCAAGCAACTTACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCC 180  
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Qy 181 TGTGCTGCCACTAATGCTGATGCTTCATGCTCTAGCAGCTGAATCCAGGCTCGCCA 240

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QY 301 GTGAGTGCAAGATGGTTCTTGAGAGCCCCCGAGAGAAAAATTCATGACAGTGTCTGGGC 360  
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; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F..  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A..  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I..  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
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; PRIOR FILING DATE: 1998-07-07  
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 870; DB 3; Length 870;

Best Local Similarity 100.0%; Pred. No. 5.2e-265; Indels 0; Gaps 0;  
Matches 870; Conservative 0; Mismatches 0;

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DB 1 CTCGCCCTCAAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACACACAGGCTGAGTATC 60  
QY 61 CTGACCTGAGTCATCCCGAGGGATCAGGAGCCTCAGCAGGGAACCTTCCATTATTTCT 120  
DB 61 CTGACCTGAGTCATCCCGAGGGATCAGGAGCCTCAGCAGGGAACCTTCCATTATTTCT 120  
QY 121 TCAAGCAACTTACAGCTGCACCGCAGTTGGGATGAAAGTTCTAATCTTCCCTCCTCC 180  
DB 121 TCAAGCAACTTACAGCTGCACCGCAGTTGGGATGAAAGTTCTAATCTTCCCTCCTCC 180  
QY 181 TGTTCCTGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGTCCCA 240  
DB 181 TGTTCCTGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGTCCCA 240  
QY 241 GAGGCCACAGGACCGAGGCCAGGGCTTCTAGAGATGGCTCAGGGAAGCGGCCAAGAT 300  
DB 241 GAGGCCACAGGACCGAGGCCAGGGCTTCTAGAGATGGCTCAGGGAAGCGGCCAAGAT 300  
QY 301 GTGAGTGCAAAAGATTGGTTCTCTGAGAGCCCGAGGAAGAAATTCATGACGTCTGGGC 360  
DB 301 GTGAGTGCAAAAGATTGGTTCTCTGAGAGCCCGAGGAAGAAATTCATGACGTCTGGGC 360  
QY 361 TGCCAAAGAACGAGTGGCTTCTGAGAGCCCGAGGAAGAAATTCATGAGCAATTCGACACC 420  
DB 361 TGCCAAAGAACGAGTGGCTTCTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACC 420  
QY 421 AAAGGCACCAAGAAAGCAAAACAGCAATTCAGAGCCTGCCAGCAATTTCTCAACAAT 480  
DB 421 AAAGGCACCAAGAAAGCAAAACAGCAATTCAGAGCCTGCCAGCAATTTCTCAACAAT 480  
QY 481 GTCAGCTAAGAGCTTTGCTCTGCTTTGTAGGAGCTCTGAGCGCCACTCTTCCAATTA 540  
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QY 541 AACATTCTCAGCAAGAAAGACAGTGAGCACACCTACACAGACACTCTTCTTCCACCTC 600

Db 541 AACATTCTCAGCCAGAAGACAGTGTAGCACACCTACCAGACACTCTTTCTCCACCTC 600  
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Db 601 ACTCTCCCACTGTACCCACCCCTAAATCATTCAGTGTCTCTCAAAAGCATGTTTTTCAA 660  
Qy 661 GATCATTTTGTGTTGTTGTTCTCTCTAGTGTCTTTCTCTCGTCAGTCTTAGCGCTGTGCC 720  
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Qy 781 AGCTAGTGTCAATTAACTTAAATGCAATCAGGAAAGTAGCAACAGAGTCAATAAATA 840  
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Qy 841 TTTTAAATGTCAAAAAAATAAAAAA 870  
Db 841 TTTTAAATGTCAAAAAAATAAAAAA 870

RESULT 4  
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; Sequence 164, Application US/09992598  
; Patent No: 6956108  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavini, Ivar J.  
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; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C20  
; CURRENT APPLICATION NUMBER: US/09/992,598  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
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Db 61 CTGACCTGAGTCAATCCCAGGGATCAGGAGCCTCCAGCAGGAACTTTCCATATATTTCT 120

Qy 121 TCAAGCAACTTACAGCTGCACCGACAGTTGGATGGAAGTTCTAATCTTTCCCTCCCTCC 180  
Db 121 TCAAGCAACTTACAGCTGCACCGACAGTTGGATGGAAGTTCTAATCTTTCCCTCCCTCC 180

Qy 181 TGTTCCTGCCACTAATGCTGATGTCATGCTCTTAGCAGCCTGAATCCAGGGGTCGCCA 240  
Db 181 TGTTCCTGCCACTAATGCTGATGTCATGCTCTTAGCAGCCTGAATCCAGGGGTCGCCA 240

Qy 241 GAGGCCACAGGGACCGAGGCCAGGCTTTAGGAGATGGCTCCAGGAAGGGCCCAAGAAAT 300  
Db 241 GAGGCCACAGGGACCGAGGCCAGGCTTTAGGAGATGGCTCCAGGAAGGGCCCAAGAAAT 300

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Db 301 GTGAGTGCAGAAAGATTGGTTCTTGAGAGCCCGAGAGAAAATTCATGACAGTGTCTGGGC 360

Qy 361 TGCCAAAGAACAGTCGCCCCCTGTCATCATTTCAAGGGCAATGTGAAGAAAAACAAGACACC 420  
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Qy 421 AAAGGCCACACAGAAAGCCAAACAAAGCAATTCAGAGCTGCCAGCAATTTCTCAAAACAAT 480  
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Qy 481 GTCAGCTAAGAAAGCTTTGCTCTGCTTGTAGGAGCTTGAGCGCCCACTCTTCCAAATTA 540  
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Qy 541 AACATTCTCAGCCCAAGAGACAGTGAGCACACCTACAGACACTCTTCTTCTCCACCTC 600  
Db 541 AACATTCTCAGCCCAAGAGACAGTGAGCACACCTACAGACACTCTTCTTCTCCACCTC 600

Qy 601 ACTCTCCACTGTACCCACCCCTAAATCAATTCAGTGTCTCAAAAAGCATGTTTTTCAA 660  
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Qy 661 GATCATTTTGTGTTGCTCTCTAGTGTCTTCTCTCTGTCAGTCTTAGCCCTGTGCC 720  
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Qy 721 CTCCTCTTACCCAGGCTTAGGCTTAAATTAACCTGAAAGATTCAGGAAACTCTAGCTTCT 780  
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Qy 841 TTTTAAATGTCAAAAAA 870  
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; Sequence 164, Application US/09989735  
; Patent No. 6972185  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
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; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC61  
; CURRENT APPLICATION NUMBER: US/09/989,735  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
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; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 870; DB 4; Length 870;
Best Local Similarity 100.0%; Pred. No. 5.2e-265;
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 TCAAGCAACTTACAGCTGCACCGACAGTTGGGATGAAAGTTCTATCTCTTCCCTCC 180
Db 121 TCAAGCAACTTACAGCTGCACCGACAGTTGGGATGAAAGTTCTATCTCTTCCCTCC 180
Qy 181 TGTGCTGCCACTAATGCTGATGTCCTAGCAGCTGNAATCCAGGGGTGCGCA 240
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Qy 421 AAAGGCACACAGAAAGCCAAACAGCATTCAGAGCTGCCAGCAATTTCTCAAAACAAT 480
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Qy 841 TTTTAAATGTCAAAAAA 870
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RESULT 6
US-09-989-726-164
; Sequence 164, Application US/09989726
; Patent No. 7018811
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
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APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC60  
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Query Match 100.0%; Score 870; DB 5; Length 870;  
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Qy	61	CTGACCTGAGTCAATCCAGGGAATCAGGAGCCTCCAGCAGGGAACTTTCCATTATATCT	120
Db	61	CTGACCTGAGTCAATCCAGGGAATCAGGAGCCTCCAGCAGGGAACTTTCCATTATATCT	120
Qy	121	TCAAGCAACTTACAGCTGCAACGACAGTTGGATGAAAGTTCTATCTCTTCCCTCCCTCC	180
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Qy	181	TGTTGCTGCCACTAAATGCTGATGTCCTAGCAGCTGTAATCAGGGGTCGCA	240
Db	181	TGTTGCTGCCACTAAATGCTGATGTCCTAGCAGCTGTAATCAGGGGTCGCA	240
Qy	241	GAGGCCACAGGACCGAGGCCAGAGCTTCTAGGAGATGGCTCCAGGAAGCGGCCAAGAT	300
Db	241	GAGGCCACAGGACCGAGGCCAGAGCTTCTAGGAGATGGCTCCAGGAAGCGGCCAAGAT	300
Qy	301	GTGAGTGCAAAGATTGGTTCTGAGAGCCCCGAGAGAAATTCATGACAGTGTCTGGGC	360
Db	301	GTGAGTGCAAAGATTGGTTCTGAGAGCCCCGAGAGAAATTCATGACAGTGTCTGGGC	360
Qy	361	TGCCAAAGAAAGCAGTGGCCCTGTGATCATTTTCAAGGGCAATGTGAAGAAAAACAACACACC	420
Db	361	TGCCAAAGAAAGCAGTGGCCCTGTGATCATTTTCAAGGGCAATGTGAAGAAAAACAACACACC	420
Qy	421	AAAGGCCACACAGAAAGCCAAACAGCATTCAGAGCCTGCAGCAATTTCTCAAACAAT	480
Db	421	AAAGGCCACACAGAAAGCCAAACAGCATTCAGAGCCTGCAGCAATTTCTCAAACAAT	480
Qy	481	GTACGCTAAGAAAGCTTTGCTCTGCTCTTGTAGGAGCTCTGAGCGGCCACTCTTCCAAATTA	540
Db	481	GTACGCTAAGAAAGCTTTGCTCTGCTCTTGTAGGAGCTCTGAGCGGCCACTCTTCCAAATTA	540
Qy	541	AACATTTCTACGCCAAGAAGACAGTGAGCACACTACAGACACTCTTTCTCCACCTC	600
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Qy	601	ACTCTCCACGTATACCCACCCCTAAATCATTTCCAGTGCTCTCAAAAGCATGTTTTTCAA	660
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Qy	841	TTTTTAAATGTCAAAAAAATAAAAAA 870	
Db	841	TTTTTAAATGTCAAAAAAATAAAAAA 870	



181	Qy	TGTTGCTGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAAATCCAGGGGTGCGCA	240
181	Db	TGTTGCTGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAAATCCAGGGGTGCGCA	240
241	Qy	GAGGCCACAGGGACCGAGGCCAGGGCTTCTAGGAGATGGCTCCAGGAAGCGGCCCAAGAAT	300
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301	Qy	GTGAGTGCAAAAGATTGGTTCTGAGAGGCCCGAGAAAGAAAATTCATGACAGTGTCTGGGC	360
301	Db	GTGAGTGCAAAAGATTGGTTCTGAGAGGCCCGAGAAAGAAAATTCATGACAGTGTCTGGGC	360
361	Qy	TGCCAAAGAAGCAGTGGCCCTGTGTATCATTTCAAGGGCAAATGCTGAAGAGAAAACAAGACACC	420
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421	Qy	AAAGGCCACACAGAAAGCCAAACAAAGCATTCAGAGCCTGCAGACAAATTTCTCAAAACAAT	480
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## RESULT 9

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US/09-397-349-164
; Sequence 164, Application US/09997349
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanovyers, Luc
; APPLICANT: Eacon, Dan L.
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Db	61	CTGACCTGAGTATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCATTATTTCT	120
QY	121	TCAAGCAACTTACAGCTGACCCGACAGTTCGATGAAAGTTCTATCTCTTCCCTCTCC	180
Db	121	TCAAGCAACTTACAGCTGACCCGACAGTTCGATGAAAGTTCTATCTCTTCCCTCTCC	180
QY	181	TGTTGCTGCCACTAATGCTGATGTCCTGATGCTCTAGCAGCCTGAATCCAGGGTCCCA	240
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QY	301	GTGAGTGCAAAAGATTGGTTCTTGAGAGCCCCGAGAGAAAAATTCATGACAGTCTGGGC	360
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QY	361	TGCCAAGNAGCAGTGCCCTCTGATCATTTCAAGGGCAATCTGAGAAAAACAAGACACC	420
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QY	421	AAAGGCACCAAGAAAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAACAAT	480
Db	421	AAAGGCACCAAGAAAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAACAAT	480
QY	481	GTGAGCTAAGAAAGCTTTGCTCTGCTCTTTGTAGAGCTCTGAGCGCCACTCTTCCAATTA	540
Db	481	GTGAGCTAAGAAAGCTTTGCTCTGCTCTTTGTAGAGCTCTGAGCGCCACTCTTCCAATTA	540

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C38
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; GENERAL INFORMATION:  
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; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
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; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Napier, Mary A.  
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; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC66  
; CURRENT APPLICATION NUMBER: US/09/989,293A  
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; PRIOR APPLICATION NUMBER: 60/089653  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/089907  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/089908  
; PRIOR FILING DATE: 1998-06-18  
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; PRIOR APPLICATION NUMBER: 60/089948  
; PRIOR FILING DATE: 1998-06-19  
; PRIOR APPLICATION NUMBER: 60/089952  
; PRIOR FILING DATE: 1998-06-19  
; PRIOR APPLICATION NUMBER: 60/090246  
; PRIOR FILING DATE: 1998-06-22  
; PRIOR APPLICATION NUMBER: 60/090252  
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; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
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; PRIOR APPLICATION NUMBER: 60/090431
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; PRIOR APPLICATION NUMBER: 60/090435
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; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-06-26
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; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 870; DB 5; Length 870;
Best Local Similarity 100.0%; Pred. No. 5.2e-265;
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGCGCCCTCAATGGGAAGCTGGCGCTGGGACTAAAGCATAGACACACAGGCTGAGTATC 60
DB      1 CTGCGCCCTCAATGGGAAGCTGGCGCTGGGACTAAAGCATAGACACACAGGCTGAGTATC 60
QY      61 CTGACCTGAGTATCCCGAGGATCAGGAGCTCCAGAGGGAACTTCCATTATATTTCT 120
DB      61 CTGACCTGAGTATCCCGAGGATCAGGAGCTCCAGAGGGAACTTCCATTATATTTCT 120
QY      121 TCAAGCAACTTACAGCTGCACCGACAGTTGCCAGTGAAGTTCTTAATCTCTTCCCTCCTCC 180
DB      121 TCAAGCAACTTACAGCTGCACCGACAGTTGCCAGTGAAGTTCTTAATCTCTTCCCTCCTCC 180
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QY      181 TGTGTGCTGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCCCA 240
DB      181 TGTGTGCTGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCCCA 240
QY      241 GAGGCCACAGGGACCGAGGCCAGGCTTCTAGAGATGGCTCCAGGAAGGGCGGCAAGAAT 300
DB      241 GAGGCCACAGGGACCGAGGCCAGGCTTCTAGAGATGGCTCCAGGAAGGGCGGCAAGAAT 300
QY      301 GTGAGTGTCAAAAGATTGGTTCTGAGAGCCCCCAGAGAAATTCATGACAGTGTCTGGGC 360
DB      301 GTGAGTGTCAAAAGATTGGTTCTGAGAGCCCCCAGAGAAATTCATGACAGTGTCTGGGC 360
QY      361 TGCCAAAGAGCAGTGCCTCTGTGATCATTTCAAGGGCAATGTGAAGAAAAACAAGACACC 420
DB      361 TGCCAAAGAGCAGTGCCTCTGTGATCATTTCAAGGGCAATGTGAAGAAAAACAAGACACC 420
QY      421 AAAGGCACACAGAAAGCCAAACAGAGCATTCAGAGCCTGCCAGCAATTTCTCAAAACAAT 480
DB      421 AAAGGCACACAGAAAGCCAAACAGAGCATTCAGAGCCTGCCAGCAATTTCTCAAAACAAT 480
QY      481 GTGAGTGTCAAAAGATTGGTTCTGAGAGCCCCCAGAGAAATTCATGACAGTGTCTGGGC 540
DB      481 GTGAGTGTCAAAAGATTGGTTCTGAGAGCCCCCAGAGAAATTCATGACAGTGTCTGGGC 540
QY      541 AACATTCTCAGCAAGAACAGACAGTGTGAGCAGCCTACAGACACTCTTCTTCTCCACCTC 600
DB      541 AACATTCTCAGCAAGAACAGACAGTGTGAGCAGCCTACAGACACTCTTCTTCTCCACCTC 600
QY      601 ACTCTCCCACTGTACCCACCCCTAAATCATTCAGTGCTCTCAAAAGCATGTTTTTCAA 660
DB      601 ACTCTCCCACTGTACCCACCCCTAAATCATTCAGTGCTCTCAAAAGCATGTTTTTCAA 660
QY      661 GATCATTTTGTGTTGCTCTCTAGTGTCTTCTCTCTCTAGTCTTCTAGCTGTAGCTGTC 720
DB      661 GATCATTTTGTGTTGCTCTCTAGTGTCTTCTCTCTCTAGTCTTCTAGCTGTAGCTGTC 720
QY      721 CTCCCTTACCAGGCTTAGGCTTAATTAACCTGAAGATTCAGGAAACTGTAGCTTCTCT 780
DB      721 CTCCCTTACCAGGCTTAGGCTTAATTAACCTGAAGATTCAGGAAACTGTAGCTTCTCT 780
QY      781 AGCTAGTGTCAATTAACCTTAATCAATCAATCAAGAAAGTAGCAAAACAGAAAGTCAATAA 840
DB      781 AGCTAGTGTCAATTAACCTTAATCAATCAATCAAGAAAGTAGCAAAACAGAAAGTCAATAA 840
QY      841 TTTTAAATGTCAAAAAAATTTTCAAAAAAATTTTCAAAAAAATTTTCAAAAAAATTTTCA 870
DB      841 TTTTAAATGTCAAAAAAATTTTCAAAAAAATTTTCAAAAAAATTTTCAAAAAAATTTTCA 870

RESULT 12
US-09-702-705-113
; Sequence 113, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, TongLong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 533
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; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-113

Query Match      60.4%; Score 525.8; DB 3; Length 533;
Best Local Similarity 99.6%; Pred. No. 4.7e-156;
Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 136 CTGCACCGACAGTTGCGATGAAAGTTCTTAATCTCTTCCCTCTCTCTGTTGTCACCTAA 195
DB 1 CTGCACCGACAGTTGCGATGAAAGTTCTTAATCTCTTCCCTCTCTCTGTTGTCACCTAA 60

QY 196 TGTGATGTTCATGTTCTTAGCAGCTTGAATCCAGGGGTGCGCAGAGGCCACAGGGACC 255
DB 61 TGTGATGTTCATGTTCTTAGCAGCTTGAATCCAGGGGTGCGCAGAGGCCACAGGGACC 120

QY 256 GAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGCGGCCAAGAAATGTGAGTGCAAAAGATT 315
DB 121 GAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGCGGCCAAGAAATGTGAGTGCAAAAGATT 180

QY 316 GGTTCCTGAGAGCCCGCAGAGAAAATTCATGACAGTGTCTGGGCTGCAAAAGAGCAGT 375
DB 181 GGTTCCTGAGAGCCCGCAGAGAAAATTCATGACAGTGTCTGGGCTGCAAAAGAGCAGT 240

QY 376 GCCCTGTGATCATTTCAAGGGCAATGTGAAGAAACAAAGACCAAGGCCACACAGAA 435
DB 241 GCCCTGTGATCATTTCAAGGGCAATGTGAAGAAACAAAGACCAAGGCCACACAGAA 300

QY 436 AGCCAAACAAGCATTTCCAGAGCCTCCAGCAATTTCTCAAAACAATGTGAGTAAAGAGCT 495
DB 301 AGCCAAACAAGCATTTCCAGAGCCTCCAGCAATTTCTCAAAACAATGTGAGTAAAGAGCT 360

QY 496 TTGCTCTGCTTTTAGGAGCTCTGAGGCCCACTCTTCCAAATTAATAATTTCTCAGCCAA 555
DB 361 TTGCTCTGCTTTTAGGAGCTCTGAGGCCCACTCTTCCAAATTAATAATTTCTCAGCCAA 420

QY 556 GAAGACAGTGAGCAGACCTTACCAGACACTCTTCTTCCACCTCAGCTCTCCACTGTAC 615
DB 421 GAAGACAGTGAGCAGACCTTACCAGACACTCTTCTTCCACCTCAGCTCTCCACTGTAC 480

QY 616 CCACCCCTAAATCATTTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATC 664
DB 481 CCACCCCTAAATCATTTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATC 529

RESULT 13
US-09-736-457-113
; Sequence 113, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-113
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Query Match      60.4%; Score 525.8; DB 3; Length 533;
Best Local Similarity 99.6%; Pred. No. 4.7e-156;
Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 136 CTGCACCGACAGTTGCGATGAAAGTTCTTAATCTCTTCCCTCTCTCTGTTGTCACCTAA 195
DB 1 CTGCACCGACAGTTGCGATGAAAGTTCTTAATCTCTTCCCTCTCTCTGTTGTCACCTAA 60

QY 196 TGTGATGTTCATGTTCTTAGCAGCTTGAATCCAGGGGTGCGCAGAGGCCACAGGGACC 255
DB 61 TGTGATGTTCATGTTCTTAGCAGCTTGAATCCAGGGGTGCGCAGAGGCCACAGGGACC 120

QY 256 GAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGCGGCCAAGAAATGTGAGTGCAAAAGATT 315
DB 121 GAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGCGGCCAAGAAATGTGAGTGCAAAAGATT 180

QY 316 GGTTCCTGAGAGCCCGCAGAGAAAATTCATGACAGTGTCTGGGCTGCAAAAGAGCAGT 375
DB 181 GGTTCCTGAGAGCCCGCAGAGAAAATTCATGACAGTGTCTGGGCTGCAAAAGAGCAGT 240

QY 376 GCCCTGTGATCATTTCAAGGGCAATGTGAAGAAACAAAGACCAAGGCCACACAGAA 435
DB 241 GCCCTGTGATCATTTCAAGGGCAATGTGAAGAAACAAAGACCAAGGCCACACAGAA 300

QY 436 AGCCAAACAAGCATTTCCAGAGCCTCCAGCAATTTCTCAAAACAATGTGAGTAAAGAGCT 495
DB 301 AGCCAAACAAGCATTTCCAGAGCCTCCAGCAATTTCTCAAAACAATGTGAGTAAAGAGCT 360

QY 496 TTGCTCTGCTTTTAGGAGCTCTGAGGCCCACTCTTCCAAATTAATAATTTCTCAGCCAA 555
DB 361 TTGCTCTGCTTTTAGGAGCTCTGAGGCCCACTCTTCCAAATTAATAATTTCTCAGCCAA 420

QY 556 GAAGACAGTGAGCAGACCTTACCAGACACTCTTCTTCCACCTCAGCTCTCCACTGTAC 615
DB 421 GAAGACAGTGAGCAGACCTTACCAGACACTCTTCTTCCACCTCAGCTCTCCACTGTAC 480

QY 616 CCACCCCTAAATCATTTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATC 664
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RESULT 14
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; Sequence 113, Application US/09614124B
; Patent No. 6830574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-614-124B-113

Query Match      60.4%; Score 525.8; DB 3; Length 533;
Best Local Similarity 99.6%; Pred. No. 4.7e-156;
Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 136 CTGCACCGACAGTTGCGATGAAAGTTCTTAATCTCTTCCCTCTCTCTGTTGTCACCTAA 195
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Db 1 CTGCACCGACAGTTGGATGAAAGTTCTAATCTCTTCCCTCTCTCTGTTGCTGCCACTAA 60  
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Db 61 TGCTGATGTCCATGGTCTCTAGCAGCTCTGAATCAGGGGTGCGCAGAGGCCACAGGGACC 120  
QY 256 GAGGCCAGGCTTCTAGGAGATGCTCCAGGAGGCGGCCAAGAAATGTGAGTGCAGAAAGATT 315  
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QY 316 GGTTCCTGAGAGCCCGGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAGAGCAGT 375  
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QY 376 GGTTCCTGAGAGCCCGGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAGAGCAGT 435  
Db 241 GGTTCCTGAGAGCCCGGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAGAGCAGT 300  
QY 436 AGCCAAACAAAGCAATTCAGAGGCTCCAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCT 495  
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QY 496 TTGCTCTGCTTTGTAGGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCT 555  
Db 361 TTGCTCTGCTTTGTAGGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCT 420  
QY 556 GAAGACAGTGAGCAGACACCTTACCAGACACTCTTCTCTCCACCTCACTCTCCACCTGTAC 615  
Db 421 GAAGACAGTGAGCAGACACCTTACCAGACACTCTTCTCTCCACCTCACTCTCCACCTGTAC 480  
QY 616 CCACCCCTAAATCAATTCAGTGTCTCTCAAAAAGCATGTTTTTCAAGATC 664  
Db 481 CCACCCCTAAATCAATTCAGTGTCTCTCAAAAAGCATGTTTTTCAAGATC 529

RESULT 15  
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; Sequence 113, Application US/09671325  
; Patent No. 6667154  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Lodes, Michael A.  
; APPLICANT: Fanger, Gary  
; APPLICANT: Vedrick, Tom  
; APPLICANT: Carter, Darrick  
; APPLICANT: Retter, Marc  
; APPLICANT: Mannion, Jane  
; APPLICANT: Fan, Liqun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: DIAGNOSIS OF LUNG CANCER  
; CURRENT APPLICATION NUMBER: US/09/671,325  
; CURRENT FILING DATE: 2000-09-26  
; NUMBER OF SEQ ID NOS: 1825  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 113  
; LENGTH: 533  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-671-325-113

Query Match 60.4%; Score 525.8; DB 3; Length 533;  
Best Local Similarity 99.6%; Pred. No. 4.7e-156;  
Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 136 CTGCACCGACAGTTGGATGAAAGTTCTAATCTCTTCCCTCTCTCTGTTGCTGCCACTAA 195  
Db 1 CTGCACCGACAGTTGGATGAAAGTTCTAATCTCTTCCCTCTCTCTGTTGCTGCCACTAA 60  
QY 196 TGCTGATGTCCATGGTCTCTAGCAGCTCTGAATCAGGGGTGCGCAGAGGCCACAGGGACC 255  
Db 61 TGCTGATGTCCATGGTCTCTAGCAGCTCTGAATCAGGGGTGCGCAGAGGCCACAGGGACC 120

QY 256 GAGGCCAGGCTTCTAGGAGATGCTCCAGGAGGCGGCCAAGAAATGTGAGTGCAGAAAGATT 315  
Db 121 GAGGCCAGGCTTCTAGGAGATGCTCCAGGAGGCGGCCAAGAAATGTGAGTGCAGAAAGATT 180  
QY 316 GGTTCCTGAGAGCCCGGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAGAGCAGT 375  
Db 181 GGTTCCTGAGAGCCCGGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAGAGCAGT 240  
QY 376 GGTTCCTGAGAGCCCGGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAGAGCAGT 435  
Db 241 GGTTCCTGAGAGCCCGGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAGAGCAGT 300  
QY 436 AGCCAAACAAAGCAATTCAGAGGCTCCAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCT 495  
Db 301 AGCCAAACAAAGCAATTCAGAGGCTCCAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCT 360  
QY 496 TTGCTCTGCTTTGTAGGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCT 555  
Db 361 TTGCTCTGCTTTGTAGGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCT 420  
QY 556 GAAGACAGTGAGCAGACACCTTACCAGACACTCTTCTCTCCACCTCACTCTCCACCTGTAC 615  
Db 421 GAAGACAGTGAGCAGACACCTTACCAGACACTCTTCTCTCCACCTCACTCTCCACCTGTAC 480  
QY 616 CCACCCCTAAATCAATTCAGTGTCTCTCAAAAAGCATGTTTTTCAAGATC 664  
Db 481 CCACCCCTAAATCAATTCAGTGTCTCTCAAAAAGCATGTTTTTCAAGATC 529

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Published Applications NA New:\*

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#### SUMMARIES

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6	870	100.0	870	8	US-11-266-748A-406176
7	870	100.0	870	8	US-11-266-748A-477222
8	856.6	98.5	1172	6	US-10-525-116-1107
9	832.2	95.7	920	8	US-11-266-748A-185141
10	819.6	94.2	1237	8	US-11-266-748A-174627
11	819.6	94.2	1237	8	US-11-266-748A-127438
12	637.6	73.3	972	6	US-10-553-436-23
13	625.6	71.9	942	6	US-10-553-436-24
14	570	65.5	877	6	US-10-553-436-25
15	525.8	60.4	533	8	US-11-301-554-113
16	476	54.7	583	8	US-11-266-748A-172627
17	329.6	37.9	442	8	US-11-266-748A-232405
18	312	35.9	312	8	US-11-301-554-43
19	43.2	5.0	3132	6	US-10-539-228-709
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C 102	35.6	4.1	1000	8	US-11-266-748A-399350	Sequence 399350,	176	35	4.0	2537	6	US-10-505-928-149	Sequence 149, App
C 103	35.6	4.1	1000	8	US-11-266-748A-400468	Sequence 400468,	177	35	4.0	2654	8	US-11-266-748A-28392	Sequence 28392, A
C 104	35.6	4.1	1000	8	US-11-266-748A-400773	Sequence 400773,	178	35	4.0	3172	8	US-11-266-748A-31781	Sequence 31781, A
C 105	35.6	4.1	1000	8	US-11-266-748A-401156	Sequence 401156,	c 179	35	4.0	31483	8	US-11-266-748A-58439	Sequence 58439, A
C 106	35.6	4.1	1000	8	US-11-266-748A-470396	Sequence 470396,	c 180	35	4.0	523643	6	US-10-540-898-308	Sequence 308, App
C 107	35.6	4.1	1000	8	US-11-266-748A-471514	Sequence 471514,	c 181	34.8	4.0	754	8	US-11-266-748A-214622	Sequence 214622,
C 108	35.6	4.1	1000	8	US-11-266-748A-471819	Sequence 471819,	182	34.8	4.0	754	8	US-11-266-748A-237158	Sequence 237158,
C 109	35.6	4.1	1000	8	US-11-266-748A-471819	Sequence 471819,	183	34.8	4.0	1000	8	US-11-266-748A-115421	Sequence 115421,
C 110	35.6	4.1	7364	6	US-11-266-748A-472202	Sequence 472202,	184	34.8	4.0	1000	8	US-11-266-748A-115494	Sequence 115494,
C 111	35.6	4.1	114854	6	US-10-486-020-33	Sequence 33,	185	34.8	4.0	1000	8	US-11-266-748A-119027	Sequence 119027,
C 112	35.6	4.1	203132	6	US-10-539-228-459	Sequence 850, App	c 186	34.8	4.0	1000	8	US-11-266-748A-157585	Sequence 157585,
C 113	35.4	4.1	249	8	US-11-266-748A-411248	Sequence 459, App	c 187	34.8	4.0	1000	8	US-11-266-748A-157658	Sequence 157658,
C 114	35.4	4.1	856	8	US-11-266-748A-50143	Sequence 50143, A	c 188	34.8	4.0	1000	8	US-11-266-748A-161191	Sequence 161191,
C 115	35.4	4.1	1000	8	US-11-266-748A-284969	Sequence 284969,	189	34.8	4.0	1000	8	US-11-266-748A-206574	Sequence 206574,
C 116	35.4	4.1	1000	8	US-11-266-748A-290799	Sequence 290799,	190	34.8	4.0	1000	8	US-11-266-748A-284640	Sequence 284640,
C 117	35.4	4.1	1000	8	US-11-266-748A-294060	Sequence 294060,	191	34.8	4.0	1000	8	US-11-266-748A-284832	Sequence 284832,
C 118	35.4	4.1	1000	8	US-11-266-748A-336398	Sequence 336398,	192	34.8	4.0	1000	8	US-11-266-748A-284900	Sequence 284900,
C 119	35.4	4.1	1000	8	US-11-266-748A-342228	Sequence 342228,	193	34.8	4.0	1000	8	US-11-266-748A-286693	Sequence 286693,
C 120	35.4	4.1	1000	8	US-11-266-748A-345489	Sequence 345489,	194	34.8	4.0	1000	8	US-11-266-748A-293177	Sequence 293177,
C 121	35.4	4.1	1234	7	US-11-376-673-63	Sequence 63, App	195	34.8	4.0	1000	8	US-11-266-748A-293237	Sequence 293237,
C 122	35.4	4.1	1234	8	US-11-101-316-63	Sequence 63, App	196	34.8	4.0	1000	8	US-11-266-748A-294057	Sequence 294057,
C 123	35.4	4.1	1498	7	US-11-218-305-18404	Sequence 18404, A	c 197	34.8	4.0	1000	8	US-11-266-748A-336069	Sequence 336069,
C 124	35.4	4.1	743	8	US-11-266-748A-34474	Sequence 5474, A	c 198	34.8	4.0	1000	8	US-11-266-748A-336261	Sequence 336261,
C 125	35.2	4.0	746	8	US-11-266-748A-45798	Sequence 45798, A	c 199	34.8	4.0	1000	8	US-11-266-748A-336329	Sequence 336329,
C 126	35.2	4.0	969	8	US-11-217-529-293	Sequence 293, App	c 200	34.8	4.0	1000	8	US-11-266-748A-338322	Sequence 338322,
C 127	35.2	4.0	1000	8	US-11-266-748A-339661	Sequence 339661,	c 201	34.8	4.0	1000	8	US-11-266-748A-344606	Sequence 344606,
C 128	35.2	4.0	1000	8	US-11-266-748A-158896	Sequence 158896,	c 202	34.8	4.0	1000	8	US-11-266-748A-344656	Sequence 344656,
C 129	35.2	4.0	1000	8	US-11-266-748A-288232	Sequence 288232,	c 203	34.8	4.0	1000	8	US-11-266-748A-345486	Sequence 345486,
C 130	35.2	4.0	1000	8	US-11-266-748A-288232	Sequence 288232,	c 204	34.8	4.0	1000	8	US-11-266-748A-393988	Sequence 393988,
C 131	35.2	4.0	1000	8	US-11-266-748A-288232	Sequence 288232,	c 205	34.8	4.0	1000	8	US-11-266-748A-394942	Sequence 394942,
C 132	35.2	4.0	1000	8	US-11-266-748A-339661	Sequence 339661,	c 206	34.8	4.0	1000	8	US-11-266-748A-397460	Sequence 397460,
C 133	35.2	4.0	1000	8	US-11-266-748A-340255	Sequence 340255,	c 207	34.8	4.0	1000	8	US-11-266-748A-397843	Sequence 397843,
C 134	35.2	4.0	1000	8	US-11-266-748A-398471	Sequence 398471,	c 208	34.8	4.0	1000	8	US-11-266-748A-405090	Sequence 405090,
C 135	35.2	4.0	1000	8	US-11-266-748A-399073	Sequence 399073,	c 209	34.8	4.0	1000	8	US-11-266-748A-405183	Sequence 405183,
C 136	35.2	4.0	1000	8	US-11-266-748A-399747	Sequence 399747,	c 210	34.8	4.0	1000	8	US-11-266-748A-406259	Sequence 406259,
C 137	35.2	4.0	1000	8	US-11-266-748A-469517	Sequence 469517,	c 211	34.8	4.0	1000	8	US-11-266-748A-465034	Sequence 465034,
C 138	35.2	4.0	1000	8	US-11-266-748A-470119	Sequence 470119,	c 212	34.8	4.0	1000	8	US-11-266-748A-465988	Sequence 465988,
C 139	35.2	4.0	1000	8	US-11-266-748A-470193	Sequence 470193,	c 213	34.8	4.0	1000	8	US-11-266-748A-468506	Sequence 468506,
C 140	35.2	4.0	1110	7	US-11-218-305-3740	Sequence 3740, Ap	c 214	34.8	4.0	1000	8	US-11-266-748A-468889	Sequence 468889,
C 141	35.2	4.0	1151	8	US-11-216-545-7947	Sequence 7947, Ap	c 215	34.8	4.0	1000	8	US-11-266-748A-476136	Sequence 476136,
C 142	35.2	4.0	1270	8	US-11-216-545-1128	Sequence 1128, Ap	c 216	34.8	4.0	1000	8	US-11-266-748A-476229	Sequence 476229,
C 143	35.2	4.0	1459	7	US-11-218-305-1862	Sequence 1862, Ap	c 217	34.8	4.0	1000	8	US-11-266-748A-477305	Sequence 477305,
C 144	35.2	4.0	1966	8	US-11-216-545-7823	Sequence 7823, Ap	c 218	34.8	4.0	1133	7	US-11-056-355B-62113	Sequence 62113, A
C 145	35.2	4.0	2317	8	US-11-266-748A-27207	Sequence 27207, A	c 219	34.8	4.0	1275	7	US-11-218-305-12535	Sequence 12535, A
C 146	35.2	4.0	2380	8	US-11-266-748A-29972	Sequence 29972, A	c 220	34.8	4.0	1607	8	US-11-216-545-1884	Sequence 1884, Ap
C 147	35.2	4.0	2522	7	US-11-218-305-24510	Sequence 24510, A	c 221	34.8	4.0	1926	7	US-11-218-305-16080	Sequence 16080, A
C 148	35.2	4.0	2630	8	US-11-266-748A-27342	Sequence 27342, A	c 222	34.8	4.0	1998	7	US-11-218-305-17499	Sequence 17499, A
C 149	35.2	4.0	4596	8	US-11-266-748A-30159	Sequence 30159, A	c 223	34.8	4.0	2434	8	US-11-266-748A-23037	Sequence 23037, A
C 150	35.2	4.0	4670	8	US-11-145-307A-39	Sequence 29, App	c 224	34.8	4.0	2435	8	US-11-266-748A-27697	Sequence 27697, A
C 151	35.2	4.0	6001	6	US-10-517-441-771	Sequence 771, App	c 225	34.8	4.0	2501	6	US-10-517-441-286	Sequence 286, App
C 152	35.2	4.0	17897	6	US-10-517-441-344	Sequence 344, App	c 226	34.8	4.0	2501	6	US-10-517-441-560	Sequence 560, App
C 153	35.2	4.0	17897	6	US-10-517-441-618	Sequence 618, App	c 227	34.8	4.0	2614	8	US-11-266-748A-23126	Sequence 23126, A
C 154	35	4.0	719	8	US-11-216-545-855	Sequence 855, App	c 228	34.8	4.0	3976	8	US-11-266-748A-27299	Sequence 27299, A
C 155	35	4.0	869	8	US-11-266-748A-44784	Sequence 44784, A	c 229	34.8	4.0	4437	8	US-11-266-748A-28422	Sequence 28422, A
C 156	35	4.0	1000	8	US-11-266-748A-119068	Sequence 119068,	c 230	34.8	4.0	5261	8	US-11-266-748A-24343	Sequence 24343, A
C 157	35	4.0	1000	8	US-11-266-748A-161232	Sequence 161232,	c 231	34.8	4.0	5297	8	US-11-266-748A-29617	Sequence 29617, A
C 158	35	4.0	1000	8	US-11-266-748A-221950	Sequence 221950,	c 232	34.8	4.0	5493	6	US-10-517-441-417	Sequence 417, App
C 159	35	4.0	1000	8	US-11-266-748A-287551	Sequence 287551,	c 233	34.8	4.0	10865	6	US-10-517-441-464	Sequence 464, App
C 160	35	4.0	1000	8	US-11-266-748A-294371	Sequence 294371,	c 234	34.8	4.0	10865	6	US-10-517-441-738	Sequence 738, App
C 161	35	4.0	1000	8	US-11-266-748A-338980	Sequence 338980,	c 235	34.8	4.0	176928	8	US-11-266-748A-60803	Sequence 60803, A
C 162	35	4.0	1000	8	US-11-266-748A-345800	Sequence 345800,	c 236	34.6	4.0	390	8	US-11-266-748A-101792	Sequence 101792,
C 163	35	4.0	1000	8	US-11-266-748A-398275	Sequence 398275,	c 237	34.6	4.0	390	8	US-11-266-748A-154603	Sequence 154603,
C 164	35	4.0	1000	8	US-11-266-748A-405945	Sequence 405945,	c 238	34.6	4.0	647	7	US-11-218-305-21341	Sequence 21341, A
C 165	35	4.0	1000	8	US-11-266-748A-406404	Sequence 406404,	c 239	34.6	4.0	1000	8	US-11-266-748A-118863	Sequence 118863,
C 166	35	4.0	1000	8	US-11-266-748A-406628	Sequence 406628,	c 240	34.6	4.0	1000	8	US-11-266-748A-161027	Sequence 161027,
C 167	35	4.0	1000	8	US-11-266-748A-469321	Sequence 469321,	c 241	34.6	4.0	1000	8	US-11-266-748A-206499	Sequence 206499,
C 168	35	4.0	1000	8	US-11-266-748A-476891	Sequence 476891,	c 242	34.6	4.0	1000	8	US-11-266-748A-206829	Sequence 206829,
C 169	35	4.0	1000	8	US-11-266-748A-477450	Sequence 477450,	c 243	34.6	4.0	1000	8	US-11-266-748A-209393	Sequence 209393,
C 170	35	4.0	1000	8	US-11-266-748A-477450	Sequence 477450,	c 244	34.6	4.0	1000	8	US-11-266-748A-233969	Sequence 233969,
C 171	35	4.0	1195	6	US-10-374-780A-722	Sequence 722, App	c 245	34.6	4.0	1000	8	US-11-266-748A-285941	Sequence 285941,
C 172	35	4.0	1545	8	US-11-216-545-1120	Sequence 1120, Ap	c 246	34.6	4.0	1000	8	US-11-266-748A-285941	Sequence 285941,



247	34.6	4.0	1000	8	US-11-266-748A-293457	Sequence 293457,	c 320	34.2	3.9	1152	7	US-11-218-305-21291	Sequence 21291, A
C 248	34.6	4.0	1000	8	US-11-266-748A-337370	Sequence 337370,	321	34.2	3.9	1153	8	US-11-216-545-1113	Sequence 1113, Ap
C 249	34.6	4.0	1000	8	US-11-266-748A-344886	Sequence 344886,	322	34.2	3.9	1305	8	US-11-216-545-4873	Sequence 4873, Ap
250	34.6	4.0	1000	8	US-11-266-748A-396292	Sequence 396292,	323	34.2	3.9	1370	8	US-11-266-748A-26242	Sequence 26242, A
251	34.6	4.0	1000	8	US-11-266-748A-405486	Sequence 405486,	324	34.2	3.9	1432	7	US-11-218-305-1986	Sequence 1986, Ap
C 252	34.6	4.0	1000	8	US-11-266-748A-467338	Sequence 467338,	c 325	34.2	3.9	1591	8	US-11-216-545-2432	Sequence 2432, Ap
C 253	34.6	4.0	1020	7	US-11-266-748A-476532	Sequence 476532,	326	34.2	3.9	1723	8	US-11-266-748A-31403	Sequence 31403, A
C 254	34.6	4.0	1020	7	US-11-305-666-132	Sequence 132, App	327	34.2	3.9	2017	7	US-11-366-001-45	Sequence 45, Appl
C 255	34.6	4.0	1020	7	US-11-317-789A-39	Sequence 39, Appl	328	34.2	3.9	2057	8	US-11-266-748A-26180	Sequence 26180, A
C 256	34.6	4.0	1314	8	US-11-216-545-3174	Sequence 3174, Ap	329	34.2	3.9	2084	8	US-11-266-748A-26502	Sequence 26502, A
257	34.6	4.0	1386	7	US-11-218-305-14787	Sequence 14787, A	330	34.2	3.9	2708	8	US-11-266-748A-27992	Sequence 27992, A
258	34.6	4.0	1467	8	US-11-266-748A-24319	Sequence 24319, A	331	34.2	3.9	2781	8	US-11-266-748A-27281	Sequence 27281, A
259	34.6	4.0	1480	8	US-11-216-545-7629	Sequence 7629, Ap	332	34.2	3.9	2781	8	US-11-266-748A-31492	Sequence 31492, A
260	34.6	4.0	1591	8	US-11-266-748A-57969	Sequence 57969, A	333	34.2	3.9	2781	8	US-11-266-748A-51492	Sequence 51492, A
261	34.6	4.0	1651	8	US-11-266-748A-178609	Sequence 178609, A	334	34.2	3.9	2781	8	US-11-266-748A-56756	Sequence 56756, A
262	34.6	4.0	2005	6	US-11-266-748A-25450	Sequence 25450, A	335	34.2	3.9	5993	6	US-10-564-311-2	Sequence 2, Appl
263	34.6	4.0	2205	6	US-10-953-349-9921	Sequence 9921, Ap	336	34.2	3.9	5993	6	US-10-517-441-308	Sequence 308, App
264	34.6	4.0	2205	7	US-11-056-355B-45587	Sequence 45587, A	337	34.2	3.9	8093	6	US-10-517-441-582	Sequence 582, App
265	34.6	4.0	3021	8	US-11-181-115-9	Sequence 9, Appl	338	34	3.9	691	8	US-11-266-748A-217675	Sequence 217675,
C 266	34.6	4.0	3294	8	US-11-266-748A-31414	Sequence 31414, A	C 339	34	3.9	691	8	US-11-266-748A-238689	Sequence 238689,
C 267	34.4	4.0	419	8	US-11-266-748A-302966	Sequence 302966,	340	34	3.9	807	6	US-10-953-349-36144	Sequence 36144, A
268	34.4	4.0	489	8	US-11-266-748A-44601	Sequence 44601, A	341	34	3.9	812	7	US-11-218-305-15354	Sequence 15354, A
269	34.4	4.0	598	8	US-11-266-748A-54876	Sequence 54876, A	342	34	3.9	950	7	US-11-218-305-18511	Sequence 18511, A
270	34.4	4.0	751	8	US-11-266-748A-42650	Sequence 42650, A	343	34	3.9	1000	8	US-11-266-748A-206408	Sequence 206408,
271	34.4	4.0	972	7	US-11-218-305-17390	Sequence 17390, A	C 344	34	3.9	1000	8	US-11-266-748A-210626	Sequence 210626,
C 272	34.4	4.0	1000	8	US-11-266-748A-117956	Sequence 117956,	345	34	3.9	1000	8	US-11-266-748A-223811	Sequence 223811,
C 273	34.4	4.0	1000	8	US-11-266-748A-160120	Sequence 160120,	346	34	3.9	1000	8	US-11-266-748A-287489	Sequence 287489,
274	34.4	4.0	1000	8	US-11-266-748A-224490	Sequence 224490,	347	34	3.9	1000	8	US-11-266-748A-288276	Sequence 288276,
275	34.4	4.0	1000	8	US-11-266-748A-286087	Sequence 286087,	348	34	3.9	1000	8	US-11-266-748A-292535	Sequence 292535,
276	34.4	4.0	1000	8	US-11-266-748A-290633	Sequence 290633,	349	34	3.9	1000	8	US-11-266-748A-338918	Sequence 338918,
277	34.4	4.0	1000	8	US-11-266-748A-290862	Sequence 290862,	350	34	3.9	1000	8	US-11-266-748A-339705	Sequence 339705,
278	34.4	4.0	1000	8	US-11-266-748A-293570	Sequence 293570,	351	34	3.9	1000	8	US-11-266-748A-343964	Sequence 343964,
C 279	34.4	4.0	1000	8	US-11-266-748A-337516	Sequence 337516,	C 352	34	3.9	1000	8	US-11-266-748A-399124	Sequence 399124,
C 280	34.4	4.0	1000	8	US-11-266-748A-342062	Sequence 342062,	353	34	3.9	1000	8	US-11-266-748A-400211	Sequence 400211,
C 281	34.4	4.0	1000	8	US-11-266-748A-342291	Sequence 342291,	354	34	3.9	1000	8	US-11-266-748A-403532	Sequence 403532,
C 282	34.4	4.0	1000	8	US-11-266-748A-344999	Sequence 344999,	355	34	3.9	1000	8	US-11-266-748A-404254	Sequence 404254,
283	34.4	4.0	1000	8	US-11-266-748A-401593	Sequence 401593,	356	34	3.9	1000	8	US-11-266-748A-404282	Sequence 404282,
284	34.4	4.0	1000	8	US-11-266-748A-401953	Sequence 401953,	357	34	3.9	1000	8	US-11-266-748A-470170	Sequence 470170,
285	34.4	4.0	1000	8	US-11-266-748A-402225	Sequence 402225,	C 358	34	3.9	1000	8	US-11-266-748A-471257	Sequence 471257,
286	34.4	4.0	1000	8	US-11-266-748A-402225	Sequence 402225,	C 359	34	3.9	1000	8	US-11-266-748A-474578	Sequence 474578,
C 287	34.4	4.0	1000	8	US-11-266-748A-405640	Sequence 405640,	C 360	34	3.9	1000	8	US-11-266-748A-475300	Sequence 475300,
C 288	34.4	4.0	1000	8	US-11-266-748A-472639	Sequence 472639,	C 361	34	3.9	1000	8	US-11-266-748A-475328	Sequence 475328,
C 289	34.4	4.0	1000	8	US-11-266-748A-472999	Sequence 472999,	362	34	3.9	1051	7	US-11-218-305-17914	Sequence 17914, A
C 290	34.4	4.0	1000	8	US-11-266-748A-473271	Sequence 473271,	363	34	3.9	1149	8	US-11-266-748A-23108	Sequence 23108, A
291	34.4	4.0	1189	7	US-11-218-305-2730	Sequence 2730, Ap	364	34	3.9	1149	8	US-11-266-748A-58461	Sequence 58461, A
292	34.4	4.0	1327	6	US-10-374-780A-732	Sequence 732, App	365	34	3.9	1312	8	US-11-266-748A-25591	Sequence 25591, A
293	34.4	4.0	1448	7	US-11-218-305-1185	Sequence 1185, Ap	366	34	3.9	1581	7	US-11-056-355B-66051	Sequence 66051, A
C 294	34.4	4.0	1591	7	US-11-218-305-24586	Sequence 24586, A	367	34	3.9	1630	7	US-11-218-305-15787	Sequence 15787, A
295	34.4	4.0	1843	6	US-10-511-937-620	Sequence 620, App	368	34	3.9	1700	6	US-10-953-349-21788	Sequence 21788, A
296	34.4	4.0	1989	8	US-11-216-545-5413	Sequence 5413, Ap	369	34	3.9	1700	7	US-11-056-355B-57271	Sequence 57271, A
297	34.4	4.0	2213	8	US-11-216-545-3411	Sequence 3411, Ap	370	34	3.9	2446	8	US-11-266-748A-23513	Sequence 23513, A
298	34.4	4.0	2708	8	US-11-266-748A-27840	Sequence 27840, A	371	34	3.9	2979	8	US-11-266-748A-23702	Sequence 23702, A
299	34.4	4.0	3883	8	US-11-266-748A-27939	Sequence 27939, A	372	34	3.9	3345	8	US-11-266-748A-27340	Sequence 27340, A
300	34.4	4.0	4089	8	US-11-266-748A-27497	Sequence 27497, A	373	34	3.9	3411	8	US-11-266-748A-27312	Sequence 27312, A
301	34.2	3.9	390	8	US-11-266-748A-58049	Sequence 58049, A	C 374	34	3.9	4894	6	US-10-511-937-566	Sequence 566, App
302	34.2	3.9	653	8	US-11-266-748A-410282	Sequence 410282,	375	34	3.9	14147	6	US-10-517-441-265	Sequence 265, App
C 303	34.2	3.9	736	8	US-11-266-748A-212952	Sequence 212952,	C 376	33.8	3.9	693	8	US-11-266-748A-211768	Sequence 211768,
304	34.2	3.9	736	8	US-11-266-748A-236207	Sequence 236207,	377	33.8	3.9	693	8	US-11-266-748A-235371	Sequence 235371,
305	34.2	3.9	893	7	US-11-218-305-1005	Sequence 1005, Ap	378	33.8	3.9	813	8	US-11-216-545-7334	Sequence 7324, Ap
306	34.2	3.9	924	8	US-11-266-748A-45588	Sequence 45588, A	C 379	33.8	3.9	899	7	US-11-218-305-10455	Sequence 10455, A
307	34.2	3.9	931	8	US-11-266-748A-40946	Sequence 40946, A	380	33.8	3.9	1000	8	US-11-266-748A-115665	Sequence 115665,
308	34.2	3.9	1000	8	US-11-266-748A-118848	Sequence 118848,	381	33.8	3.9	1000	8	US-11-266-748A-116660	Sequence 116660,
C 309	34.2	3.9	1000	8	US-11-266-748A-161012	Sequence 161012,	C 382	33.8	3.9	1000	8	US-11-266-748A-157829	Sequence 157829,
310	34.2	3.9	1000	8	US-11-266-748A-206477	Sequence 206477,	C 383	33.8	3.9	1000	8	US-11-266-748A-158824	Sequence 158824,
311	34.2	3.9	1000	8	US-11-266-748A-209665	Sequence 209665,	384	33.8	3.9	1000	8	US-11-266-748A-224245	Sequence 224245,
312	34.2	3.9	1000	8	US-11-266-748A-287498	Sequence 287498,	385	33.8	3.9	1000	8	US-11-266-748A-224579	Sequence 224579,
313	34.2	3.9	1000	8	US-11-266-748A-288969	Sequence 288969,	386	33.8	3.9	1000	8	US-11-266-748A-287437	Sequence 287437,
314	34.2	3.9	1000	8	US-11-266-748A-293408	Sequence 293408,	387	33.8	3.9	1000	8	US-11-266-748A-291640	Sequence 291640,
C 315	34.2	3.9	1000	8	US-11-266-748A-338927	Sequence 338927,	388	33.8	3.9	1000	8	US-11-266-748A-292902	Sequence 292902,
C 316	34.2	3.9	1000	8	US-11-266-748A-340398	Sequence 340398,	C 389	33.8	3.9	1000	8	US-11-266-748A-338856	Sequence 338856,
C 317	34.2	3.9	1000	8	US-11-266-748A-340337	Sequence 340337,	C 390	33.8	3.9	1000	8	US-11-266-748A-343069	Sequence 343069,
318	34.2	3.9	1000	8	US-11-266-748A-398211	Sequence 398211,	C 391	33.8	3.9	1000	8	US-11-266-748A-344331	Sequence 344331,
C 319	34.2	3.9	1000	8	US-11-266-748A-469257	Sequence 469257,	392	33.8	3.9	1000	8	US-11-266-748A-395395	Sequence 395395,

393	33.8	3.9	1000	8	US-11-266-748A-398108	Sequence 398108,	C 467	33.6	3.9	1121	7	US-11-218-305-22972	Sequence 22972, A
394	33.8	3.9	1000	8	US-11-266-748A-398448	Sequence 398448,	468	33.6	3.9	1124	7	US-11-218-305-19059	Sequence 19059, A
395	33.8	3.9	1000	8	US-11-266-748A-403132	Sequence 403132,	469	33.6	3.9	1334	7	US-11-218-305-7219	Sequence 7319, Ap
396	33.8	3.9	1000	8	US-11-266-748A-404754	Sequence 404754,	470	33.6	3.9	1351	8	US-11-266-748A-56863	Sequence 56863, A
397	33.8	3.9	1000	8	US-11-266-748A-405042	Sequence 405042,	471	33.6	3.9	1368	8	US-11-266-748A-32768	Sequence 32768, A
398	33.8	3.9	1000	8	US-11-266-748A-405073	Sequence 405073,	C 472	33.6	3.9	1415	7	US-11-218-305-21764	Sequence 21764, A
399	33.8	3.9	1000	8	US-11-266-748A-466441	Sequence 466441,	C 473	33.6	3.9	1630	6	US-10-517-441-552	Sequence 552, App
400	33.8	3.9	1000	8	US-11-266-748A-469154	Sequence 469154,	C 474	33.6	3.9	1678	8	US-11-216-545-1613	Sequence 1613, Ap
401	33.8	3.9	1000	8	US-11-266-748A-469494	Sequence 469494,	C 475	33.6	3.9	1753	8	US-11-216-545-1680	Sequence 1680, Ap
402	33.8	3.9	1000	8	US-11-266-748A-474178	Sequence 474178,	476	33.6	3.9	1783	8	US-11-216-545-5349	Sequence 5349, Ap
403	33.8	3.9	1000	8	US-11-266-748A-475800	Sequence 475800,	477	33.6	3.9	2036	7	US-11-218-305-3322	Sequence 3322, Ap
404	33.8	3.9	1000	8	US-11-266-748A-475808	Sequence 475808,	478	33.6	3.9	2286	7	US-11-266-748A-30211	Sequence 30211, A
405	33.8	3.9	1000	8	US-11-266-748A-477019	Sequence 477019,	C 479	33.6	3.9	2303	7	US-11-218-305-15401	Sequence 15401, A
406	33.8	3.9	1023	6	US-10-374-780A-1317	Sequence 1317, Ap	480	33.6	3.9	2315	7	US-11-218-305-15574	Sequence 15574, A
407	33.8	3.9	1316	6	US-10-953-349-14397	Sequence 14397, A	481	33.6	3.9	2419	8	US-11-266-748A-27485	Sequence 27485, A
408	33.8	3.9	1316	6	US-11-216-545-7178	Sequence 7178, Ap	482	33.6	3.9	2566	8	US-11-216-545-5967	Sequence 5967, Ap
409	33.8	3.9	1428	7	US-11-218-305-10458	Sequence 10458, A	483	33.6	3.9	2627	8	US-11-266-748A-26574	Sequence 26574, Ap
410	33.8	3.9	1621	8	US-11-266-748A-26773	Sequence 26773, A	C 484	33.6	3.9	2679	8	US-11-216-545-1918	Sequence 1918, Ap
411	33.8	3.9	1685	8	US-11-266-748A-57523	Sequence 57523, A	485	33.6	3.9	2714	8	US-11-266-748A-23931	Sequence 23931, Ap
412	33.8	3.9	1777	7	US-11-218-305-10457	Sequence 10457, A	486	33.6	3.9	3575	8	US-11-266-748A-24461	Sequence 24461, A
413	33.8	3.9	1857	8	US-11-216-545-8563	Sequence 8563, Ap	487	33.6	3.9	3930	8	US-11-266-748A-26576	Sequence 26576, A
414	33.8	3.9	1874	7	US-11-218-305-20059	Sequence 20059, A	488	33.6	3.9	4496	7	US-11-317-330A-16	Sequence 16, Appl
415	33.8	3.9	2117	7	US-11-218-305-18284	Sequence 18284, A	489	33.6	3.9	4731	8	US-11-266-748A-27174	Sequence 27174, A
416	33.8	3.9	2181	8	US-11-216-545-4687	Sequence 4687, Ap	490	33.6	3.9	5895	7	US-11-218-305-8517	Sequence 8517, Ap
417	33.8	3.9	2261	6	US-10-511-937-415	Sequence 415, Appl	491	33.6	3.9	9747	8	US-11-266-748A-28362	Sequence 28362, A
418	33.8	3.9	2261	7	US-11-346-759-99	Sequence 99, Appl	492	33.6	3.9	15964	8	US-11-266-748A-22815	Sequence 22815, A
419	33.8	3.9	2270	8	US-11-266-748A-26193	Sequence 26193, A	C 493	33.6	3.9	15983	6	US-10-540-898-1688	Sequence 868, App
420	33.8	3.9	2379	8	US-11-266-748A-25071	Sequence 25071, A	494	33.4	3.8	617	7	US-11-218-305-12814	Sequence 12814, A
421	33.8	3.9	2414	6	US-10-374-780A-1604	Sequence 1604, Ap	C 495	33.4	3.8	627	8	US-11-266-748A-212396	Sequence 212396, A
422	33.8	3.9	4081	8	US-11-266-748A-23051	Sequence 23051, A	496	33.4	3.8	627	8	US-11-266-748A-235835	Sequence 235835, A
423	33.8	3.9	7132	8	US-11-266-748A-28498	Sequence 28498, A	C 497	33.4	3.8	697	8	US-11-266-748A-44345	Sequence 44345, A
424	33.8	3.9	138754	8	US-11-266-748A-23615	Sequence 23615, A	C 498	33.4	3.8	714	8	US-11-266-748A-17742	Sequence 17742, A
425	33.8	3.9	286	6	US-10-488-619-2977	Sequence 2977, Ap	499	33.4	3.8	958	8	US-11-266-748A-118706	Sequence 118706, A
426	33.6	3.9	626	8	US-11-266-748A-211275	Sequence 211275,	C 500	33.4	3.8	958	8	US-11-266-748A-160870	Sequence 160870, A
427	33.6	3.9	626	8	US-11-266-748A-234983	Sequence 234983,	501	33.4	3.8	958	8	US-11-266-748A-404762	Sequence 404762, A
428	33.6	3.9	705	8	US-11-266-748A-58294	Sequence 58294, A	C 502	33.4	3.8	958	8	US-11-266-748A-475808	Sequence 475808, A
429	33.6	3.9	932	8	US-11-266-748A-27640	Sequence 27640, A	503	33.4	3.8	960	8	US-11-266-748A-284744	Sequence 284744, A
430	33.6	3.9	1000	8	US-11-266-748A-118509	Sequence 118509,	C 504	33.4	3.8	960	8	US-11-266-748A-336173	Sequence 336173, A
431	33.6	3.9	1000	8	US-11-266-748A-160673	Sequence 160673,	505	33.4	3.8	1000	8	US-11-266-748A-222773	Sequence 222773, A
432	33.6	3.9	1000	8	US-11-266-748A-221596	Sequence 221596,	506	33.4	3.8	1000	8	US-11-266-748A-224499	Sequence 224499, A
433	33.6	3.9	1000	8	US-11-266-748A-223510	Sequence 223510,	507	33.4	3.8	1000	8	US-11-266-748A-289874	Sequence 289874, A
434	33.6	3.9	1000	8	US-11-266-748A-286954	Sequence 286954,	508	33.4	3.8	1000	8	US-11-266-748A-290880	Sequence 290880, A
435	33.6	3.9	1000	8	US-11-266-748A-289020	Sequence 289020,	509	33.4	3.8	1000	8	US-11-266-748A-291206	Sequence 291206, A
436	33.6	3.9	1000	8	US-11-266-748A-289939	Sequence 289939,	510	33.4	3.8	1000	8	US-11-266-748A-292531	Sequence 292531, A
437	33.6	3.9	1000	8	US-11-266-748A-291166	Sequence 291166,	511	33.4	3.8	1000	8	US-11-266-748A-293595	Sequence 293595, A
438	33.6	3.9	1000	8	US-11-266-748A-291187	Sequence 291187,	C 512	33.4	3.8	1000	8	US-11-266-748A-341303	Sequence 341303, A
439	33.6	3.9	1000	8	US-11-266-748A-292342	Sequence 292342,	C 513	33.4	3.8	1000	8	US-11-266-748A-342309	Sequence 342309, A
440	33.6	3.9	1000	8	US-11-266-748A-292918	Sequence 292918,	514	33.4	3.8	1000	8	US-11-266-748A-342635	Sequence 342635, A
441	33.6	3.9	1000	8	US-11-266-748A-292918	Sequence 292918,	C 515	33.4	3.8	1000	8	US-11-266-748A-343960	Sequence 343960, A
442	33.6	3.9	1000	8	US-11-266-748A-293194	Sequence 293194,	C 516	33.4	3.8	1000	8	US-11-266-748A-345024	Sequence 345024, A
443	33.6	3.9	1000	8	US-11-266-748A-338383	Sequence 338383,	517	33.4	3.8	1000	8	US-11-266-748A-394052	Sequence 394052, A
444	33.6	3.9	1000	8	US-11-266-748A-344347	Sequence 344347,	518	33.4	3.8	1000	8	US-11-266-748A-402244	Sequence 402244, A
445	33.6	3.9	1000	8	US-11-266-748A-344623	Sequence 344623,	C 519	33.4	3.8	1000	8	US-11-266-748A-402604	Sequence 402604, A
446	33.6	3.9	1000	8	US-11-266-748A-394282	Sequence 394282,	520	33.4	3.8	1000	8	US-11-266-748A-403917	Sequence 403917, A
447	33.6	3.9	1000	8	US-11-266-748A-342595	Sequence 342595,	521	33.4	3.8	1000	8	US-11-266-748A-404276	Sequence 404276, A
448	33.6	3.9	1000	8	US-11-266-748A-342616	Sequence 342616,	522	33.4	3.8	1000	8	US-11-266-748A-405674	Sequence 405674, A
449	33.6	3.9	1000	8	US-11-266-748A-343771	Sequence 343771,	523	33.4	3.8	1000	8	US-11-266-748A-405674	Sequence 405674, A
450	33.6	3.9	1000	8	US-11-266-748A-344347	Sequence 344347,	C 524	33.4	3.8	1000	8	US-11-266-748A-465098	Sequence 465098, A
451	33.6	3.9	1000	8	US-11-266-748A-344623	Sequence 344623,	C 525	33.4	3.8	1000	8	US-11-266-748A-473290	Sequence 473290, A
452	33.6	3.9	1000	8	US-11-266-748A-399964	Sequence 399964,	526	33.4	3.8	1000	8	US-11-266-748A-473650	Sequence 473650, A
453	33.6	3.9	1000	8	US-11-266-748A-402555	Sequence 402555,	C 527	33.4	3.8	1000	8	US-11-266-748A-474963	Sequence 474963, A
454	33.6	3.9	1000	8	US-11-266-748A-403897	Sequence 403897,	528	33.4	3.8	1000	8	US-11-266-748A-475322	Sequence 475322, A
455	33.6	3.9	1000	8	US-11-266-748A-404781	Sequence 404781,	C 529	33.4	3.8	1000	8	US-11-266-748A-476720	Sequence 476720, A
456	33.6	3.9	1000	8	US-11-266-748A-405112	Sequence 405112,	530	33.4	3.8	1047	7	US-11-218-305-7255	Sequence 7255, Ap
457	33.6	3.9	1000	8	US-11-266-748A-405655	Sequence 405655,	C 531	33.4	3.8	1106	7	US-11-218-305-20472	Sequence 20472, A
458	33.6	3.9	1000	8	US-11-266-748A-405629	Sequence 405629,	532	33.4	3.8	1178	8	US-11-216-545-991	Sequence 991, App
459	33.6	3.9	1000	8	US-11-266-748A-465328	Sequence 465328,	C 533	33.4	3.8	1214	8	US-11-266-748A-31148	Sequence 31148, A
460	33.6	3.9	1000	8	US-11-266-748A-471010	Sequence 471010,	534	33.4	3.8	1234	7	US-11-218-305-23945	Sequence 23945, A
461	33.6	3.9	1000	8	US-11-266-748A-473601	Sequence 473601,	C 535	33.4	3.8	1629	8	US-11-266-748A-28193	Sequence 28193, A
462	33.6	3.9	1000	8	US-11-266-748A-474943	Sequence 474943,	536	33.4	3.8	1661	8	US-11-266-748A-26508	Sequence 26508, A
463	33.6	3.9	1000	8	US-11-266-748A-475827	Sequence 475827,	537	33.4	3.8	1750	8	US-11-266-748A-31545	Sequence 31545, A
464	33.6	3.9	1000	8	US-11-266-748A-476158	Sequence 476158,	538	33.4	3.8	1885	8	US-11-266-748A-28499	Sequence 28499, A
465	33.6	3.9	1000	8	US-11-266-748A-476701	Sequence 476701,	C 539	33.4	3.8	1958	7	US-11-218-305-16733	Sequence 16733, A
466	33.6	3.9	1000	8	US-11-266-748A-477575	Sequence 477575,	539	33.4	3.8	2059	8	US-11-266-748A-57711	Sequence 57711, A

540	33.4	3.8	2408	8	US-11-266-748A-26410	Sequence 26410, A	613	33.2	3.8	1344	7	US-11-218-305-3321	Sequence 3321, Ap
541	33.4	3.8	2735	8	US-11-266-748A-27563	Sequence 27563, A	614	33.2	3.8	1350	8	US-11-266-748A-158384	Sequence 58384, A
542	33.4	3.8	2909	3	US-11-216-545-5685	Sequence 5685, Ap	615	33.2	3.8	1370	7	US-11-218-305-15856	Sequence 15856, A
543	33.4	3.8	3098	6	US-10-539-228-716	Sequence 716, App	616	33.2	3.8	1596	8	US-11-266-748A-20200	Sequence 20200, A
544	33.4	3.8	3551	8	US-11-266-748A-24371	Sequence 24371, A	617	33.2	3.8	1646	8	US-11-266-748A-27752	Sequence 27752, A
545	33.4	3.8	3593	7	US-11-340-429-10	Sequence 10, Appl	618	33.2	3.8	1758	8	US-11-266-748A-57522	Sequence 57522, A
546	33.4	3.8	4023	8	US-11-266-748A-30712	Sequence 30712, A	619	33.2	3.8	1828	8	US-11-216-545-8656	Sequence 8656, Ap
547	33.4	3.8	4023	8	US-11-266-748A-57006	Sequence 57006, A	620	33.2	3.8	1843	8	US-11-266-748A-24276	Sequence 24276, A
548	33.4	3.8	4384	8	US-11-266-748A-28246	Sequence 28246, A	621	33.2	3.8	1850	7	US-11-056-355B-53395	Sequence 53395, A
549	33.4	3.8	4930	6	US-10-517-441-627	Sequence 627, App	622	33.2	3.8	1983	7	US-11-218-305-23832	Sequence 23832, A
550	33.4	3.8	6001	6	US-10-517-441-786	Sequence 786, App	623	33.2	3.8	2110	8	US-11-216-545-2569	Sequence 2569, Ap
551	33.4	3.8	7833	6	US-10-517-441-623	Sequence 623, App	624	33.2	3.8	2939	8	US-11-216-545-4350	Sequence 4350, Ap
552	33.4	3.8	47322	6	US-10-539-228-507	Sequence 507, App	625	33.2	3.8	2955	8	US-11-266-748A-28001	Sequence 28001, A
553	33.4	3.8	48643	6	US-10-539-228-715	Sequence 715, App	626	33.2	3.8	3315	8	US-11-266-748A-27139	Sequence 27139, A
554	33.4	3.8	70019	8	US-10-539-228-823	Sequence 823, App	627	33.2	3.8	3844	8	US-11-266-748A-27661	Sequence 27661, A
555	33.4	3.8	113539	8	US-11-266-748A-60002	Sequence 60002, A	628	33.2	3.8	4365	8	US-11-266-748A-28358	Sequence 28358, A
556	33.2	3.8	342	8	US-11-266-748A-61402	Sequence 61402, A	629	33.2	3.8	4382	8	US-11-266-748A-27432	Sequence 27432, A
557	33.2	3.8	574	7	US-11-056-355B-62259	Sequence 62259, A	630	33.2	3.8	5133	8	US-11-266-748A-29007	Sequence 29007, A
558	33.2	3.8	808	8	US-11-266-748A-46111	Sequence 46111, A	631	33.2	3.8	75217	6	US-10-517-441-526	Sequence 526, App
559	33.2	3.8	1000	8	US-11-266-748A-115981	Sequence 115981, A	632	33.2	3.8	75217	8	US-11-266-748A-29045	Sequence 29045, A
560	33.2	3.8	1000	8	US-11-266-748A-117802	Sequence 117802, A	633	33	3.8	434	8	US-11-266-748A-36150	Sequence 96150, A
561	33.2	3.8	1000	8	US-11-266-748A-158145	Sequence 158145, A	634	33	3.8	434	8	US-11-266-748A-148961	Sequence 148961, A
562	33.2	3.8	1000	8	US-11-266-748A-159966	Sequence 159966, A	635	33	3.8	502	8	US-11-266-748A-57937	Sequence 57937, A
563	33.2	3.8	1000	8	US-11-266-748A-206836	Sequence 206836, A	636	33	3.8	588	8	US-11-266-748A-50474	Sequence 50474, A
564	33.2	3.8	1000	8	US-11-266-748A-223110	Sequence 223110, A	637	33	3.8	651	8	US-11-266-748A-50145	Sequence 50145, A
565	33.2	3.8	1000	8	US-11-266-748A-223198	Sequence 223198, A	638	33	3.8	687	8	US-11-266-748A-213934	Sequence 213934, A
566	33.2	3.8	1000	8	US-11-266-748A-224355	Sequence 224355, A	639	33	3.8	687	8	US-11-266-748A-236725	Sequence 236725, A
567	33.2	3.8	1000	8	US-11-266-748A-284621	Sequence 284621, A	640	33	3.8	688	8	US-11-266-748A-57859	Sequence 57859, A
568	33.2	3.8	1000	8	US-11-266-748A-285872	Sequence 285872, A	641	33	3.8	688	8	US-11-266-748A-21144	Sequence 21144, A
569	33.2	3.8	1000	8	US-11-266-748A-286670	Sequence 286670, A	642	33	3.8	688	8	US-11-266-748A-234874	Sequence 234874, A
570	33.2	3.8	1000	8	US-11-266-748A-288892	Sequence 288892, A	643	33	3.8	692	8	US-11-266-748A-207686	Sequence 207686, A
571	33.2	3.8	1000	8	US-11-266-748A-289534	Sequence 289534, A	644	33	3.8	898	8	US-11-216-545-56	Sequence 56, Appl
572	33.2	3.8	1000	8	US-11-266-748A-289689	Sequence 289689, A	645	33	3.8	898	8	US-11-266-748A-116386	Sequence 116386, A
573	33.2	3.8	1000	8	US-11-266-748A-290205	Sequence 290205, A	645	33	3.8	1000	8	US-11-266-748A-158550	Sequence 158550, A
574	33.2	3.8	1000	8	US-11-266-748A-292998	Sequence 292998, A	646	33	3.8	1000	8	US-11-266-748A-158550	Sequence 158550, A
575	33.2	3.8	1000	8	US-11-266-748A-293191	Sequence 293191, A	647	33	3.8	1000	8	US-11-266-748A-220618	Sequence 220618, A
576	33.2	3.8	1000	8	US-11-266-748A-293222	Sequence 293222, A	648	33	3.8	1000	8	US-11-266-748A-222188	Sequence 222188, A
577	33.2	3.8	1000	8	US-11-266-748A-336050	Sequence 336050, A	649	33	3.8	1000	8	US-11-266-748A-222655	Sequence 222655, A
578	33.2	3.8	1000	8	US-11-266-748A-337301	Sequence 337301, A	650	33	3.8	1000	8	US-11-266-748A-285076	Sequence 285076, A
579	33.2	3.8	1000	8	US-11-266-748A-338099	Sequence 338099, A	651	33	3.8	1000	8	US-11-266-748A-285121	Sequence 285121, A
580	33.2	3.8	1000	8	US-11-266-748A-340321	Sequence 340321, A	652	33	3.8	1000	8	US-11-266-748A-289196	Sequence 289196, A
581	33.2	3.8	1000	8	US-11-266-748A-340963	Sequence 340963, A	653	33	3.8	1000	8	US-11-266-748A-289639	Sequence 289639, A
582	33.2	3.8	1000	8	US-11-266-748A-341118	Sequence 341118, A	654	33	3.8	1000	8	US-11-266-748A-293355	Sequence 293355, A
583	33.2	3.8	1000	8	US-11-266-748A-341634	Sequence 341634, A	655	33	3.8	1000	8	US-11-266-748A-336505	Sequence 336505, A
584	33.2	3.8	1000	8	US-11-266-748A-344427	Sequence 344427, A	656	33	3.8	1000	8	US-11-266-748A-336550	Sequence 336550, A
585	33.2	3.8	1000	8	US-11-266-748A-344620	Sequence 344620, A	657	33	3.8	1000	8	US-11-266-748A-340625	Sequence 340625, A
586	33.2	3.8	1000	8	US-11-266-748A-344651	Sequence 344651, A	658	33	3.8	1000	8	US-11-266-748A-341068	Sequence 341068, A
587	33.2	3.8	1000	8	US-11-266-748A-393007	Sequence 393007, A	659	33	3.8	1000	8	US-11-266-748A-344784	Sequence 344784, A
588	33.2	3.8	1000	8	US-11-266-748A-397198	Sequence 397198, A	660	33	3.8	1000	8	US-11-266-748A-393751	Sequence 393751, A
589	33.2	3.8	1000	8	US-11-266-748A-400583	Sequence 400583, A	661	33	3.8	1000	8	US-11-266-748A-395310	Sequence 395310, A
590	33.2	3.8	1000	8	US-11-266-748A-400752	Sequence 400752, A	662	33	3.8	1000	8	US-11-266-748A-397358	Sequence 397358, A
591	33.2	3.8	1000	8	US-11-266-748A-401393	Sequence 401393, A	663	33	3.8	1000	8	US-11-266-748A-397994	Sequence 397994, A
592	33.2	3.8	1000	8	US-11-266-748A-401882	Sequence 401882, A	664	33	3.8	1000	8	US-11-266-748A-398971	Sequence 398971, A
593	33.2	3.8	1000	8	US-11-266-748A-405110	Sequence 405110, A	665	33	3.8	1000	8	US-11-266-748A-400181	Sequence 400181, A
594	33.2	3.8	1000	8	US-11-266-748A-405159	Sequence 405159, A	666	33	3.8	1000	8	US-11-266-748A-400533	Sequence 400533, A
595	33.2	3.8	1000	8	US-11-266-748A-406650	Sequence 406650, A	667	33	3.8	1000	8	US-11-266-748A-400695	Sequence 400695, A
596	33.2	3.8	1000	8	US-11-266-748A-406650	Sequence 406650, A	668	33	3.8	1000	8	US-11-266-748A-402856	Sequence 402856, A
597	33.2	3.8	1000	8	US-11-266-748A-468244	Sequence 468244, A	669	33	3.8	1000	8	US-11-266-748A-404496	Sequence 404496, A
598	33.2	3.8	1000	8	US-11-266-748A-471629	Sequence 471629, A	670	33	3.8	1000	8	US-11-266-748A-404497	Sequence 404497, A
599	33.2	3.8	1000	8	US-11-266-748A-471798	Sequence 471798, A	671	33	3.8	1000	8	US-11-266-748A-464797	Sequence 464797, A
600	33.2	3.8	1000	8	US-11-266-748A-472439	Sequence 472439, A	672	33	3.8	1000	8	US-11-266-748A-466356	Sequence 466356, A
601	33.2	3.8	1000	8	US-11-266-748A-475928	Sequence 475928, A	673	33	3.8	1000	8	US-11-266-748A-468404	Sequence 468404, A
602	33.2	3.8	1000	8	US-11-266-748A-476156	Sequence 476156, A	674	33	3.8	1000	8	US-11-266-748A-469040	Sequence 469040, A
603	33.2	3.8	1000	8	US-11-266-748A-476205	Sequence 476205, A	675	33	3.8	1000	8	US-11-266-748A-470017	Sequence 470017, A
604	33.2	3.8	1000	8	US-11-266-748A-477696	Sequence 477696, A	676	33	3.8	1000	8	US-11-266-748A-471227	Sequence 471227, A
605	33.2	3.8	1018	8	US-11-266-748A-483725	Sequence 483725, A	677	33	3.8	1000	8	US-11-266-748A-471579	Sequence 471579, A
606	33.2	3.8	1038	7	US-11-218-305-17388	Sequence 17388, A	678	33	3.8	1000	8	US-11-266-748A-471741	Sequence 471741, A
607	33.2	3.8	1155	8	US-11-266-748A-259577	Sequence 259577, A	679	33	3.8	1000	8	US-11-266-748A-473902	Sequence 473902, A
608	33.2	3.8	1155	8	US-11-266-748A-320094	Sequence 320094, A	680	33	3.8	1000	8	US-11-266-748A-475542	Sequence 475542, A
609	33.2	3.8	1226	8	US-11-266-748A-193829	Sequence 193829, A	681	33	3.8	1000	8	US-11-266-748A-475543	Sequence 475543, A
610	33.2	3.8	1226	8	US-11-266-748A-227351	Sequence 227351, A	682	33	3.8	1174	8	US-11-266-748A-25800, A	Sequence 25800, A
611	33.2	3.8	1229	8	US-11-266-748A-172863	Sequence 172863, A	683	33	3.8	1190	7	US-11-218-305-15133	Sequence 15133, A
612	33.2	3.8	1318	7	US-11-218-305-12279	Sequence 12279, A	684	33	3.8	1283	7	US-11-218-305-18128	Sequence 18128, A
						Sequence 12279, A	685	33	3.8	1352	8	US-11-216-545-23	Sequence 23, Appl

686	33	3.8	1459	6	US-10-953-349-27966	Sequence 27966, A	c 759	32.8	3.8	1000	8	US-11-266-748A-159905	Sequence 159905,
687	33	3.8	1459	7	US-11-056-355B-64482	Sequence 64482, A	c 760	32.8	3.8	1000	8	US-11-266-748A-160717	Sequence 160717,
688	33	3.8	1517	8	US-11-216-545-1233	Sequence 1233, Ap	761	32.8	3.8	1000	8	US-11-266-748A-205673	Sequence 205673,
689	33	3.8	1589	8	US-11-266-748A-25642	Sequence 25642, A	762	32.8	3.8	1000	8	US-11-266-748A-221139	Sequence 221139,
690	33	3.8	1641	8	US-11-266-748A-57204	Sequence 57204, A	763	32.8	3.8	1000	8	US-11-266-748A-221753	Sequence 221753,
691	33	3.8	1645	8	US-11-266-748A-57204	Sequence 57204, A	764	32.8	3.8	1000	8	US-11-266-748A-223853	Sequence 223853,
692	33	3.8	1685	6	US-10-533-868-25	Sequence 25, Appl	765	32.8	3.8	1000	8	US-11-266-748A-287052	Sequence 287052,
693	33	3.8	1751	8	US-11-216-545-212	Sequence 212, App	766	32.8	3.8	1000	8	US-11-266-748A-289331	Sequence 289331,
694	33	3.8	1825	8	US-11-216-545-8590	Sequence 8590, Ap	767	32.8	3.8	1000	8	US-11-266-748A-289425	Sequence 289425,
695	33	3.8	1842	7	US-11-218-305-9077	Sequence 9077, Ap	768	32.8	3.8	1000	8	US-11-266-748A-290020	Sequence 290020,
696	33	3.8	1858	7	US-11-218-305-234	Sequence 234, App	769	32.8	3.8	1000	8	US-11-266-748A-290653	Sequence 290653,
697	33	3.8	1922	7	US-11-218-305-5933	Sequence 5933, Ap	770	32.8	3.8	1000	8	US-11-266-748A-292069	Sequence 292069,
698	33	3.8	2005	8	US-11-266-748A-27282	Sequence 27282, A	771	32.8	3.8	1000	8	US-11-266-748A-292374	Sequence 292374,
699	33	3.8	2037	8	US-11-266-748A-26997	Sequence 26997, A	772	32.8	3.8	1000	8	US-11-266-748A-293044	Sequence 293044,
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701	33	3.8	2133	8	US-11-266-748A-29684	Sequence 29684, A	c 774	32.8	3.8	1000	8	US-11-266-748A-340760	Sequence 340760,
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703	33	3.8	2494	8	US-11-266-748A-23443	Sequence 23443, A	c 776	32.8	3.8	1000	8	US-11-266-748A-341449	Sequence 341449,
704	33	3.8	2510	8	US-11-266-748A-27211	Sequence 27211, A	c 777	32.8	3.8	1000	8	US-11-266-748A-342082	Sequence 342082,
c 705	33	3.8	2608	7	US-11-218-305-22500	Sequence 22500, A	c 778	32.8	3.8	1000	8	US-11-266-748A-343498	Sequence 343498,
706	33	3.8	2618	8	US-11-266-748A-29724	Sequence 29724, A	c 779	32.8	3.8	1000	8	US-11-266-748A-343803	Sequence 343803,
707	33	3.8	2668	8	US-11-266-748A-27838	Sequence 27838, A	c 780	32.8	3.8	1000	8	US-11-266-748A-344473	Sequence 344473,
708	33	3.8	2942	7	US-11-218-305-16147	Sequence 16147, A	781	32.8	3.8	1000	8	US-11-266-748A-395719	Sequence 395719,
709	33	3.8	3298	8	US-11-266-748A-26098	Sequence 26098, A	782	32.8	3.8	1000	8	US-11-266-748A-396553	Sequence 396553,
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712	33	3.8	3883	8	US-11-266-748A-28593	Sequence 28593, A	785	32.8	3.8	1000	8	US-11-266-748A-401175	Sequence 401175,
c 713	33	3.8	5027	7	US-11-218-305-24326	Sequence 24326, A	786	32.8	3.8	1000	8	US-11-266-748A-401976	Sequence 401976,
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715	33	3.8	5976	6	US-10-517-441-554	Sequence 554, App	788	32.8	3.8	1000	8	US-11-266-748A-404057	Sequence 404057,
716	33	3.8	6181	8	US-11-266-748A-24504	Sequence 24504, A	789	32.8	3.8	1000	8	US-11-266-748A-404760	Sequence 404760,
c 717	33	3.8	7001	6	US-10-517-441-513	Sequence 513, App	790	32.8	3.8	1000	8	US-11-266-748A-404931	Sequence 404931,
c 718	33	3.8	7001	6	US-10-517-441-787	Sequence 787, App	c 791	32.8	3.8	1000	8	US-11-266-748A-466765	Sequence 466765,
c 719	33	3.8	8900	6	US-10-517-441-428	Sequence 428, App	c 792	32.8	3.8	1000	8	US-11-266-748A-467599	Sequence 467599,
c 720	33	3.8	11429	6	US-10-517-441-479	Sequence 479, App	c 793	32.8	3.8	1000	8	US-11-266-748A-468691	Sequence 468691,
c 721	33	3.8	11429	6	US-10-517-441-753	Sequence 753, App	c 794	32.8	3.8	1000	8	US-11-266-748A-471506	Sequence 471506,
c 722	33	3.8	14147	6	US-10-517-441-539	Sequence 539, App	c 795	32.8	3.8	1000	8	US-11-266-748A-472221	Sequence 472221,
c 723	33	3.8	261789	8	US-11-260-842-1	Sequence 1, Appl	c 796	32.8	3.8	1000	8	US-11-266-748A-473022	Sequence 473022,
c 724	32.8	3.8	417	8	US-11-266-748A-293050	Sequence 293050, A	c 797	32.8	3.8	1000	8	US-11-266-748A-473022	Sequence 473022,
c 725	32.8	3.8	417	8	US-11-266-748A-344519	Sequence 344519, A	c 798	32.8	3.8	1000	8	US-11-266-748A-474710	Sequence 474710,
c 726	32.8	3.8	459	8	US-11-266-748A-7608	Sequence 7608, Ap	c 799	32.8	3.8	1000	8	US-11-266-748A-475103	Sequence 475103,
c 727	32.8	3.8	459	8	US-11-266-748A-81577	Sequence 81577, A	c 800	32.8	3.8	1000	8	US-11-266-748A-475806	Sequence 475806,
c 728	32.8	3.8	459	8	US-11-266-748A-111081	Sequence 111081, A	c 801	32.8	3.8	1118	7	US-11-218-305-12485	Sequence 12485, A
c 729	32.8	3.8	459	8	US-11-266-748A-134388	Sequence 134388, A	c 802	32.8	3.8	1163	8	US-11-105-233-108	Sequence 108, App
c 730	32.8	3.8	459	8	US-11-266-748A-177744	Sequence 177744, A	c 803	32.8	3.8	1175	8	US-11-266-748A-27680	Sequence 27680, A
c 731	32.8	3.8	459	8	US-11-266-748A-251094	Sequence 251094, A	c 804	32.8	3.8	1306	8	US-11-216-545-2259	Sequence 2259, Ap
c 732	32.8	3.8	459	8	US-11-266-748A-311611	Sequence 311611, A	c 805	32.8	3.8	1425	8	US-11-266-748A-58244	Sequence 58244, A
c 733	32.8	3.8	459	8	US-11-266-748A-358300	Sequence 358300, A	c 806	32.8	3.8	1448	8	US-11-266-748A-27177	Sequence 27177, A
c 734	32.8	3.8	459	8	US-11-266-748A-41679	Sequence 41679, A	c 807	32.8	3.8	1607	7	US-11-218-305-22253	Sequence 22253, A
c 735	32.8	3.8	459	8	US-11-266-748A-400949	Sequence 400949, A	c 808	32.8	3.8	1658	8	US-11-216-545-3140	Sequence 3140, Ap
c 736	32.8	3.8	532	8	US-11-266-748A-471995	Sequence 471995, A	c 809	32.8	3.8	1741	8	US-11-266-748A-26965	Sequence 26965, A
c 737	32.8	3.8	580	8	US-11-266-748A-53319	Sequence 53319, A	c 810	32.8	3.8	1886	6	US-10-449-902-548	Sequence 548, App
c 738	32.8	3.8	581	8	US-11-266-748A-371855	Sequence 371855, A	c 811	32.8	3.8	1914	7	US-11-366-001-34	Sequence 34, Appl
c 739	32.8	3.8	581	8	US-11-266-748A-455234	Sequence 455234, A	c 812	32.8	3.8	1946	7	US-11-218-305-2525	Sequence 2525, Ap
c 740	32.8	3.8	678	8	US-11-266-748A-209877	Sequence 209877, A	c 813	32.8	3.8	1952	7	US-11-218-305-18680	Sequence 18680, A
c 741	32.8	3.8	678	8	US-11-266-748A-234234	Sequence 234234, A	c 814	32.8	3.8	1990	8	US-11-266-446-76	Sequence 76, Appl
c 742	32.8	3.8	702	8	US-11-266-748A-209926	Sequence 209926, A	c 815	32.8	3.8	2057	8	US-11-266-748A-28575	Sequence 28575, A
c 743	32.8	3.8	721	8	US-11-266-748A-42254	Sequence 42254, A	c 816	32.8	3.8	2105	8	US-11-216-545-6720	Sequence 6720, Ap
c 744	32.8	3.8	764	8	US-11-216-545-4622	Sequence 4622, Ap	c 817	32.8	3.8	2307	8	US-11-216-545-1611	Sequence 1611, Ap
c 745	32.8	3.8	788	7	US-11-056-355B-60582	Sequence 60582, A	c 818	32.8	3.8	2442	6	US-10-953-349-35802	Sequence 35802, A
c 746	32.8	3.8	807	7	US-11-218-305-21335	Sequence 21335, A	c 819	32.8	3.8	2426	7	US-11-218-305-18102	Sequence 18102, A
c 747	32.8	3.8	883	6	US-10-953-349-15521	Sequence 15521, A	c 820	32.8	3.8	2530	8	US-11-145-307A-70	Sequence 70, Appl
c 748	32.8	3.8	931	8	US-11-266-748A-25720	Sequence 25720, A	c 821	32.8	3.8	2530	8	US-11-266-748A-56717	Sequence 56717, A
c 749	32.8	3.8	944	8	US-11-216-545-7493	Sequence 7493, Ap	c 822	32.8	3.8	2530	8	US-11-266-748A-24373	Sequence 24373, A
c 750	32.8	3.8	976	8	US-11-266-748A-81578	Sequence 81578, A	c 823	32.8	3.8	2745	7	US-11-218-305-18483	Sequence 18483, A
c 751	32.8	3.8	976	8	US-11-266-748A-111082	Sequence 111082, A	c 824	32.8	3.8	2848	6	US-10-449-902-16718	Sequence 16718, A
c 752	32.8	3.8	976	8	US-11-266-748A-134389	Sequence 134389, A	c 825	32.8	3.8	3158	6	US-10-504-973-76	Sequence 76, Appl
c 753	32.8	3.8	1000	8	US-11-266-748A-116497	Sequence 116497, A	c 826	32.8	3.8	3183	8	US-11-266-748A-27495	Sequence 27495, A
c 754	32.8	3.8	1000	8	US-11-266-748A-117511	Sequence 117511, A	c 827	32.8	3.8	3183	8	US-11-266-748A-57723	Sequence 57723, A
c 755	32.8	3.8	1000	8	US-11-266-748A-117741	Sequence 117741, A	c 828	32.8	3.8	3189	8	US-11-266-748A-25316	Sequence 25316, A
c 756	32.8	3.8	1000	8	US-11-266-748A-118553	Sequence 118553, A	c 829	32.8	3.8	3189	8	US-10-449-902-17285	Sequence 17285, A
c 757	32.8	3.8	1000	8	US-11-266-748A-158661	Sequence 158661, A	c 830	32.8	3.8	3606	8	US-11-266-748A-26097	Sequence 26097, A
c 758	32.8	3.8	1000	8	US-11-266-748A-159675	Sequence 159675, A	c 831	32.8	3.8	3666	7	US-11-218-305-18860	Sequence 18860, A

832	32.8	3.8	3741	8	US-11-266-748A-31177	Sequence 31177, A	C 905	32.6	3.7	1000	8	US-11-266-748A-469819	Sequence 469819, A
833	32.8	3.8	3998	8	US-11-266-748A-24597	Sequence 24597, A	C 906	32.6	3.7	1000	8	US-11-266-748A-470713	Sequence 470713, A
834	32.8	3.8	4039	6	US-10-449-902-25532	Sequence 25532, A	C 907	32.6	3.7	1000	8	US-11-266-748A-471567	Sequence 471567, A
835	32.8	3.8	4086	8	US-11-201-554-1801	Sequence 1801, Ap	C 908	32.6	3.7	1000	8	US-11-266-748A-471981	Sequence 471981, A
836	32.8	3.8	4538	8	US-11-266-748A-30642	Sequence 30642, A	C 909	32.6	3.7	1000	8	US-11-266-748A-472868	Sequence 472868, A
837	32.8	3.8	5976	6	US-10-517-441-280	Sequence 280, App	C 910	32.6	3.7	1000	8	US-11-266-748A-473266	Sequence 473266, A
838	32.8	3.8	11021	6	US-10-517-441-450	Sequence 450, App	C 911	32.6	3.7	1000	8	US-11-266-748A-474525	Sequence 474525, A
839	32.8	3.8	11021	6	US-10-517-441-724	Sequence 724, App	C 912	32.6	3.7	1000	8	US-11-266-748A-475047	Sequence 475047, A
840	32.8	3.8	81463	6	US-10-540-898-659	Sequence 659, App	C 913	32.6	3.7	1000	8	US-11-266-748A-475679	Sequence 475679, A
841	32.8	3.8	81463	6	US-10-539-228-773	Sequence 773, App	C 914	32.6	3.7	1000	8	US-11-266-748A-475969	Sequence 475969, A
842	32.8	3.8	152331	8	US-11-175-714-86	Sequence 86, Appl	C 915	32.6	3.7	1000	8	US-11-266-748A-477571	Sequence 477571, A
843	32.8	3.8	197526	6	US-10-539-228-498	Sequence 187, App	C 916	32.6	3.7	1035	8	US-11-216-545-1996	Sequence 1996, Ap
844	32.8	3.8	586	8	US-11-145-307A-187	Sequence 187, App	C 917	32.6	3.7	1041	7	US-11-218-305-16933	Sequence 16933, A
845	32.6	3.7	658	8	US-11-266-748A-52927	Sequence 52927, A	C 918	32.6	3.7	1045	7	US-11-218-305-16933	Sequence 20430, A
846	32.6	3.7	755	8	US-11-266-748A-41499	Sequence 41499, A	C 919	32.6	3.7	1072	8	US-11-216-545-4808	Sequence 4808, Ap
847	32.6	3.7	762	6	US-10-953-349-30826	Sequence 30826, A	C 920	32.6	3.7	1154	8	US-11-266-748A-26212	Sequence 26212, A
848	32.6	3.7	844	8	US-11-216-545-1182	Sequence 1182, Ap	C 921	32.6	3.7	1196	7	US-11-218-305-18365	Sequence 18365, A
849	32.6	3.7	919	6	US-10-374-780A-1356	Sequence 1356, Ap	C 922	32.6	3.7	1214	8	US-11-216-545-1387	Sequence 1287, Ap
850	32.6	3.7	922	8	US-11-216-545-3692	Sequence 3692, Ap	C 923	32.6	3.7	1225	8	US-11-216-545-3858	Sequence 3858, Ap
851	32.6	3.7	960	8	US-11-266-748A-57978	Sequence 57978, A	C 924	32.6	3.7	1225	8	US-11-216-545-4292	Sequence 4292, Ap
852	32.6	3.7	1000	8	US-11-266-748A-116866	Sequence 116866, A	C 925	32.6	3.7	1270	7	US-11-174-307B-2729	Sequence 2729, Ap
853	32.6	3.7	1000	8	US-11-266-748A-116892	Sequence 116892, A	C 926	32.6	3.7	1309	7	US-11-184-982-29	Sequence 29, Appl
854	32.6	3.7	1000	8	US-11-266-748A-117261	Sequence 117261, A	C 927	32.6	3.7	1309	8	US-11-134-445-29	Sequence 29, Appl
855	32.6	3.7	1000	8	US-11-266-748A-117921	Sequence 117921, A	C 928	32.6	3.7	1309	8	US-11-216-545-3759	Sequence 3759, Ap
856	32.6	3.7	1000	8	US-11-266-748A-118579	Sequence 118579, A	C 929	32.6	3.7	1326	8	US-11-216-545-3452	Sequence 3452, Ap
857	32.6	3.7	1000	8	US-11-266-748A-118579	Sequence 159030, A	C 930	32.6	3.7	1327	8	US-11-216-545-3518	Sequence 3518, Ap
858	32.6	3.7	1000	8	US-11-266-748A-159056	Sequence 159056, A	C 931	32.6	3.7	1361	8	US-11-216-545-6682	Sequence 6682, Ap
859	32.6	3.7	1000	8	US-11-266-748A-159425	Sequence 159425, A	C 932	32.6	3.7	1416	7	US-11-218-305-17282	Sequence 17282, A
860	32.6	3.7	1000	8	US-11-266-748A-160085	Sequence 160085, A	C 933	32.6	3.7	1429	8	US-11-216-545-3534	Sequence 3534, Ap
861	32.6	3.7	1000	8	US-11-266-748A-160743	Sequence 160743, A	C 934	32.6	3.7	1433	8	US-11-266-748A-24728	Sequence 24728, A
862	32.6	3.7	1000	8	US-11-266-748A-222123	Sequence 222123, A	C 935	32.6	3.7	1783	8	US-11-266-748A-27762	Sequence 27762, A
863	32.6	3.7	1000	8	US-11-266-748A-222476	Sequence 222476, A	C 936	32.6	3.7	1802	7	US-11-056-358B-106553	Sequence 106553, A
864	32.6	3.7	1000	8	US-11-266-748A-222520	Sequence 222520, A	C 937	32.6	3.7	1802	7	US-11-056-358B-117792	Sequence 117792, A
865	32.6	3.7	1000	8	US-11-266-748A-222796	Sequence 222796, A	C 938	32.6	3.7	1859	8	US-11-266-748A-27709	Sequence 27709, A
866	32.6	3.7	1000	8	US-11-266-748A-223380	Sequence 223380, A	C 939	32.6	3.7	1878	8	US-11-266-748A-5428	Sequence 5428, Ap
867	32.6	3.7	1000	8	US-11-266-748A-223976	Sequence 223976, A	C 940	32.6	3.7	1914	8	US-11-218-305-14872	Sequence 14872, A
868	32.6	3.7	1000	8	US-11-266-748A-224299	Sequence 224299, A	C 941	32.6	3.7	1937	7	US-11-218-305-14872	Sequence 30, Appl
869	32.6	3.7	1000	8	US-11-266-748A-224736	Sequence 224736, A	C 942	32.6	3.7	2026	7	US-11-366-001-30	Sequence 27048, A
870	32.6	3.7	1000	8	US-11-266-748A-287053	Sequence 287053, A	C 943	32.6	3.7	2026	8	US-11-266-748A-27048	Sequence 5037, Ap
871	32.6	3.7	1000	8	US-11-266-748A-289831	Sequence 289831, A	C 944	32.6	3.7	2080	8	US-11-216-545-5037	Sequence 25894, A
872	32.6	3.7	1000	8	US-11-266-748A-291204	Sequence 291204, A	C 945	32.6	3.7	2166	8	US-11-266-748A-25894	Sequence 724, App
873	32.6	3.7	1000	8	US-11-266-748A-291919	Sequence 291919, A	C 946	32.6	3.7	2204	6	US-10-540-898-724	Sequence 14584, A
874	32.6	3.7	1000	8	US-11-266-748A-292335	Sequence 292335, A	C 947	32.6	3.7	2245	8	US-11-218-305-14584	Sequence 59040, A
875	32.6	3.7	1000	8	US-11-266-748A-292457	Sequence 292457, A	C 948	32.6	3.7	2258	8	US-11-266-748A-59040	Sequence 99, Appl
876	32.6	3.7	1000	8	US-11-266-748A-292457	Sequence 292457, A	C 949	32.6	3.7	2327	8	US-11-216-545-99	Sequence 57404, A
877	32.6	3.7	1000	8	US-11-266-748A-293089	Sequence 293089, A	C 950	32.6	3.7	2327	8	US-11-266-748A-57404	Sequence 25961, A
878	32.6	3.7	1000	8	US-11-266-748A-293648	Sequence 293648, A	C 951	32.6	3.7	2618	8	US-11-266-748A-25961	Sequence 29880, A
879	32.6	3.7	1000	8	US-11-266-748A-294287	Sequence 294287, A	C 952	32.6	3.7	2747	8	US-11-266-748A-29880	Sequence 23618, A
880	32.6	3.7	1000	8	US-11-266-748A-338482	Sequence 338482, A	C 953	32.6	3.7	2784	8	US-11-266-748A-23618	Sequence 1, Appl
881	32.6	3.7	1000	8	US-11-266-748A-341260	Sequence 341260, A	C 954	32.6	3.7	3053	8	US-11-247-437-1	Sequence 30143, A
882	32.6	3.7	1000	8	US-11-266-748A-342633	Sequence 342633, A	C 955	32.6	3.7	3240	8	US-11-266-748A-30143	Sequence 9070, Ap
883	32.6	3.7	1000	8	US-11-266-748A-343348	Sequence 343348, A	C 956	32.6	3.7	3561	7	US-11-218-305-9070	Sequence 2121, Ap
884	32.6	3.7	1000	8	US-11-266-748A-343764	Sequence 343764, A	C 957	32.6	3.7	3740	8	US-11-216-545-2121	Sequence 57391, A
885	32.6	3.7	1000	8	US-11-266-748A-343886	Sequence 343886, A	C 958	32.6	3.7	3861	8	US-11-266-748A-57391	Sequence 28365, A
886	32.6	3.7	1000	8	US-11-266-748A-344518	Sequence 344518, A	C 959	32.6	3.7	4133	8	US-11-266-748A-28365	Sequence 21828, A
887	32.6	3.7	1000	8	US-11-266-748A-345077	Sequence 345077, A	C 960	32.6	3.7	4241	7	US-11-218-305-21828	Sequence 24733, A
888	32.6	3.7	1000	8	US-11-266-748A-345078	Sequence 345078, A	C 961	32.6	3.7	4860	6	US-11-266-748A-24733	Sequence 318, App
889	32.6	3.7	1000	8	US-11-266-748A-345716	Sequence 345716, A	C 962	32.6	3.7	5203	6	US-10-517-441-318	Sequence 532, App
890	32.6	3.7	1000	8	US-11-266-748A-397646	Sequence 397646, A	C 963	32.6	3.7	5203	6	US-10-517-441-592	Sequence 57364, A
891	32.6	3.7	1000	8	US-11-266-748A-398693	Sequence 398693, A	C 964	32.6	3.7	5288	8	US-11-266-748A-57364	Sequence 32592, A
892	32.6	3.7	1000	8	US-11-266-748A-398773	Sequence 398773, A	C 965	32.6	3.7	6035	8	US-11-266-748A-32592	Sequence 416, App
893	32.6	3.7	1000	8	US-11-266-748A-399667	Sequence 399667, A	C 966	32.6	3.7	15355	6	US-10-517-441-416	Sequence 416, App
894	32.6	3.7	1000	8	US-11-266-748A-400521	Sequence 400521, A	C 967	32.6	3.7	15355	6	US-10-517-441-690	Sequence 650, App
895	32.6	3.7	1000	8	US-11-266-748A-400935	Sequence 400935, A	C 968	32.6	3.7	168732	6	US-10-539-228-560	Sequence 560, App
896	32.6	3.7	1000	8	US-11-266-748A-401822	Sequence 401822, A	C 969	32.6	3.7	313287	6	US-10-539-228-48	Sequence 48, Appl
897	32.6	3.7	1000	8	US-11-266-748A-402220	Sequence 402220, A	C 970	32.6	3.7	634	8	US-11-197-712-231	Sequence 231, App
898	32.6	3.7	1000	8	US-11-266-748A-403479	Sequence 403479, A	C 971	32.4	3.7	635	8	US-11-197-712-230	Sequence 230, App
899	32.6	3.7	1000	8	US-11-266-748A-404001	Sequence 404001, A	C 972	32.4	3.7	651	8	US-11-266-748A-212486	Sequence 212486, A
900	32.6	3.7	1000	8	US-11-266-748A-404633	Sequence 404633, A	C 973	32.4	3.7	651	8	US-11-266-748A-235908	Sequence 235908, A
901	32.6	3.7	1000	8	US-11-266-748A-404923	Sequence 404923, A	C 974	32.4	3.7	680	8	US-11-266-748A-211895	Sequence 211895, A
902	32.6	3.7	1000	8	US-11-266-748A-406525	Sequence 406525, A	C 975	32.4	3.7	680	8	US-11-266-748A-235440	Sequence 235440, A
903	32.6	3.7	1000	8	US-11-266-748A-468692	Sequence 468692, A	C 976	32.4	3.7	798	7	US-11-218-305-14209	Sequence 14209, A
904	32.6	3.7	1000	8	US-11-266-748A-469739	Sequence 469739, A	C 977	32.4	3.7	827	8	US-11-266-748A-83798	Sequence 83798, A

c 978	32.4	3.7	827	8	US-11-266-748A-111685	Sequence 111685,	1051	32.4	3.7	6707	8	US-11-266-748A-24508	Sequence 24508, A
c 979	32.4	3.7	827	8	US-11-266-748A-136609	Sequence 136609,	c1052	32.4	3.7	7833	6	US-10-517-441-349	Sequence 349, App
c 980	32.4	3.7	886	8	US-11-266-748A-186709	Sequence 186709,	c1053	32.4	3.7	8900	6	US-10-517-441-701	Sequence 701, App
c 981	32.4	3.7	985	8	US-11-266-748A-356904	Sequence 356904,	c1054	32.4	3.7	146733	6	US-10-540-898-387	Sequence 387, App
c 982	32.4	3.7	985	8	US-11-266-748A-386138	Sequence 386138,	c1055	32.4	3.7	390183	6	US-10-540-898-937	Sequence 937, App
c 983	32.4	3.7	985	8	US-11-266-748A-440283	Sequence 440283,	c1056	32.4	3.7	1421559	8	US-11-266-748A-28208	Sequence 28208, A
c 984	32.4	3.7	1000	8	US-11-266-748A-206699	Sequence 206699,	1057	32.2	3.7	263	8	US-11-266-748A-273348	Sequence 273348,
c 985	32.4	3.7	1000	8	US-11-266-748A-207140	Sequence 207140,	c1058	32.2	3.7	263	8	US-11-266-748A-273348	Sequence 273348,
c 986	32.4	3.7	1000	8	US-11-266-748A-209380	Sequence 209380,	c1059	32.2	3.7	425	6	US-10-953-349-14130	Sequence 14130, A
c 987	32.4	3.7	1000	8	US-11-266-748A-224360	Sequence 224360,	1060	32.2	3.7	461	8	US-11-266-748A-55654	Sequence 55654, A
c 988	32.4	3.7	1000	8	US-11-266-748A-281705	Sequence 281705,	1061	32.2	3.7	515	8	US-11-266-748A-40037	Sequence 40037, A
c 989	32.4	3.7	1000	8	US-11-266-748A-286326	Sequence 286326,	1062	32.2	3.7	687	8	US-11-242-317-38	Sequence 38, App1
c 990	32.4	3.7	1000	8	US-11-266-748A-289245	Sequence 289245,	1063	32.2	3.7	715	8	US-11-266-748A-76767	Sequence 76767, A
c 991	32.4	3.7	1000	8	US-11-266-748A-291280	Sequence 291280,	1064	32.2	3.7	715	8	US-11-266-748A-109550	Sequence 109550,
c 992	32.4	3.7	1000	8	US-11-266-748A-293235	Sequence 293235,	c1065	32.2	3.7	715	8	US-11-266-748A-129578	Sequence 129578,
c 993	32.4	3.7	1000	8	US-11-266-748A-294340	Sequence 294340,	c1066	32.2	3.7	727	8	US-11-266-748A-211264	Sequence 211264,
c 994	32.4	3.7	1000	8	US-11-266-748A-308345	Sequence 308345,	1067	32.2	3.7	727	8	US-11-266-748A-234974	Sequence 234974,
c 995	32.4	3.7	1000	8	US-11-266-748A-337755	Sequence 337755,	1068	32.2	3.7	743	7	US-11-218-305-21197	Sequence 21197, A
c 996	32.4	3.7	1000	8	US-11-266-748A-340674	Sequence 340674,	1069	32.2	3.7	790	8	US-11-266-748A-54836	Sequence 54836, A
c 997	32.4	3.7	1000	8	US-11-266-748A-342709	Sequence 342709,	1070	32.2	3.7	880	8	US-11-216-545-5474	Sequence 5474, Ap
c 998	32.4	3.7	1000	8	US-11-266-748A-344664	Sequence 344664,	1071	32.2	3.7	880	8	US-11-216-545-5492	Sequence 5492, Ap
c 999	32.4	3.7	1000	8	US-11-266-748A-345769	Sequence 345769,	1072	32.2	3.7	921	8	US-11-266-748A-43946	Sequence 43946, A
c1000	32.4	3.7	1000	8	US-11-266-748A-350767	Sequence 350767,	1073	32.2	3.7	1000	8	US-11-266-748A-117348	Sequence 117348
c1001	32.4	3.7	1000	8	US-11-266-748A-395550	Sequence 395550,	1074	32.2	3.7	1000	8	US-11-266-748A-117619	Sequence 117619,
c1002	32.4	3.7	1000	8	US-11-266-748A-396751	Sequence 396751,	1075	32.2	3.7	1000	8	US-11-266-748A-117648	Sequence 117648,
c1003	32.4	3.7	1000	8	US-11-266-748A-401198	Sequence 401198,	1076	32.2	3.7	1000	8	US-11-266-748A-117715	Sequence 117715,
c1004	32.4	3.7	1000	8	US-11-266-748A-402705	Sequence 402705,	1077	32.2	3.7	1000	8	US-11-266-748A-118133	Sequence 118133,
c1005	32.4	3.7	1000	8	US-11-266-748A-405176	Sequence 405176,	1078	32.2	3.7	1000	8	US-11-266-748A-118312	Sequence 118312,
c1006	32.4	3.7	1000	8	US-11-266-748A-406596	Sequence 406596,	1079	32.2	3.7	1000	8	US-11-266-748A-118652	Sequence 118652,
c1007	32.4	3.7	1000	8	US-11-266-748A-466596	Sequence 466596,	1080	32.2	3.7	1000	8	US-11-266-748A-118824	Sequence 118824,
c1008	32.4	3.7	1000	8	US-11-266-748A-467797	Sequence 467797,	1081	32.2	3.7	1000	8	US-11-266-748A-119105	Sequence 119105,
c1009	32.4	3.7	1000	8	US-11-266-748A-472244	Sequence 472244,	c1082	32.2	3.7	1000	8	US-11-266-748A-159512	Sequence 159512,
c1010	32.4	3.7	1000	8	US-11-266-748A-473751	Sequence 473751,	c1083	32.2	3.7	1000	8	US-11-266-748A-159783	Sequence 159783,
c1011	32.4	3.7	1000	8	US-11-266-748A-476222	Sequence 476222,	c1084	32.2	3.7	1000	8	US-11-266-748A-159812	Sequence 159812,
c1012	32.4	3.7	1000	8	US-11-266-748A-477642	Sequence 477642,	c1085	32.2	3.7	1000	8	US-11-266-748A-159879	Sequence 159879,
c1013	32.4	3.7	1000	8	US-11-266-748A-477642	Sequence 477642,	c1086	32.2	3.7	1000	8	US-11-266-748A-160297	Sequence 160297,
c1014	32.4	3.7	1123	8	US-11-216-545-2723	Sequence 481485,	c1087	32.2	3.7	1000	8	US-11-266-748A-160476	Sequence 160476,
c1015	32.4	3.7	1181	8	US-11-266-748A-27693	Sequence 2723, Ap	c1088	32.2	3.7	1000	8	US-11-266-748A-160816	Sequence 160816,
c1016	32.4	3.7	1238	7	US-11-218-305-11544	Sequence 27693, A	c1089	32.2	3.7	1000	8	US-11-266-748A-160988	Sequence 160988,
c1017	32.4	3.7	1245	3	US-11-216-545-953	Sequence 11544, A	c1090	32.2	3.7	1000	8	US-11-266-748A-161269	Sequence 161269,
c1018	32.4	3.7	1488	7	US-11-056-355B-7215	Sequence 953, App	c1091	32.2	3.7	1000	8	US-11-266-748A-209775	Sequence 209775,
c1019	32.4	3.7	1558	8	US-11-266-748A-28194	Sequence 28194, A	c1092	32.2	3.7	1000	8	US-11-266-748A-221109	Sequence 221109,
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c1021	32.4	3.7	2078	8	US-11-266-748A-27633	Sequence 27633, A	c1094	32.2	3.7	1000	8	US-11-266-748A-223013	Sequence 223013,
c1022	32.4	3.7	2158	8	US-11-266-748A-31443	Sequence 31443, A	c1095	32.2	3.7	1000	8	US-11-266-748A-223791	Sequence 223791,
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c1024	32.4	3.7	2265	8	US-11-266-748A-26265	Sequence 26265, A	c1097	32.2	3.7	1000	8	US-11-266-748A-285381	Sequence 285381,
c1025	32.4	3.7	2275	8	US-11-266-748A-27117	Sequence 27117, A	c1098	32.2	3.7	1000	8	US-11-266-748A-289027	Sequence 289027,
c1026	32.4	3.7	2314	7	US-11-218-305-13396	Sequence 13396, A	c1099	32.2	3.7	1000	8	US-11-266-748A-289760	Sequence 289760,
c1027	32.4	3.7	2445	8	US-11-266-748A-23326	Sequence 23326, A	c1100	32.2	3.7	1000	8	US-11-266-748A-289813	Sequence 289813,
c1028	32.4	3.7	2494	8	US-11-266-748A-27412	Sequence 27412, A	c1101	32.2	3.7	1000	8	US-11-266-748A-289950	Sequence 289950,
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c1042	32.4	3.7	3930	8	US-11-266-748A-56192	Sequence 56192, A	c1115	32.2	3.7	1000	8	US-11-266-748A-342568	Sequence 342568,
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c1048	32.4	3.7	5377	8	US-11-266-748A-28394	Sequence 28394, A	c1121	32.2	3.7	1000	8	US-11-266-748A-394480	Sequence 394480,
c1049	32.4	3.7	6001	6	US-10-517-441-512	Sequence 512, App	c1122	32.2	3.7	1000	8	US-11-266-748A-396895	Sequence 396895,
c1050	32.4	3.7	6299	7	US-11-218-305-12285	Sequence 12285, A	c1123	32.2	3.7	1000	8	US-11-266-748A-397609	Sequence 397609,



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1172	32.2	3.7	1698	7	US-11-056-355B-73744	Sequence 73744, A	1245	32	3.7	1000	8	US-11-266-748A-220955	Sequence 220955,
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1183	32.2	3.7	1993	8	US-11-266-748A-57024	Sequence 57024, A	1256	32	3.7	1000	8	US-11-266-748A-290170	Sequence 290170,
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1196	32.2	3.7	3720	8	US-11-266-748A-26582	Sequence 26582, A	1269	32	3.7	1000	8	US-11-266-748A-340929	Sequence 340929,

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